Regulation of respiratory pathways for the energy generation in *D. shibae* under nitrate respiratory conditions

Von der Fakultät für Lebenswissenschaften
der Technischen Universität Carolo-Wilhelmina
zu Braunschweig
zur Erlangung des Grades eines
Doktors der Naturwissenschaften
(Dr. rer. nat.)
genehmigte
D i s s e r t a t i o n

von Sebastian Walter Friedrich Laaß

aus Salzgitter

1. Referent: Prof. Dr. Dieter Jahn

2. Referent: Prof. Dr. Dietmar Schomburg

eingereicht am: 02.11.2015

mündliche Prüfung (Disputation) am: 29.02.2016

Druckjahr 2016

Vorveröffentlichungen der Dissertation

Teilergebnisse aus dieser Arbeit wurden mit Genehmigung der Fakultät für Lebenswissenschaften, vertreten durch den Mentor der Arbeit, in folgenden Beiträgen vorab veröffentlicht:

Publikationen

Ebert, M., Laaß, S., Burghartz, M., Petersen, J., Koßmehl, S., Wöhlbrand, L,. Rabus, R., Wittmann, C., Tielen, P., Jahn, D.: Transposon Mutagenesis Identified Chromosomal and Plasmid Genes Essential for Adaptation of the Marine Bacterium *Dinoroseobacter shibae* to Anaerobic Conditions. J. Bacteriol. 195 4769-4777 (2013)

Laass, S., Kleist, S., Bill, N., Drüppel, K., Kossmehl, S., Wöhlbrand, L., Rabus, R., Klein, J., Rohde, M., Bartsch, A., Wittmann, C., Schmidt-Hohagen, K., Tielen, P., Jahn, D., Schomburg, D.: Gene Regulatory and Metabolic Adaptation Processes of *Dinoroseobacter shibae* DFL12T during Oxygen Depletion. J. Biol. Chem., 289, 13219-13231 (2014)

Vorträge

Laass, S., Piekarski, T., Tielen, P., Jahn, D.: Regulatory networks of the *Dinoroseobacter shibae* energy metabolism. 2nd Status Seminar Status Seminar of the Transregio 51, Oldenburg (2011)

Laass, S., Klein, J., Jahn, D., Tielen, P.: Regulation of anaerobic respiratory pathways in *Dinoroseobacter shibae*. VAAM Jahrestagung 2012 in Tübingen (2012)

Laass, S., Klein, J., Jahn, D., Tielen, P.: Regulation of anaerobic respiratory pathways in *Dinoroseobacter shibae*. Mibi Retreat des Instituts für Mikrobiologie, Helmstedt (2012)

Laaß, S., Jacobs, J., Ebert, M., Heisig, M., Rhode, M., Tielen, P., Jahn, D.: Regulation of anaerobic respiratory pathways in *Dinoroseobacter shibae*. 6th Status Seminar of the Transregio 51, Braunschweig (2012)

Laass, S., Klein, J., Heisig, M., Rhode, M., Tielen, P., Jahn, D.: Regulation of anaerobic respiratory pathways in *Dinoroseobacter shibae*. VAAM Jahrestagung 2013 zusammen mit der KNVM in Bremen (2013)

Poster

Laass, S., Klein, J., Heisig, M., Rhode, M., Tielen, P., Jahn, D.: Regulation of anaerobic respiratory pathways in *Dinoroseobacter shibae*. Gordan Research Conference Marine Microbes Lucca (2012)

Jacobs, J., Laass, S., Heyber S., Engelmann S., Härtig E., Jahn D.: Iron regulation in the marine microorganism *Dinoroseobacter shibae*. VAAM Jahrestagung 2015 in Marburg (2015)

„Siehst du den Horizont? Direkt überm Boden fängt der Himmel an und wär ich dort, dann würd ich wetten, dass ich ihn erreichen kann. Doch hier hat es den Anschein bin ich dafür zu klein“

Thomas D (1997)

Table of Contents

Abbreviations

°C	Degree Celsius
µ	Micro
AAP	Aerobic anoxygenic photosynthesis
AHL	Acyl homoserine lactone
ALA	Aminolevulinic acid
Anr	Anaerobic regulation of arginine deiminase and nitrate reduction
ATP	Adenosine triphosphate
B_1	Thiamine
B_{12}	Cobalamin
bp	Base pair
CARD-FISH	Catalyzed reporter deposition fluorescent *in situ* hybridization
Crp	cAMP receptor protein
Cy3	Carbocyanine 3 (fluorescent dye)
Cy5	Carbocyanine 5 (fluorescent dye)
DMS	Dimethyl sulfide
DMSP	Dimetyhlsulfoniopropionate
DOM	Disolved organic matter
DNA	Deoxyribonucleic acid
DSM	Dissolved organic matter
Dnr	Dissimilatory nitrate respiration regulator
e.g.	exempli gratia (lat.)
Fig	Figure
Fnr	Fumarate and nitrate reductase regulator
g	acceleration of gravity
g	Gram
h	Hour
hMB	Half concentated Marine Bouillon
HTH	Helix-Turn-Helix
IPTG	Isopropyl-β-D-1-thiogalactopyranoside
JGI	Joint Genome Institut
kDa	KiloDalton
l	liter

m	Meter/Milli
M	Molar concentration/molarity
MB	Marine Bouillon
Mbp	Mega base pairs
min	Minute
mg	Milligram
ml	Milliliter
mol	Mole (amount of substance)
n	Nano
N_2	Nitrogen
NH_3	Ammonia
NO_3^-	Nitrate
NO_2^-	Nitrite
NO	Nitric oxide
N_2O	Nitrous oxide
OD_x	Optical density at x nanometer
OMZ	Oxygen minimal zone
PAGE	Polyacrylamide gel electrophoresis
PCR	Polymerase chain reaction
PHB	Polyhydroxybutanoate
PMF	Proton motive force
ppb	Parts per Billion
RNA	Ribonucleic acid
rpm	Rounds per minute
rRNA	Ribosomal ribonucleic acid
s	Second
SDS	Sodium dodecyl sulfate
SWM	Saltwater medium
TDA	Tropodithietic acid
TMAO	Triethylamin-N-oxid
U	Unit

1 Introduction

1.1 Roseobacter clade

In the world`s oceans microbes play an essential role. Phytoplankton is referred to be responsible for one half of the global primary production. Half of this productivity results in dissolved organic matter (DOM), which is assimilated by heterotrophic bacteria and archaea (Geng & Belas, 2010). Beside this contribution to the carbon cycle, marine bacteria also play an important role in the sulfur cycle by converting dimethylsulfoniopropionate (DMSP) into dimethyl sulfide (DMS), which in turn has an impact on clouding and therefore on the earth`s climate (Malin, 2006). Furthermore, marine microbes are involved in the nitrogen cycle by nitrogen fixation, nitrification and marine nitrogen loss via denitrification (Brinkhoff *et al.*, 2008; Moran *et al.*, 2007; Buchan *et al.*, 2005).

The bacterial community in the world`s oceans can be subdivided into nine major clades. The *Roseobacter* clade is being one of these. This α-3 subclass of the *Proteobacteria* shares > 89 % 16S rRNA identity and represent up to 20 % of the costal and 15 % of mixed-layer ocean bacterioplankton communities. Furthermore, they can be found free-living in the water column, in the sediment, particle associated or also in association with marine eukaryotes (Buchan *et al.*, 2005). In some of these habitats, members of the *Roseobacter* clade are foundas part of microbial biofilms (Bruhn *et al.*, 2007). However, they differ in their physiological and morphological features, which lead to the assumption of a highly efficient adaptation to various marine environments (Buchan *et al.*, 2005; Wagner-Döbler & Biebl, 2006).

Some members have the ability to synthesize bacteriochlorophyll *a* for aerobic anoxygenic photosynthesis (AAP), while others do not. Some members of the *Roseobacter* clade are able to use alternative electron acceptors under microaerobic and/or anaerobic conditions while prevailing in the sediment, in biofilms or in oxygen minimal zones (OMZ) of the oceans. Under anaerobic conditions, *Roseobacter denitrificans* and *Dinoroseobacter shibae* DFL12^T are able to reduce nitrate instead of oxygen for respiration (Biebl *et al.*, 2005; Shiba, 1991). *D. shibae* also possesses genes for pyruvate and arginine fermentation pathways (Wagner-Döbler *et al.*, 2010). Furthermore, some members can use dimethyl sulfoxide (DMSO) or triethylamin-N-oxide (TMAO) as alternative electron acceptors (Arata *et al.*, 1992; González *et al.*,

1999; Ansede *et al.*, 2001). The synthesis of secondary metabolites like the antibiotic tropodithietic acid (TDA) was observed in *Phaeobacter inhibens* DSM 17395 (Brinkhoff *et al.*, 2004). TDA seems to offer the bacterium a significant advantage for colonization of microalga against bacterial competitors and in protection of the host from bacterial pathogens (Brinkhoff *et al.*, 2004; Berger *et al.*, 2011). Furthermore, bacteria of this clade are able to degrade aromatic compounds, synthesize quorum sensing molecules like *N*-acyl homoserine lactones (AHL) and to produce toxins (Buchan *et al.*, 2005; Wagner-Döbler *et al.*, 2005; Moran *et al.*, 2007). Additionally, this group plays an important role on the global carbon and sulfur cycle as some of the members are able to oxidize carbon monoxide as well as organic sulfur compounds such as DMSP (Moran *et al.*, 2004; González *et al.*, 1999).

Interestingly, some of the genes encoding for this metabolic diversity are located on plasmids. For example, genes for siderophore secretion, biofilm formation and the production of the antibiotic TDA are located on extrachromosomal elements in *P. inhibens* DSM 17395 (Petersen *et al.*, 2013). The *puf* genes encoding the enzymes of the light harvesting complex are also plasmid locelized in *Roseobacter litoralis* (Pradella *et al.*, 2004). Localization of these genes on plasmids permits potentially to evolution *via* horizontal gene transfer to other bacteria and therefore contributes their adaptation to new habitats (Brinkhoff *et al.*, 2008).

This versatile metabolic capability allows for a high adaptability to several ecological niches. Surely, it is one of the major reasons for the ecological success for the *Roseobacter* clade in the world oceans.

There are isolates of members of the *Roseobacter* clade, which can be used as model organisms for investigation of the evolutionary, genetic and physiological principles contributing to the ecological success in the oceans. Beside *P. inhibens* DSM17395, *D. shibae* DFL12^T is one of the model organisms which were chosen due to its metabolic capabilities, the ability for growth under defined culture conditions and its accessibility of genetic manipulation.

1.2 Dinoroseobacter shibae DFL12^T

The marine bacterium *D. shibae* is systematically classified as a member of the *Alphaproteobacteria* and of the Rhodobacteraceae family. Biebl classified *Dinoroseobacter* as a new genus within the *Roseobacter* clade and described the type

strain DFL12^T (=DSM 16493^T =NCIMB 14021^T) (Biebl 2005). *D. shibae* DFL12^T was named after Professor Tsuneo Shiba, who discovered the marine aerobic anoxygenic phototrophic bacteria in 1979 (Shiba *et al.*, 1979; Biebl *et al.*, 2005). A characteristic feature of the cocci or ovoid rod forming bacterium is its strong pigmentation (Fig. 1.1).

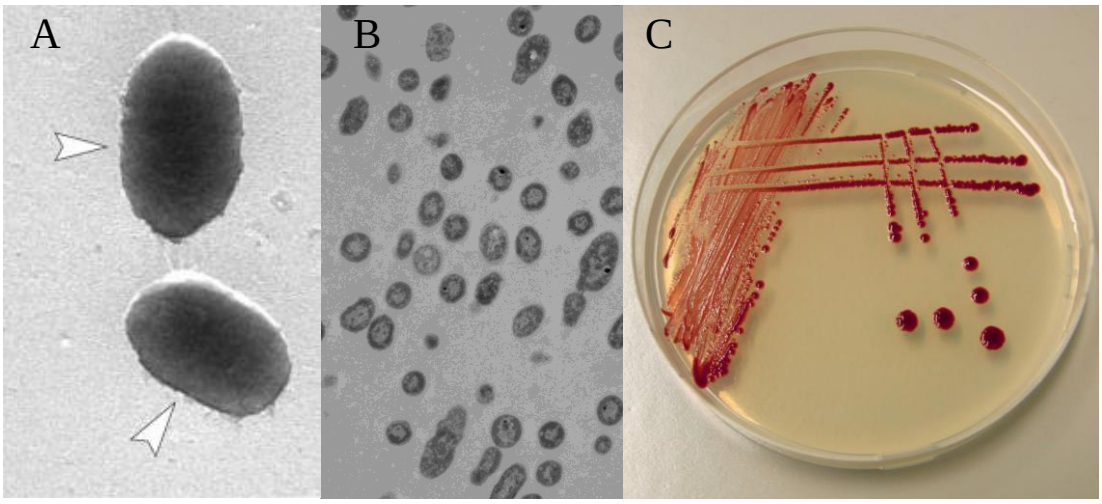


Fig. 1.1: Electron micrograph and pigmentation of *D. shibae* cells. A: Scanning electron microscope picture of short rod-shape cells (white arrows) (Biebl *et al.*, 2005). B: Transmission electron microscope picture of different cell types (Laass *et al.*, 2014). C: Agar plate of aerobically grown *D. shibae* with red pigmentation (Wozniczka DSMZ).

Liquid cultures grown in the dark appear pink or light red, whereas those grown under illumination look weak beige. This redish pigmentation is due to the carotenoid spheroidenone. *D. shibae* is able to grow between 15 and 38 °C. The optimal growth was observed at 33 °C. The pH optimum was found between 6.5 and 8.8. At least 1 % of salinity is necessary for efficient growth. *D. shibae* is still able to grow at a concentration of 7 % salt, twice the salinity of normal sea water (Biebl *et al.*, 2005) (Biebletal.,È. Additionally, three vitamins (biotin, nicotinic acid and 4-aminobenzoic acid) are requiredfor growth, whereas the addition of amino acids is not necessary.

The bacterium is able to utilize a wide spectrum of organic substances as carbon source, such as acetate, succinate, fumarate, lactate, citrate, glutamate, pyruvate, fructose, glycerol. Weak growths was observed with ethanol. The closest phylogenetic neighbors of *D. shibae* are *Jannaschia helgolandis*, *Ruegeria atlantica* and *Rhodobacter veldkampii* with similarities on 16S rRNA level between 94.1, 93.7 to 93.4 %, respectively. Surprisingly, the G+C content of *D. shibae* (64.8 mol %) is clearly different to the values usually reported for the genus *Roseobacter* (56.7 – 59.6 mol %).

Several strains of *D. shibae* were found associated with dinoflagellates. The type strain *D. shibae* DFL12^T was isolated from the surface of the dinoflagellate *Prorocentrum lima*, whereas the strain *D. shibae* DFL27 was found associated with *Alexandrium ostenfeldii* (Allgaier *et al.*, 2003). The successful isolation of *D. shibae* strains from a broad range of dinoflagellates excluded a restriction to a single or small group of marine microalgae. A potential symbiosis of *D. shibae* with the microalgae was deduced from by the fact that the bacterial cells were found attached to *P. lima* in a catalyzed reporter deposition fluorescent *in situ* hybridization (CARD-FISH) assay (Fig. 1.2) (Wagner-Döbler *et al.*, 2010).

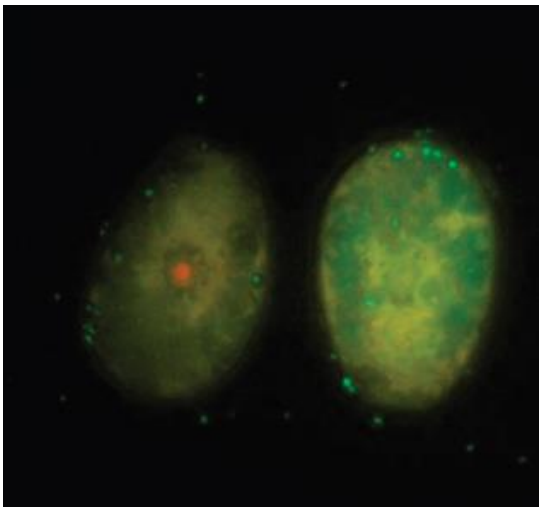


Fig. 1.2: Attachment of *D. shibae* to the dinoflagelate host *P. lima*. Catalyzed reporter deposition fluorescent *in situ* hybridization (CARD-FISH) shows *D. shibae* cells (green dots) attached to the dinoflagela (Wagner-Döbler *et al.*, 2010).

One contribution of *D. shibae* to the symbiosis with the dinoflagellate might be supplementation of the vitamins thiamine (B_1) and cobalamin (B_{12}). It was shown that the growth of the B_1 and B_{12} auxotrophic *Prorocentrum minimum* was stimulated by *D. shibae*. The bacterium itself might benefit by metabolic products discharged by the algae. Furthermore, it is currently discussed whether *D. shibae* profits from the collapse of an algae bloom and of switching to a parasitic mode of life (Wagner-Döbler *et al.*, 2010).

The genome of *D. shibae* DFL12^T was sequenced by the Joint Genome Institute (JGI) and published in 2010 (Wagner-Döbler *et al.*, 2010). The genome size of 4417 kbp is similar to that of other *Roseobacter* genomes like that of *R. denitrificans* (OCH 114), *Silicibacter pomeroyi* (DSS-3) and *J. helgolandis*. It contains 4198 protein-encoding genes. For about 28 % of the annotated gene products no function is currently known.

The DNA sequence indicates a circular conformation of the 3.78 Mbp chromosome and the presence of five circular plasmids pDS191, pDS153, pDS126, pDS82 and pDS76 with a size of 191 kbp, 153 kbp, 126 kbp, 82 kbp and 76 kbp, respectively. Interestingly, 80 % of the pDS126 extrachromosomal element is homologous to the pDS191 sequence (Wagner-Döbler *et al.*, 2010)

D. shibae possesses most of previously described energy metabolic capacities observed for other fully sequenced *Roseobacter* isolates, such as aerobic anoxygenic photosynthesis (*pufLM* genes), carbon monoxide oxidation (*cox* genes), aromatic compound degradation (*pcaGH* and *boxC* genes), sulfur oxidation (*soxB*), denitrification (*nirS, norB, nosZ*), nitrate assimilation (*nasA, nasDE*), phosphonate utilization (*phn*), type IV secretion (*vir* genes) and dimethylsulfoniopropionate (DMSP) degradation (*dmdA*). The potential for DNA mobilization is indicated by 61 transposase, 43 integrase and 11 site-specific recombinase/resolvase genes. Interestingly, some of these genes were found encoded on the plasmids. The *vir* operon, which encodes the type IV secretion system, is located in one copy on pDS191 and an additional copy on pDS126. The 153 kb plasmid harbors genes for the degradation of aromatic compounds. The *cox* operonen coding cytochrome *c* oxidase is found on the 72 kb plasmid (Wagner-Döbler *et al.*, 2010).

1.3 Anaerobic metabolism

The world oceans offer a broad spectrum of ecological niches. Beside oxygen-rich enviroments in surface water and in deep sea, microaerobic to anaerobic conditions are found in mid layer water masses between 200 and 1000 m of the water column, named oxygen minimum zones (OMZs) (Lam *et al.*, 2009), Marine sediments (Glud, 2008) and deeper layers of a surface attached and free floating biofilm constitute additional anaerobic enviroments (Folsom *et al.*, 2010). The genome annotation of *D. shibae* revealed genes encoding enzymes for an advanced anaerobic metabolism. A dimethylsulfoxide reductase and the enzymes for a complete denitrification pathway are available for the reduction of the alternative electron acceptors DMSO, nitrate, nitrite, nitric oxide and nitrous oxide. Furthermore, *D. shibae* possesses genes for the pathways of arginine and pyruvate fermentation, which can be used for anaerobic growth or survival in the absence of alternative electron acceptors (Wagner-Döbler *et al.*, 2010).

Growth under nitrate reducing conditions and the corresponding induction of genes encoding for the denitrification enzymes was shown (Piekarski *et al.*, 2009).

1.3.1 Denitrification in *D. shibae*

Denitrification is a part of the global nitrogen cycle mainly conducted by prokaryotes. In this cycle elemental nitrogen (N_2) is removed from the biosphere by nitrogen fixating microorganisms, which convert N_2 to ammonia (NH_4). NH_4 itself can be used for the synthesis of nitrogen-containing biomolecules like amino acids and nucleotides. NH_4 is oxidized to nitrate (NO_3^-) via the nitrification pathway. In a two-step reaction NH_4 is oxidized to nitrite (NO_2^-) (ammonia oxidation) and subsequently to NO_3^- (nitrite oxidation). The reverse pathway is used for nitrate assimilation. Oxidized nitrogen gets reduced to NH_4 and furthermore utilized for nitrogen-containing biomolecules. The nitrogen cycle is closed by the reduction of NO_3^- to N_2 via the denitrification pathway (Fig. 1.3) (Zumft, 1997; Moreno-Vivián *et al.*, 1999; Zehr & Kudela, 2011).

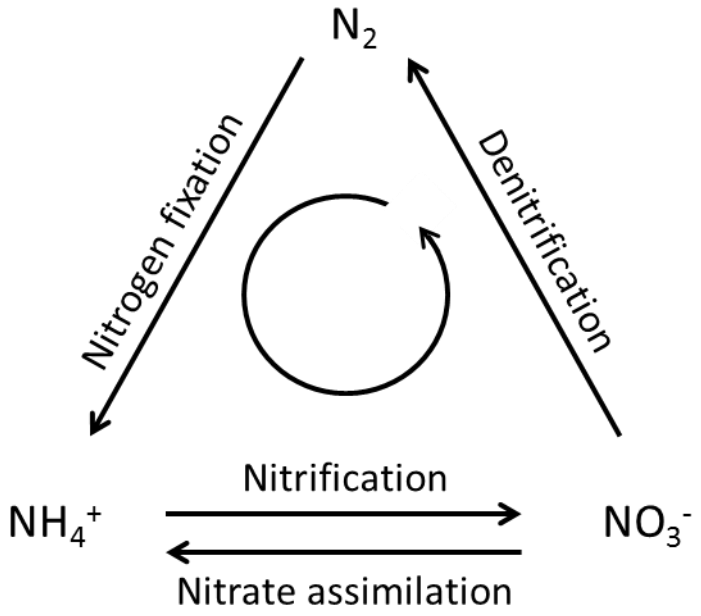


Fig. 1.3: Schematic overview of the global nitrogen cycle mainly sustained by prokaryotes.
(Modified from (Zumft, 1997))

The denitrification pathway consists of four single reactions. The first reduction of NO_3^- to NO_2^- is performed by the cytoplasmatic membrane localized nitrate reductase Nar or by the periplasmatic nitrate reductase Nap. Interestingly, *D. shibae* only possesses genes encoding the periplasmatic nitrate reductase Nap (*napFDAGHBC*), which is active

under aerobic and anaerobic conditions and genes encoding the assimilatory nitrate reductase NasA (*nasA*). The genes encoding the cytoplasmatic membrane bound nitrate reductase (Nar), are missing in the genome, (Wagner-Döbler *et al.*, 2010). For the dissimilatory periplasmatic nitrate reductase Nap different physiological functions have been proposed. Beside the role in nitrate respiration in *Haemophilus influenza* (Brigé *et al.*, 2001) and the denitrifying bacterium *Pseudomonas* sp. strain G-179 (Bedzyk *et al.*, 1999), Nap is involved in magnetite biomineralization in *Magnetospirillum gryphiswaldense* (Li *et al.*, 2012), takes part in the aerobic denitrification in *Thiosphaera panthotropha* (Bell *et al.*, 1990) and plays a role in respiratory ammonification and cellular redox balancing in *Shewanella* species (Simpson *et al.*, 2010). The periplasmatic nitrate reductase Nap consists of three subunits. The membrane bound tetraheme cytochrome NapC, which is responsible for the electron transfer from the quinone pool to the NapAB complex. The periplasmatic NapAB complex is divided into the smaller subunit NapB and the larger catalytic subunit NapA. NapA harbors a molybdenum cofactor and an iron-sulfur cluster of the [4Fe-4S] type (Zumft, 1997; González *et al.*, 2006; Richardson *et al.*, 2001; Chen *et al.*, 2011). The membrane bound cytoplasmatic nitrate reductase Nar is responsible for nitrate respiration under anaerobic conditions and is therefore involved in the generation of a proton motive force (PMF). The reduction of nitrate can be performed by three different enzymes in bacteria. The assimilatory nitrate reductase NasA, which is localized in the cytoplasm, is responsible for the utilization of nitrate as a nitrogen source for N-containing biomolecules.

The further reduction of NO_2^- to nitric oxide (NO) is catalyzed by the nitrite reductase Nir. Two different dissimilatory nitrite reductases are known in nature. *Pseudomonas aeruginosa* possesses the tetraheme protein cytochrome cd_1 as respiratory cd_1 nitrate reductase Nir (NirS), whereas *R. sphaeroides* utilizes the copper-containing nitrite reductase CuNir (Zumft, 1997). *D. shibae* possesses genes encoding for the cytochrome cd_1 nitrite reductase NirS (*nirSECFDGHJN*).

The toxic NO is reduced in the next step by the membrane bound nitric oxide reductase NorBC to nitrous oxide (N_2O). The membrane integrated enzyme nitric oxide reductase and consists of two subunits NorB and NorC. The small subunit NorC possesses a heme *c*, the larger NorB contains three iron centers, two b-type hemes (heme *b*, heme b_3) and a non-heme bound iron (Zumft, 1997; Hino *et al.*, 2012; Shiro *et al.*, 2012; Spiro, 2012). In *D. shibae* the enzyme is encoded by the *norCBQDEF* operon.

The conversion of N_2O to N_2 represents the last step of the denitrification pathway. This reduction is catalyzed by the nitrous oxide reductase NosZ (Zumft, 1997). . NosZ is a periplasmatic, cytoplasmic membrane associated homodimeric protein. Each monomer of the homodimeric protein contains two copper atoms as a cofactor (Zumft, 1997; Spiro, 2012). The enzyme is encoded by the *nosRZDFYLX* operon in *D. shibae*. A schematic overview of the denitrification pathway in *D. shibae* is shown in Fig. 1.4.

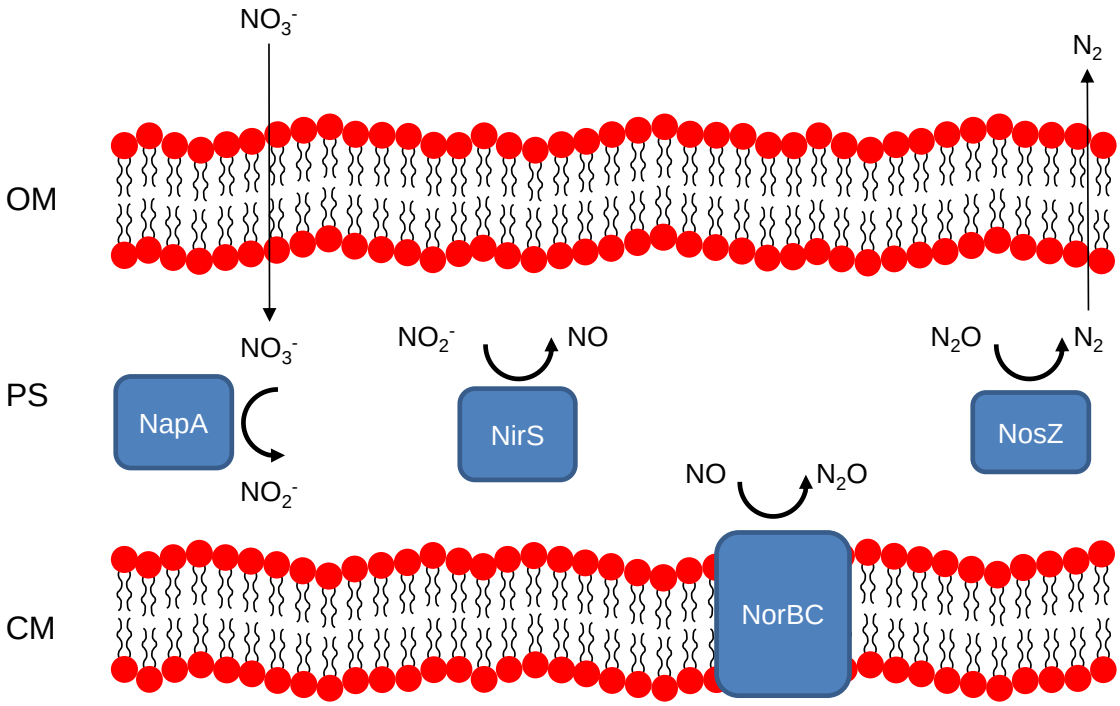


Fig. 1.4: Schematic representation of the denitrification apparatus in *D. shibae*. NapA: periplasmatic nitrate reductase, NirS: nitrite reductase, NorCB nitric oxide reductase, NosZ: nitrous oxide reductase, OM: outer membrane, PS: periplasmatic space, CM: cytoplasma membrane.

All operons which encode genes for the denitrification pathway can be found next to each other in the *D. shibae* genome. The *nap*-operon is encoded by Dshi_3167-Dshi_3161, the *nir*-operon by Dshi_3180-Dshi_3182, the *nor*-operon by Dshi_3183-Dshi_3188 and the *nos*-operon by Dshi_3194-Dshi_3199. Furthermore, genes encoding the possible regulators for the anaerobic metabolism DnrD (Dshi_3189), DnrE (Dshi_3191) and NosR (Dshi_3193) are located in this area (Fig. 1.5).

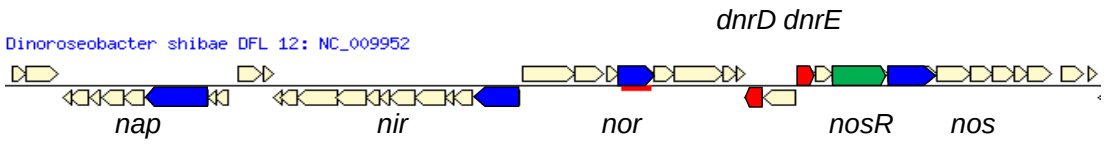


Fig. 1.5: **Arrangement of genes/operons involved in denitrification pathway.** Blue: genes coding for catalytic enzymes (*napA*, *nirS norB*, *nosZ* form left to right), red: genes encoding for Dnr like regulators (*dnrD*, *dnrE*), green: *nosR3*. Modified from: img.jgi.doe.gov/cgi-bin/pub/main.cgi

1.3.2 Regulation of anaerobic pathways

The successful response to changing environmental conditions needs a fine tuned regulation of gene expression. The synthesis of the denitrification machinery is mainly dependent on low oxygen tension and respirable N-oxides as signals. Furthermore, metal ions are essential for several enzymes. Iron, copper and molybdenum are essential for the enzymes of the denitrification machinery or for the corresponding electron carriers, which are synthesized *de novo* upon the change to anaerobic conditions (Zumft, 1997). Moreover, a fine tuned regulation of the different enzymes involved in denitrification is required to avoid accumulation of toxic intermediates such as NO_2^-, NO and N_2O. Crp/Fnr-like transcription factors (cAMP receptor protein, fumarate and nitrate reductase regulator) are involved in this regulatory network in many other bacteria (Körner *et al.*, 2003). Despite their low overall amino acid sequence identity of 25 %, this group of transcription factors share common structural features. The proteins are composed of 230-250 amino acid residues. All homodimers contain an N-terminal sensor domain, a dimerization helix and a C-terminal DNA binding domain with a Helix-Turn-Helix (HTH) motif. A conformational change due to the binding of an effector molecule to the sensor domain leads to the active conformation and appropriate binding of the corresponding DNA sequence (Körner *et al.*, 2003; Giardina *et al.*, 2011). The superfamily is divided into several subgroups depending on their phylogenetic affiliations (Fig. 1.6). However, a functional prediction within one phylogenetic cluster is not possible. For example binding of a signal percepting cofactor leads to a distinct physiological function but does result in a distinct phylogenetic subgroup. The [4Fe-4S] cluster containing *Bacillus subtilis* Fnr belongs to the PfrA subfamily and not to the classical Fnr subfamily, which contains most regulators of a similar function and cofactor content (Körner *et al.*, 2003).

Fig. 1.6: Phylogenetic tree of the Crp/Fnr family. The clusters are named by the most important representatives. Larger groups without known lead member are shown by one capital letters and smaller branches by the use of small letters (Körner *et al.*, 2003).

1.3.3 The global transcription factor Fnr

The transcriptional activation of genes involved in denitrification requires the global transcription factor Fnr (e.g. *E. coli*) or one of the Fnr-like transcription factors Anr (*P. aeruginosa*), FnrA (*Pseudomonas stutzeri*), FnrL (*R. sphaeroides*) or FnrP (*P. denitrificans*) all belonging to the same subgroup (Zumft, 1997). In *P. aeruginosa* a second Crp/Fnr-like regulator Dnr is involved in regulation of the *nirS*, *norCB*, and *nosR* promoters (Arai *et al.*, 1995; Arai *et al.*, 2003). *P. stutzeri* possesses four *fnr*-like genes, *fnrA*, *dnrD*, *dnrE* and *dnrS*, all co-expressed under denitrifying conditions (Vollack *et al.*, 1999). In *D. shibae* 7 Crp/Fnr-like regulators are described (Dshi_0660, Dshi_3189, Dshi_3191, Dshi_0447, Dshi_2521, Dshi_2528, Dshi_3270). However, only Dshi_0660 carries the typical four cysteine residues for iron sulfer cluster

formation as known from the Fnr protein of *E. coli* or Anr from *P. aeruginosa* (Wagner-Döbler *et al.*, 2010).

Under anaerobic conditions the Fnr protein of *E. coli* exists as a homodimer with an [4Fe-4S] cluster that can bind to a palindromic DNA sequence named Fnr box with the consensus sequence 5`-TTGAT-N6-ATCAA-3` (Körner *et al.*, 2003). The binding of Fnr to a target site is described for two different promoter types. For the class I promoters a binding site exists at positions 61.5, 71.5, 82.5 and 92.5 upstream the transcriptional starting site, while the class II promoter, which is found more often, is located 41.5 bp upstream of the transcriptional start site (Tielen, Schobert, Härtig, & Jahn, 2012; Williams *et al.*, 1997). *Via* the iron-sulfur cluster, Fnr is a direct sensor for oxygen availability. Under aerobic conditions the [4Fe-4S] cluster is first oxidized to a [3Fe-3S] cluster and in a second step to a [2Fe-2S] cluster. Without the [4Fe-4S] cluster Fnr becomes a monomer and gets inactive (Khoroshilova *et al.*, 1997; Crack *et al.*, 2008). Durand and Storz could show the involvement of a small RNA FnrS in the extended regulon of Fnr (Tielen, Schobert, Härtig, & Jahn, 2012; Körner *et al.*, 2003; Fleischhacker & Kiley, 2011; Durand & Storz, 2010).

1.3.4 The NO sensing regulator Dnr

The dissimilatory nitrate respiration regulator (Dnr) is also a member of the Crp/Fnr like regulators family. Dnr is not able to detect oxygen with an iron-sulfur cluster as it lacks the four cysteine residues for cluster formation. Nitric oxide is the major signal detected by a non covalently bound heme, which is essential for the Dnr activation of a target promoter in *E. coli* (Castiglione *et al.*, 2009). The expression of the *dnr* gene is controlled by Anr. Computational prediction of a Dnr regulon is not possible because the consensus sequence of the DNA binding site is identical to that of Anr (Rompf *et al.*, 1998; Arai *et al.*, 2003; Arai *et al.*, 1997; Körner *et al.*, 2003). By know it is not known how Anr and Dnr distinguish between their target promoters. Transcriptome and genetic analyses of the Dnr regulon in *P. aeruginosa* showed that in the presence of NO Dnr induces the expression of *nirS*, *norC* and *nosR*, which are involved in the denitrification pathway (Schreiber *et al.*, 2007; Arai *et al.*, 2003; Trunk *et al.*, 2010; Fleischhacker & Kiley, 2011).

In 2009 Giardina *et al*. published the crystal structure of *P. aeruginosa* Dnr (Fig. 1.7) (Giardina *et al.*, 2009). Similar to other members of the Crp/Fnr superfamily the Dnr

monomer structure revealed a N-terminal sensor domain composed of a β-barrel core (β-sheets 1-8) and three α-helices (α-helix A-C), a dimerization helix (α-helix D) and a C-terminal DNA binding domain consisting of three α-helices (α-helix E-G) and two β-sheets (β-sheets 9 and 10). The α-G helix is the recognition helix of the HTH and responsible for DNA binding. A comparison with the structure of *E. coli* Crp in the active ON conformation in complex with DNA, after activation of two molecules of the cofactor cAMP, identifies Dnr in the OFF conformation. In comparison to the structure of the ON conformation of Crp, the DNA binding domain of the two Dnr dimers were found rotated by 155°. In this OFF conformation of Dnr the α-helix G of one monomer (colored) is directed towards the sensing domain of the second monomer (grey). Furthermore, the comparison of the Dnr structure with the structures of CooA (Crp/Fnr type regulator, activated by carbon monoxide via binding to a heme cofactor) and CrpK (Dnr homologue, activated by o-chlorophenolacetic acid via binding to the reduced protein) shows the position of the sensor domain of Dnr is rotated by 65° (OFF CooA), 60° (ON CooA) 49° (OFF CrpK) and 54° (ON CrpK). Due to the similarity of Dnr, Crp, CooA and CrpK, the active form of Dnr (ON) is suggested to share the same topology of its sensory and DNA binding domains in the ON from. Therefore, Dnr OFF has to undergo a large conformational rearrangement to reach the Dnr ON conformation (Giardina *et al.*, 2008; Giardina *et al.*, 2009).

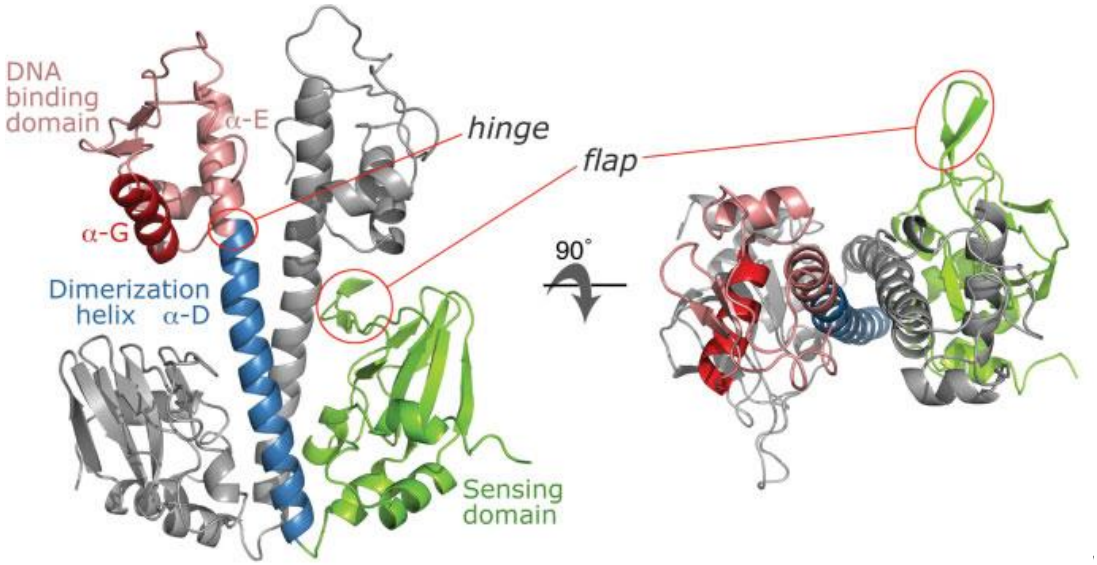


Fig. 1.7: 3D structure of a Dnr dimer in side and top view. Sensor domain: green; dimerization helix: blue; recognition helix α-G: red; DNA binding domain: salmon; second monomer: grey (Giardina *et al.*, 2009).

1.3.5 Regulation of the anoxic metabolism in *D. shibae*

A fine-tuned regulatory network is needed for the successful adaptation of bacteria to microoxic or anoxic conditions. The expression of genes encoding for enzymes involved in energy generation and cofactor biosynthesis is usually regulated in depended of oxygen absence and the alternative electron acceptors (Tielen, Schobert, Härtig, & Jahn, 2012; Zumft, 1997; Körner *et al.*, 2003). The following predicted regulation of the anoxic metabolism in *D. shibae* is proposed in analogy to the regulation mechanism in *P. aeruginosa* (Schobert & Tielen, 2010) (Fig. 1.8).

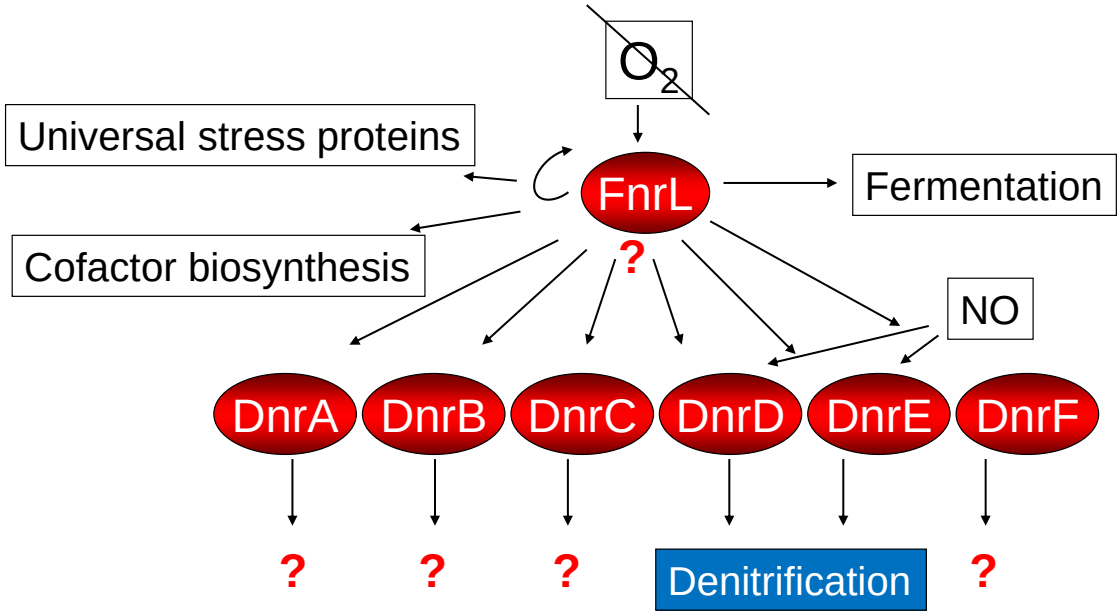


Fig. 1.8: Predicted regulatory network in *D. shibae*. The global transcriptional regulator FnrL, on top of the control hierarchy induces the expression of genes involved in the response to anoxic conditions.

Working hypothesis: Due to low oxygen partial pressure a [4Fe-4S] cluster is assembled in the *D. shibae* Anr homologue FnrL and induces the expression of genes encoding for enzymes involved in stress response, cofactor biosynthesis and fermentation. Furthermore, FnrL induces the expression of its own gene as well as the regulator Dnr encoding gene *dnr*. In *P. aeruginosa*, the Anr regulator also induces the expression of the *narXL* genes encoding the nitrate detecting two component system NarXL. However, this system is missing in the *D. shibae* genome and it is not clear how the availability of nitrate is detected in *D. shibae*. Dnr detects nitric oxide with its bound cofactor heme and induces the expression of the *nap*-operon, *nir*-operon, *nor*-operon and *nos*-operon encoding for the nitrate reductase NapA, the nitrite reductase NirS, the nitric oxide reductase NorBC and the nitrous oxide reductase NosZ, respectivley.

Furthermore, the expression of the *nirQ* gene is induced, which encodes a posttranslational activation protein of NirS. Until now it is not known whether all Dnr-like regulators are involved in the regulation of the anaerobic metabolism in *D. shibae* or if regulation is only mediated by DnrD and DnrE, which are encoded between the denitrification operons.

The *D. shibae* genome was searched for possible Fnr binding sites using a position weight matrix approach (Wagner-Döbler *et al.*, 2010). Possible Fnr boxes were found in the promoter region of genes encoding for high-affinity oxygen-dependent cytochrome *c* oxidases (cbb_3 type) (Dshi_0248), an NADH dehydrogenase (Dshi_1378), universal stress proteins (Dshi_1338, Dshi_2213, Dshi_2686), DnaK suppressor proteins (Dshi_0812, Dshi_1411) and cofactor biosynthesis (*hemN1*, *hemN2*, *hemA2*, *moaC*). Furthermore, in some of the promoter regions of the bacteriochlorophyll biosynthesis genes also Fnr binding sites are present (Wagner-Döbler *et al.*, 2010). This leads to the suggestion of an involvement of FnrL in the regulation of the photosynthetic apparatus like in *R. sphaeroides* (Körner *et al.*, 2003).

1.4 Polyhydroxybutanoate production

In response to an imbalanced nutrient supply or during impaired denitrification, polyhydroxybutanoate (PHB) is synthesized by numerous bacteria (Madison & Huisman, 1999; Xiao & Jiao, 2011; Trautwein *et al.*, 2008). The microbial biosynthesis of the polymer starts with the condensation of two acetyl-CoA to acetoacetyl-CoA as an intermediate which is subsequently reduced to (R)-3-hydroxybutanoyl-CoA.

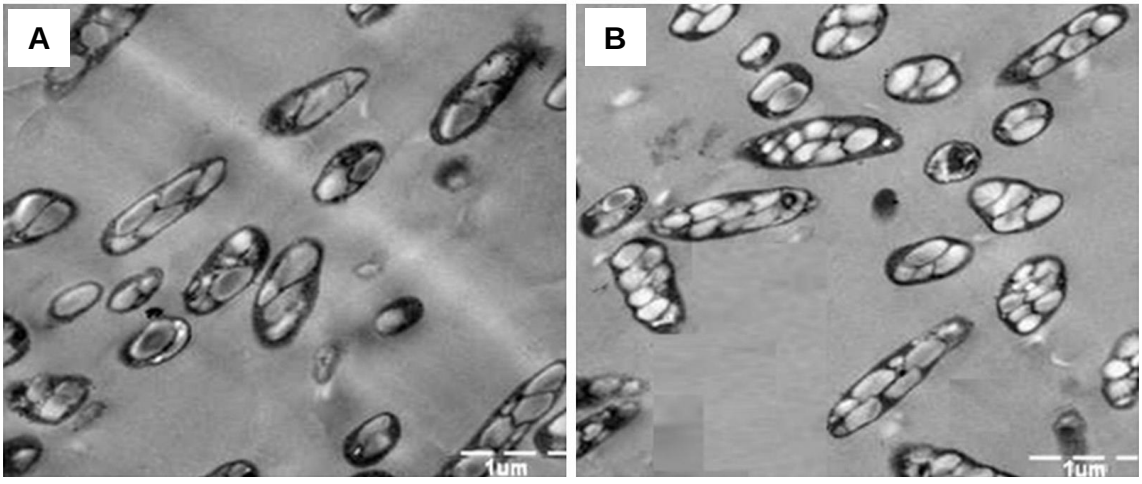


Fig. 1.9: TEM of *Dinoroseobacter* sp. JL 1447 cultured in glucose medium producing PHB granules.
A: exponential phase, B: stationary phase (Xiao *et al.*, 2015).

This monomer is then polymerized to PHB. *Dinoroseobacter* sp. JL 1447 produces PHB granules in the mid exponential and stationary phase (Fig. 1.9) (Xiao *et al.*, 2015). *D. shibae* possesses the polyhydroxybutyrate polymerase (Dshi_2233) and the genes Dshi_2231 and Dshi_2232, which show homology to polyhydroxyalkanoate associated proteins (e.g. *Jannaschia* sp. Jann_1118), for the synthesis of PHB. Furthermore *D. shibae* exhibits the genes for the polyhydroxyalkanoate synthesis repressor, PhaR (*phaR*) and for the polyhydroxyalkanoate depolymerase (Dshi_2234).

1.5 Objectives of the Work

The aim of this work was the elucidation of the unknown gene regulatory and metabolic network for the adaptation of the marine bacterium *Dinoroseobacter shibae* to anoxic conditions using nitrate as alternative electron acceptor.

For this purpose, a continuously cultivation of D. shibae in a chemostat with the ability of a shift from oxic to anoxic conditions had to be established. Time-resolved, combined analyses of transcriptome, proteome and metabolome should foster to a systems biology approach revealing the intergated transcriptional, proteomic and metabolic network for the adaptation of *D. shibae* to anoxic conditions. Furthermore, the involvement of several Fnr/Dnr type transcriptional regulators was expected. For their functional characterization the heterologous production of *D. shibae* Dnr-like proteins was an objective of this work.

In a second approach transposon mutagenesis should be used to identify genes encoding proteins, which are essential for the survival under anoxic denitrifying conditions.

2 Part I: Transposon mutagenesis identified chromosomal and plasmid encoded genes essential for the adaptation of the marine bacterium *Dinoroseobacter shibae* to anaerobic conditions

Matthias Ebert[1§], Sebastian Laaß[1§], Melanie Burghartz[1], Jörn Petersen[2], Sebastian Koßmehl[3], Lars Wöhlbrand[3], Ralf Rabus[3], Christoph Wittmann[4], Petra Tielen[1#], Dieter Jahn[1]

[1]Institute for Microbiology, Technische Universität Braunschweig, D-38106 Braunschweig, Germany
[2]Leibniz-Institut DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Inhoffenstraße 7 B, D-38124 Braunschweig, Germany
[3]Institut für Chemie und Biologie des Meeres, Carl von Ossietzky Universität Oldenburg, Carl-von-Ossietzky Str. 9-11, D-26111 Oldenburg
[4]Institute of Biochemical Engineering, Technische Universität Braunschweig, D-38106 Braunschweig, Germany

[§]Authors contributed equally.

corresponding author:
Dr. Petra Tielen
p.tielen@tu-bs.de

My contribution: design of experiments (with D.J. and P.T.); establishment of continuously cultivation of *D. shibae* in a chemostate; experimental procedure of transcriptome analyses; guidance of M.E. in transposon mutagenesis experiments; analyses of transposon insertion sites, transcriptome and proteome data; first draft of manuscript.

2.1 Abstract Part I

Anaerobic growth and survival are integral parts of the life cycle of many marine bacteria. To identify genes essential for the anoxic life of *Dinoroseobacter shibae* a transposon library was screened for strains impaired in anaerobic denitrifying growth. Transposon insertions in 35 chromosomal and 18 plasmid encoded genes were detected. The essential contribution of plasmid encoded genes to anaerobic growth was confirmed with plasmid-cured *D. shibae* strains. A combined transcriptome and proteome approach identified oxygen tension regulated genes. Transposon insertions sites of a total of 1527 mutants without anaerobic growth phenotype were determined to identify anaerobically induced, but not essential genes. A surprisingly low degree of overlap of only 3 genes (*napA*, *phaA* and the Na^+/P_i antiporter gene Dshi_0543) between anaerobically essential and induced genes was found. Interestingly, transposon mutations in genes involved in dissimilatory and assimilatory nitrate reduction (*napA*, *nasA*) and corresponding cofactor biosynthesis (genomic *moaB*, *moeB*, *dsbC*, plasmid encoded *dsbD*, *ccmH*) were identified to cause anaerobic growth defects. In contrast, mutation of anaerobically induced genes encoding proteins required for the later denitrification steps (*nirS*, *nirJ*, *nosD*), dimethyl sulfoxide reduction (*dmsA1*) and fermentation (*pdhB1*, *arcA*, *aceE*, *pta*, *acs*) did not result in decreased anaerobic growth under tested conditions. Additional essential components (ferredoxin, *cccA*) of the anaerobic electron transfer chain and central metabolism (*pdhB*) were identified. Another surprise was the importance of sodium gradient-dependent membrane processes and genomic rearrangements via viruses, transposons and IS elements for anaerobic growth. These processes and the observed contribution of cell envelope restructuring (*lysM*, *mipA*, *fadK*), C4-dicarboxylate transport (*dctM1*, *dctM3*) and protease function to anaerobic growth require further investigations to unravel the novel underlying adaptation strategies.

2.2 Introduction Part I

The *Roseobacter* clade is one of the most abundant groups of bacteria in oceans. The ecological success of the *Roseobacter* clade can be attributed to its broad metabolic capabilities (Wagner-Döbler & Biebl, 2006; Brinkhoff *et al.*, 2008). One of the model organisms for the *Roseobacter* clade is *Dinoroseobacter shibae*. It is a mixotrophic bacterium that can utilize various organic carbon sources including several carboxylic acids, glucose, glycerol and succinate (Wagner-Döbler & Biebl, 2006; Brinkhoff *et al.*, 2008; Biebl *et al.*, 2005). Fluxome analyses showed that *D. shibae* lacks phosphofructokinase activity during growth on glucose and uses preferentially the Entner-Doudoroff pathway instead of glycolysis for sugar metabolization (Fürch *et al.*, 2009). Moreover, *D. shibae* can gain additional energy by aerobic anoxygenic photosynthesis, but it is unable to grow photoautotrophically. Annotation of the 4.4 Mb genome of *D. shibae* DFL12^T discovered genes that indicated the use of alternative electron acceptors such as nitrate and dimethyl sulfoxide (DMSO) in the absence of molecular oxygen (Wagner-Döbler *et al.*, 2010). In agreement, the anaerobic growth by denitrification was shown recently (Piekarski *et al.*, 2009). The bacterium possesses *nap*-, *nir*-, *nor*- and *nos*-operons encoding the nitrate reductase NapAB, the nitrite reductase NirS, the nitric oxide reductase NorCB and the nitrous oxide reductase NosZ (Zumft, 1997). Notably, *D. shibae* possesses the genes encoding the periplasmic NapAB nitrate reductases instead of the genes for the membrane localized, nitrate reductase NarGHI (Wagner-Döbler *et al.*, 2010; Zumft, 1997). Additionally, genes for high-affinity cbb_3-type cytochrome *c* oxidases and various alternative NADH dehydrogenase systems were identified. These might be also involved in energy conversation under low oxygen conditions (Wagner-Döbler *et al.*, 2010). Various electron donating primary dehydrogenase genes were annotated (*gcd* for glucose, *gld* for gluconate, *lld* and *dld* for lactate, *glp* for glycerol-3-phosphate and *fda* for formate). Moreover, the capacity for substrate level phosphorylation processes including the arginine deiminase pathway and a mixed-acid type fermentation can be deduced from the *D. shibae* genome (Wagner-Döbler *et al.*, 2010).

However, the members of the anaerobic modulon remain to be experimentally defined for this important class of marine bacteria. The contribution of the five plasmids of *D. shibae* to these processes is completely unknown.

Here we present the identification of genes involved in the adaptation process of *D. shibae* to anaerobic conditions via transposon mutagenesis and combined transcriptome and proteome analyses. Chromosomal and plasmid encoded genes were found essential. Only a low degree

of overlap between the genes found necessary for anaerobic growth and those induced under these conditions was detected. A novel type of anaerobic adaption strategy was deduced.

2.3 Material and Methods Part I

2.3.1 Bacterial strains, growth conditions and plasmid transfer

The type strain *D. shibae* DFL12^T (Biebl *et al.*, 2005) was cultured aerobically in Marine-Bouillon (MB, Roth, Karlsruhe, Germany) at 30 °C in bottle flasks shaking at 200 rpm in the dark. The mariner transposon (Kulasekara *et al.*, 2005) located on the plasmid pBT20 (Fig. 2.2, Supplemental Material) was used for transposon mutagenesis of *D. shibae* DFL12^T. For selection of *D. shibae* mutants 80 µg/ml gentamycin were added after conjugation to half-concentrated MB (hMB) (Piekarski *et al.*, 2009). *Escherichia coli* ST18, a Δ*hemA*-mutant of *E. coli* S17, served as donor strain for the conjugative transfer of plasmid DNA (Thoma & Schobert, 2009). Luria-Bertani (LB, Roth, Karlsruhe, Germany) medium supplemented with 50 µg/ml aminolevulinic acid adjusted to pH 7 was used for its cultivation at 37 °C and 200 rpm. For solid medium, agar was added to final concentration of 1.5 % (w/v).

The conjugative plasmid transfer into *D. shibae* DFL12^T was performed as described previously with modifications outlined in the Supplemental Material (Piekarski *et al.*, 2009). For selection of *D. shibae* transposon mutants with an anaerobic growth deficiency all clones were cultivated aerobically and anaerobically at 30 °C in 96 well plates with hMB supplemented with 80 µg/µl gentamycin, respectively. For anaerobic cultivation 25 mM nitrate were added. Growth was followed by optical density measurements at 595 nm in a microtiter plate reader (Model 680, Biorad, Munich, Germany). Strains showing growth deficiencies under anaerobic conditions were isolated for further studies. The growth behavior of the selected *D. shibae* DFL12^T transposon mutants was analyzed aerobically and anaerobically in artificial seawater medium (SWM) with 16.9 mM succinate, respectively (Tomasch *et al.*, 2011). For anaerobic cultivation 25 mM nitrate was added. The cultivation occurred in 48 well flower plates (m2p-labs, Baesweiler/Aachen, Germany) at 30 °C for 60 h with 800 rpm in a parallel bioreactor system (Biolector type Micro Fermentation System, m2p-labs GmbH, Aachen, Germany). Every hour the optical density at 620 nm, the pH and the oxygen partial pressure were measured automatically.

2.3.2 Identification of transposon integration site

First an arbitrary PCR protocol was established according to the publication of O'Toole and coworkers (O'Toole *et al.*, 1999). For this purpose, two different PCR analyses were performed. The first PCR included the genomic DNA from a grown transposon mutant colony and primer 1 (oJG016: 5'-TCT ACG TGC AAG CAG ATT ACG GTG AC -3') which hybridized to the transposon DNA. Random primer 2 (oJG007: 5'-GGC CAC GCG TCG ACT AGT CAN NNN NNN NNN GAT AT-3') and primer 3 (oJG008: 5'-GGC CAC GCG TCG ACT AGT CAN NNN NNN NNN GAT CC-3') were added. The initial incubation at 95 °C (5 min) was followed by six cycles of DNA denaturation at 94 °C (30 sec), annealing at 30 °C (30 sec) and elongation at 70 °C (1 min). In a second part of the PCR the annealing temperature was increased up to 45 °C for further 30 cycles, followed by a final elongation phase at 72 °C (5 min). The second PCR involved primer 4 (oJG005: 5'-GAT ATC GAC CCA AGT ACC GCC ACC TA-3') and primer 5 (oJG009: 5'-GGC CAC GCG TCG ACT AGT AC-3'). The employed conditions were chosen according to the first PCR protocol. PCR products were subjected to DNA sequence determination. The resulting FASTA sequences were aligned to the genome sequence of *D. shiabe* DFL12^T (GenBank accession number NC_009952 and NC_009955-59).

2.3.3 Cultivation of *D. shibae* in a chemostat

Continuous cultivation of *D. shibae* DFL12^T for transcriptome and proteome analyses was performed in SWM (Tomasch *et al.*, 2011) in an Infors HT Multifor 2 bioreactor (Infors, Bottmingen, Switzerland) at 30°C, pH 8.0, with aeration of 0.7 l air per minute and a stirring speed of 150 rpm. The bioreactor had a working volume of 1 l. The pH was adjusted automatically using 500 mM H_3PO_4 and 500 mM NaOH. In the steady state the oxygen saturation of the culture in the bioreactor was stabilized to approximately 85 %. To avoid aerobic anoxygenic photosynthesis of *D. shibae* during the experiment the chemostat was protected from light by covering with aluminium foil. The bioreactor was inoculated to a starting optical density of OD_{578} of 0.02 with an appropriate pre-culture. Feeding with fresh medium was started after the culture reached an OD_{578} of 0.5. The dilution rate was 0.1 h^{-1}, establishing a half-maximum growth rate of *D. shibae* in the exponential phase. The anaerobic shift was initialized after 20 hours of continuous cultivation by stopping of the aeration. The oxygen concentration in the reactor was determined with an InPro 6820 oxygen electrode

(Mettler Toledo, Gießen, Germany) as well as with a sensor spot O_2 (PreSence, Regensburg, Germany). Anaerobic conditions were reached approximately after 20 min.

2.3.4 DNA microarray experiments and data analysis

A customized whole genome DNA microarray (Agilent, Santa Clara, USA 8 x 15K format) containing three different 60 nt oligonucleotides covering 96% of the genes of *D. shibae* DFL12^T was designed using the eArray platform from Agilent (https://earray.chem.agilent.com/earray/) and used as described before (Tomasch *et al.*, 2011). The investigated time points were 0 min and 30 min after the oxygen supply had been switched off. Two µg of isolated total cellular RNA were either labeled with Cy3 or Cy5, using the ULS^{TM} Fluorescent Labeling Kit for Agilent arrays (Kreatech, Amsterdam, the Netherlands) according to the manufacturers manual. Subsequently, 300 ng of each labeled RNA were pooled, fragmented and hybridized according to the "two-colour microarray" protocol from Agilent. The DNA microarrays were scanned using an Agilent C scanner with the Agilents scan control 8.4.1 software and the feature extraction 10.7.3.1 software. Data processing was performed in the R environment (http://www.cran.r-project.org/) using the limma package, BioBASE package and the GPLOTS package of the BioConductor project q(http:// www.bioconductor.org/) (Smyth *et al.*, 2005; Miller & Alachi, 1996). Three biological and three technical replicates were performed. Only genes with a logarithmic change of >0.8 in their expression between aerobic (0 min) and anaerobic (30 min) conditions and a P-value of <0.05 were considered in subsequent analyses. The data discussed in this publication have been deposited in NCBI's Gene Expression Omnibus (Edgar *et al.*, 2002) and are accessible through GEO Series accession number GSE47445 (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE47445).

2.3.5 Shotgun proteome analysis by nanoliquid chromatography-electrospray ionization tandem mass spectrometry (nanoLC-ESI MS/MS)

Cell pellets of approximately 50 mg wet weight from bioreactor growth were resuspended in 200 µl lysis buffer and cells disrupted using the PlusOne grinding kit (GE Healthcare, Munich, Germany) as described before (Zech *et al.*, 2013b). Protein concentrations were determined as described before (Bradford, 1976). Following the reduction and the alkylation of 50 µg total cellular protein the proteolytic digest was performed overnight with 0.5 µg

trypsin GOLD (Promega, Mannheim, Germany). Finally, 1 µg of digested protein was separated using an UltiMate 3000 nanoLC system (Thermo Scientific, Bremen, Germany) by applying a linear gradient of increasing acetonitrile concentration over 215 min online coupled to an electrospray-ionization ion trap mass spectrometer (amaZon ETD, Bruker Daltonik GmbH, Bremen, Germany) as described before (Zech *et al.*, 2013b). Three biological replicates were analyzed. Protein identification was performed with ProteinScape (version 3.0; Bruker Daltonik GmbH) on a Mascot server (version 2.3; Matrix Science Ltd, London, UK) by searching against a genomic database of *D. shibae* DFL12^T translated into amino acid sequences, with a target-decoy strategy. Searching was restricted to doubly and triply charged peptides. A false discovery rate of <1.0% was set. Only peptides with a mascot score of >25 were considered for protein identification.

2.3.6 Analysis of the membrane protein-enriched fraction by nanoLC-ESI MS

Preparation and SDS-PAGE separation of the membrane protein-enriched fraction was performed as described recently (Zech *et al.*, 2013b). For each sample, one gel lane was cut into 11 slices that were further cut into smaller pieces for washing, reduction, alkylation and tryptic digest as described before (Zech *et al.*, 2013b). Separation of generated peptides was performed with an UltiMate 3000 nanoLC (Thermo Scientific, Bremen, Germany) applying a 95 minute linear gradient of increasing acetonitrile concentration (Zech *et al.*, 2013b). Mass spectrometric analysis of the LC eluent was performed with an online-coupled ion trap mass spectrometer (amazon ETD; Brucker Daltomics GmbH) as described before (Zech *et al.*, 2013b). Protein identification was performed as outlined above.

2.3.7 Plasmid curing in *D. shibae*

The curing of the 191 kb plasmid pDSHI01 (NC_009955.1) from *D. shibae* DSM 16493^T was performed as recently described (Petersen *et al.*, 2013). The RepABC-9 type replication module of 4,500 bp, which encodes the replicase gene, the origin of replication (*ori*V), the *parAB* partitioning operon and the putative cis-acting palindromic anchor sequence 5´-AAACTCCAATCTTGAACGCGTTCAAGATTGGAGTTT-3´ (Petersen *et al.*, 2009), was amplified and the primers P046 (5´-GACCGGCGCTGGCTACTTCAC-3´) and P047 (5´-TCACAAAACCCGAAGGACACT-3´). The PCR product was cloned within the *Sma*I site of

a pBluescript SK+ vector containing an additional gentamicin resistance cassette (Petersen *et al.*, 2011). Complete DNA sequencing of the 4.5 kb insert revealed the integrity of the replication module. The preparation of electrocompetent *D. shibae* cells and transformation of the plasmid containing RepABC-9 type replication module construct was conducted as described before (Dower *et al.*, 1988). The transformants were plated on marine broth medium with 40 µg/ml gentamicin and streaked out additional three times. The successful elimination of the original 191 kb plasmid was verified via PCR using purified plasmid DNA (NucleoSpin Plasmid DNA kit, Macherey-Nagel) and the following primer combinations for all five extrachromosomal elements of *D. shibae* (pDSHI01 [191 kb], P430: 5´-TCTGGCTGCGTGGTGGCTTTC-3´, P431: 5´-TGCGCTATAGTGCTCTCAACA-3´; pDSHI02 [153 kb], P252: 5´-CCAAGGGGCGGCGGGAGATGC-3´, P253: 5´-CGCACGCCGCCCAGTTCTTCG-3´; pDSHI03 [126 kb], P432: 5´-GGCACCATCGTCGGAACCAAT-3´, P433: 5´-TGGTATCAGGCATTCGCTTCA-3´; pDSHI04 [86 kb], P421: 5´-GATTTTGAAACGGGCATTGAT-3´, P422: 5´-TATAGAATTCGCGGATAGAAGGGGGTGGTTT-3´; pDSHI05 [72 kb], P562: 5´-ATGGCGACGCAGAAGAAGGTT-3´, P563: 5´-AAGACACCAGCCCCGCCACAT-3´). Single colonies of strains of interest were streaked out on MB-medium without the addition of antibiotics. The procedure was repeated five times for the spontaneous loss of the RepABC-9 replication module containing vector (Petersen *et al.*, 2009). The loss of the plasmid was confirmed by the absence of the gentamicin cassette. That was tested via PCR with the primers P024 (5´-GGAAACGGATGAAGGCACCAA-3´) and P025 (5´-GCCCAGCGCCAGCAGGAAC-3´). The resulting *D. shibae* Δ191 kb plasmid cured mutant was subsequently used for growth experiments under aerobic and anaerobic conditions. Curing of the 86 kb plasmid was performed analogously.

2.4 Results and Discussion Part I

2.4.1 Rationale of the approach

A mariner-based transposon mutagenesis in combination with a PCR-based integration site determination and anaerobic growth phenotype testing was used to identify genes essential for anaerobic growth of *D. shibae* under denitrifying conditions. Furthermore, the integration sites of the transposon of most obtained transposon mutants were determined to allow for the identification of mutations in known genes of the anaerobic metabolism without anaerobic growth phenotype. The resulting representative transposon mutant collection of *D. shibae* will be made available to other researches in the field. Furthermore anaerobically expressed genes and formed proteins were identified using a combined transcriptomics and proteomics approach. Obtained results were compared and discussed in light of the currently available literature. A molecular adaption strategy of *D. shibae* to anaerobic growth conditions was deduced.

2.4.2 Transposon mutagenesis, chemostate cultivation, transcriptome and proteome analyses

A transposon mutagenesis of *D. shibae* was performed using the mariner transposon localized on the plasmid pBT20 (Tomasch *et al.*, 2011). The loci of transposon integration into the chromosome and the plasmids were determined using a PCR-based approach. Only single transposon carrying strains were subjected to further analyses. Details are given in the Supplemental Material.

A total of 4500 *D. shibae* transposons mutants were isolated and further screened for growth defects under anaerobic denitrifying conditions. Random integration of the transposon was observed (Fig. 2.1). For the 1580 sequenced transposon mutants 1134 showed different loci of integration (Table S1 Supplemental Material Part I). Taking approximately 12% of essential genes into account the saturation of mutagenesis reached 82 % of the genome. Fifty three mutants, 35 with transposon integration in chromosomal and 18 in plasmid encoded genes, showed a significantly decrease or even a loss of anaerobic growth (Table 2.1). Clearly, complementation experiments are required to ultimately confirm the observed loci of transposon integration as responsible for the observed phenotype. Again, for details please consult the Supplemental Material.

For the transcriptome and proteome analyses a chemostate cultivation with a standardized protocol for the shift from aerobic to anaerobic conditions was developed. The transcriptome analysis revealed 474 genes differentially expressed during the shift from aerobic to anaerobic conditions, with 207 showing an increase and 267 showing a decrease in expression. The proteome analyses detected 878 different proteins in the whole cell protein shot-gun approach and 1215 different proteins in the membrane fraction covering approximately 25 % of the predicted *D. shibae* proteins. The results of the various experimental approaches were interpreted and discussed in the light of their functional consequences below.

2.4.3 Plasmids are essential for anaerobic growth of *D. shibae*

Besides the chromosome *D. shibae* DFL12^T contains five plasmids (Wagner-Döbler *et al.*, 2010). The results of transposon mutagenesis revealed an unexpected impact of these plasmids on the anaerobic growth of *D. shibae*. The both sister plasmids pDSHI01 and pDSHI03 as well as plasmid pDSHI02 seemed to be essential for anaerobic growth (Table 2.1). No transposon mutant affecting anaerobic growth was found for plasmid pDSHI05.

In order to unambiguously demonstrate the contribution of the plasmid encoded genes to anaerobic growth plasmid deficient *D. shibae* strains were generated. The strains were cured for the plasmids pDSH01 and pDSH04 and tested for aerobic versus anaerobic growth. Both plasmid-cured *D. shibae* strains had lost their ability to grow anaerobically. These observations clearly demonstrate the requirement of plasmid provided genetic information for anaerobic growth.

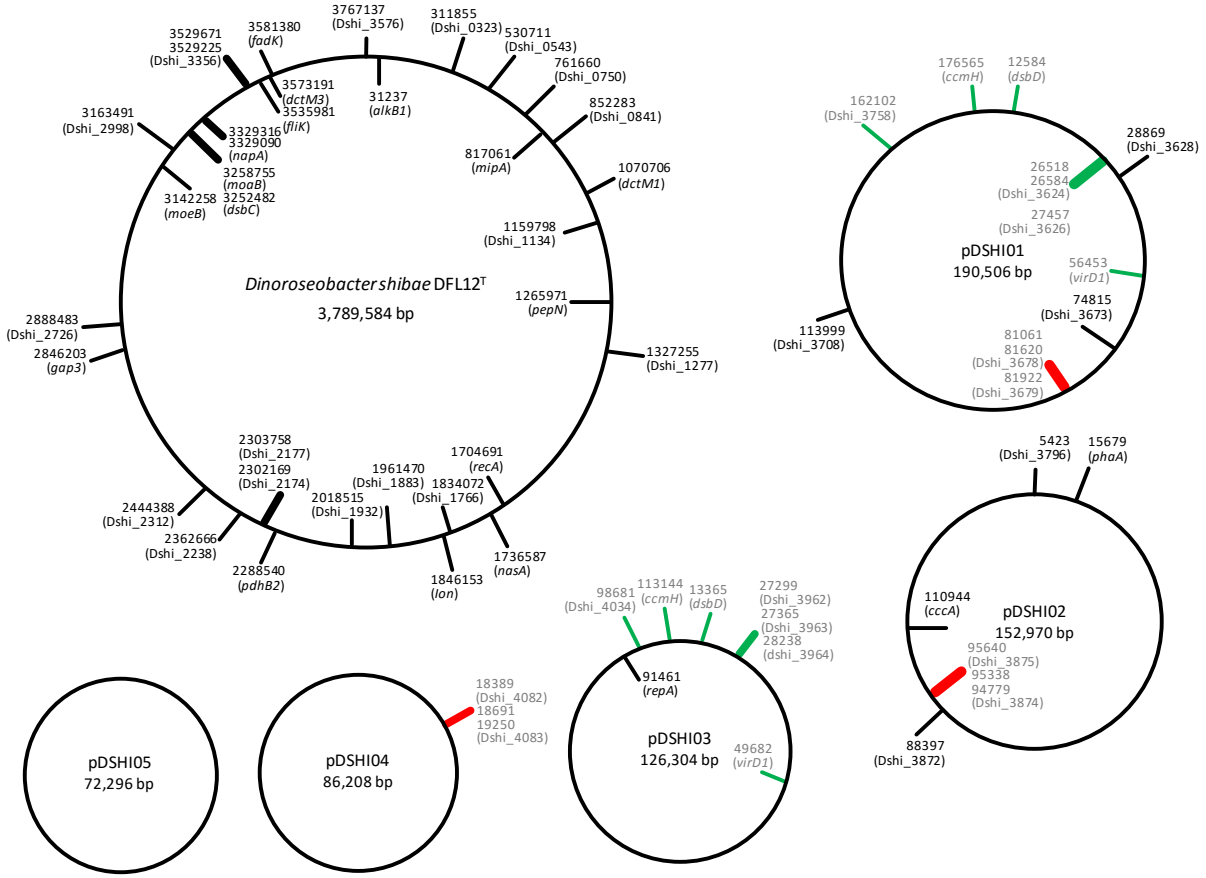


Fig. 2.1: Genomic distribution of transposon insertion sites. Shown are the chromosomal and extrachromosomal DNA of *D. shibae*. Labels on the exterior of the cycle specifies the loci of insertion in the plus orientation. Marks on the cycle interior show insertions in the minus orientation. Numbers denote the point of insertion according to chromosome annotation of *D.shibae* DFL12^T (Refseq number: NC_009952.1, NC_009955.1, NC_009956.1, NC_009957.1, NC_009958.1, NC_009959.1)

2.4.4 Denitrification is induced, but only nitrate reduction is essential for anaerobic growth

Under anaerobic conditions *D. shibae* is able to grow via denitrification with nitrate, nitrite, NO and N_2O as terminal electron acceptors (Piekarski *et al.*, 2009). The first step of denitrification is the reduction of nitrate to nitrite (Zumft, 1997). Accordingly, *napA* (Dshi_3165) encoding the catalytic subunit of the periplasmic dissimilatory nitrate reductase NapAB was identified by transposon mutagenesis as one of the essential genes under anaerobic denitrifying conditions (Table 2.1). Nap is encoded by the *napFDAGHBC*-operon (Dshi_3161-Dshi_3167). The expression of the operon was found slightly induced upon oxygen depletion in the transcriptome analysis. The NapA protein was also detected under aerobic as well as under anaerobic conditions in the proteome analyses (Table 2.3). *D. shibae* possesses only the periplasmatic NapAB but not the membrane spanning, NarGHI nitrate reductase (Wagner-Döbler *et al.*, 2010). Obviously, in the two obtained *napA* mutants energy

conversation via nitrate respiration became limiting. The later steps of denitrification cannot substitute for the process due to the missing production of nitrite, NO and N_2O in this mutant. Consequently mutations in this gene led to a lethal phenotype under anaerobic conditions (Table 2.1). Similar observations for an essential role of the NapAB nitrate reductase for denitrification and anaerobic growth were recently made for the *Magnetospirillum gryphiswaldense* enzyme *(Li et al., 2012a).*

Several transposon insertions in other genes encoding enzymes of the denitrification pathway were found without effect on anaerobic growth (Table 2.1). For example mutations in the nitrite reductase *nirS* (Dshi_3180) and the nitrous oxide reductase maturation protein *nosD* (Dshi_3195) failed to cause a lethal phenotype under anaerobic denitrifying conditions. Similarly, the defect in the nitrous oxide regulator *nosR2* gene (Dshi_3181) did not lead to any growth defect. However, all of these genes (*napH*, *napF*, *nirS*, *nosD*) were found induced under denitrifying conditions. The corresponding proteins were also found abundant under anaerobic conditions in the proteomics investigation (Table 2.2).

Table 2.1: *D.shibae* DFL12^T transposon mutants showing a decrease in anaerobic growth under denitrifying conditions. 2 = normal growth; 1 = decreased growth, 0 = no growth

Locus tag	Function of the geneproduct	Gene name	Position in ORF	Integartion position	TD[1]	Growth	
						aerobic	anaerobic
Nitrate reductases and electron transfer							
Dshi_1669	Nitrate reductase	*nasA*	(283) 2622	1736587 chromosome	F	2	0-1
Dshi_3165	Periplasmic nitrate reductase	*napA*	(1875) 2496	3329316 chromosome	R	2	0
Dshi_3165	Periplasmic nitrate reductase	*napA*	(2101) 2496	3329090 chromosome	R	2	0
Dshi_0323	Ferredoxin		(65) 624	311855 chromosome	F	2	0
Molybdopterin biosynthesis and cytochrome *c* biogenesis							
Dshi_1932	Putative glutathione S-transferase		(703) 870	2018515 chromosome	R	0-1	0
Dshi_2974	Molybdopterin biosynthesis protein	*moeB*	(427) 1041	3142258 chromosome	R	2	0
Dshi_3089	Molybdopterin biosynthesis protein	*moaB*	(475) 543	3258755 chromosome	R	2	1
Dshi_3082	Putative *c*-type cytochrome biosynthesis protein	*dsbC*	(709) 810	3252482 chromosome	R	2	0
Dshi_3606 Dshi_3944	Cytochrome *c* biogenesis protein transmembrane region	*dsbD*	(385) 723	12584 pDSHI01 13365 pDSHI03	F	0-1	0
Dshi_3887	Class I cytochrome *c*	*cccA*	(150) 432	110944 pDSHI02	R	2	0
Dshi_3777 Dshi_4053	Cytochrome *c* biogenesis protein	*ccmH*	(269) 474	176565 pDSHI01 113144 pDSHI03	F	2	0
Na^+-dependent processes							
Dshi_0543	Na^+/P_i-cotransporter		(765) 1851	530711 chromosome	F	2	0
Dshi_1037	TRAP dicarboxylate transporter	*dctM1*	(1268) 1305	1070706 chromosome	F	2	0
Dshi_1195	TRAP transporter solute receptor		(430) 993	1234801 chromosome	R	2	0

Dshi_2998	Putative mechanosensitive ion channel		(1158) 2481	3163491 chromosome	F	2	0
Dshi_3395	C4-dicarboxylate transport system permease DctM subunit	*dctM3*	(1342) 1449	3573191 chromosome	R	2	0-1
Dshi_3708	AraC-like ligand binding domain		(227) 837	113999 pDSHI01	F	2	0
Dshi_3805	NADH dehydrogenase	*phaA*	(2761) 2910	15679 pDSHI02	F	2	0
Peptidases							
Dshi_0841	Hypothetical protein		(-3) 1029	852283 chromosome	F	2	0
Dshi_1223	Aminopeptidase N	*pepN*	(877) 2556	1265975 chromosome	R	2	0
Dshi_1777	ATP-dependent protease		(874) 2409	1846153 chromosome	F	2	0
Dshi_1883	Putative ClpA/ClpB family protein		(15) 843	1961470 chromosome	R	1	1
Dshi_3625 Dshi_3963	Hypothetical protein		(-17) 566	26584 pDSHI01 27365 pDSHI03	F	2	0
Dshi_3872	Hemolysin-type calcium-binding protein		(43) 5688	88397 pDSHI02	F	2	1
Central metabolism							
Dshi_1134	3-Oxo acid-CoA-transferase (B subunit)		(460) 627	1159798 chromosome	R	2	0
Dshi_2159	Pyruvate dehydrogenase	*pdhB2*	(677) 1356	2288540 chromosome	F	1	0
Phages, Transposons and DNA restructuring							
Dshi_1643	Bacterial DNA recombination	*recA*	(1067) 1068	1704691 chromosome	R	0-1	0
Dshi_2174	Putative phage capsid protein		(446) 1218	2302169 chromosome	R	2	0
Dshi_2177	Phage portal protein, HK97 family		(931) 1191	2303758 chromosome	R	2	0-1
Dshi_2312	Type I restriction-modification system (R subunit) - dsDNase		(511) 516	2444388 chromosome	F	2	1
Dshi_3356	Transposase		(-424) 267	3529671 chromosome	F	2	0
Dshi_3356	Transposase		(-870) 267	3529225 chromosome	F	2	1
Dshi_3655 Dshi_3988	Type VI secretion system protein, TraG/TraD family protein	*virD1*	(911) 2004 (912) 2001	56453 pDshi01 49682 pDshi03	R	2	0
Dshi_3758 Dshi_4034	Transposase		(80) 390	162102 pDSHI01 98681 pDSHI03	F	2	0
Dshi_3679 Dshi_3875 Dshi_4082	Integrase catalytic region (transposase)		(1411) 1494	81922 pDSHI01 95640 pDSHI02 18389 pDSHI04	F R R	2	0
Dshi_3678 Dshi_3874 Dshi_4083	ATP-binding protein, putative transposase		(782)825	81061 pDSHI01 94779 pDSHI02 19250 pDSHI04	F R R	2	0
Dshi_3678 Dshi_3874 Dshi_4083	ATP-binding protein, putative transposase		(223) 825	81620 pDSHI01 95338 pDSHI02 18691 pDSHI04	F R R	0-1	0
Dshi_4023	Plasmid partitioning protein RepA	*repA*	(-173) 1188	91461 pDSHI03	R	2	0
Cell envelope							
Dshi_0027	Fatty acid desaturase	*alkB2*	(570) 1155	31237 chromosome	R	2	0
Dshi_0808	Membrane bound transglycosylase and penicillin-binding protein	*mipA*	(-11) 744	817061 chromosome	R	2	0
Dshi_1766	Pepidoglycan-binding protein LysM	*lysM*	(103) 1596	1834072 chromosome	R	2	0
Dshi_2238	Periplasmic binding protein/LacI transcriptional regulator		(676) 1035	2362666 chromosome	F	2	1
Dshi_3403	AMP-dependent synthetase and	*fadK*	(1114) 1740	3581380	F	2	0

	ligase			chromosome			
Dshi_3576	Glycosyl transferase family 2		(1223) 1233	3767137 chromosome	F	2	0
Dshi_3628	Bacterial outer membrane protein		(113) 696	28869 pDshi01	F	2	0
Transport							
Dshi_3624 Dshi_3962	Co/Zn/Cd efflux system component		(607) 621	26518 pDSHI01 27299 pDSHI03	F	2	0
Dshi_3626 Dshi_3964	Co/Zn/Cd resistance protein		(303) 966	27457 pDSHI01 28238 pDSHI03	F	2	0
Dshi_3796	ABC transporter (importer) ATP-binding protein	*oppD*	(1686) 1002	5423 pDSHI02	F	0-1	0
Others							
Dshi_0750	Conserved hypothetical protein		(665) 795	761660 chromosome	F	2	1
Dshi_1277	Hypothetical protein		(181) 243	1327255 chromosome	F	2	0
Dshi_2726	Hypothetical protein		(157) 405	2888483 chromosome	F	2	1
Dshi_3364	Flagellar hook-length control protein	*fliK*	(314) 2337	3535981 chromosome	R	2	0
Dshi_3673	Hypothetical protein		(176) 969	74815 pDSHI01	R	2	0-1

[1]Transposon direction

Surprisingly, also mutation of the assimilatory NADH-dependent nitrate reductase encoding gene *nasA* (Dshi_1669) led to a significant decrease in anaerobic growth (Table 2.1). The *nasA* gene is localized upstream of the *nasDE* genes encoding the assimilatory nitrite reductase. During nitrogen assimilation, ammonium is generated through the reduction of nitrate via nitrite in the cytoplasm (Moreno-Vivián *et al.*, 1999). However, the growth medium was supplemented with sufficient ammonium during the selection process excluding a general defect in the nitrogen metabolism. In agreement, no aerobic phenotype was observed. Furthermore, mutation in the *nasD* gene (Dshi_1667) encoding one of the assimilatory nitrite reductase subunits, did not result in an anaerobic growth phenotype under denitrifying conditions (Table 2.3). Nevertheless, the amount of transcript of the whole *nas*-operon did not change between aerobic and anaerobic conditions. In conclusion, the observed anaerobic growth phenotype for the *nasA* mutant in the presence of ammonium underscores the importance of this enzyme for dissimilatory denitrifying growth. Alternatively, a novel yet unknown function of nitrite under anaerobic growth conditions can be conducted.

Table 2.2: Comparison of growth phenotypes, fold change of gene expression after 30 min of oxygen depletion and presence of cytoplasmic and membrane proteins under anaerobic, denitrifying conditions. The (2) stands for normal growth, (1) for decreased growth, (-) for no growth, (o) not detected, (+) for detected. In red are the induced genes which revealed an anaerobic growth phenotype upon transposon insertion.

Locus Tag	Gene Name	Function of gene product	Transposon insertion	Growth phenotype	Fold change Transcript anaerob	Presence Protein anaerob
Dshi_3180	*nirS*	Nitrite reductase precursor	+	2	31.6	+
Dshi_3192		Hypothetical protein	+	2	14.2	o
Dshi_3195	*nosD*	Nitrous oxide maturation protein	+	2	12.8	o
Dshi_2278	*dmsA1*	Dimethyl sulfoxide reductase precursor	+	2	11.7	o
Dshi_0542		Phosphate transporter	+	2	8.3	o
Dshi_3173	*nirJ*	Putative nitrite reductase heme biosynthesis J protein	+	2	6.6	o
Dshi_2304		Putative regulator of cell morphogenesis and NO signaling	+	nD	6.2	+
Dshi_0664	*fixP*	Cytochrome *c* oxidase, *cbb3*-type, subunit III	+	2	5.7	+
Dshi_3165	*napA*	Nitrate reductase catalytic subunit	+	-	4.4	+
Dshi_0543		Na^+/P_i-cotransporter	+	-	3.5	o
Dshi_3152		Protein of unknown function DUF1445	+	1	3.5	o
Dshi_1449		TonB-dependent receptor	+	nD	3.3	o
Dshi_3163	*napH*	Ferredoxin-type protein NapH	+	2	3.2	o
Dshi_2233	*phbC*	Poly-beta-hydroxybutyrate polymerase	+	2	3.1	+
Dshi_3558		Hypothetical protein	+	2	3.1	+
Dshi_1968	*aceE*	Pyruvate dehydrogenase subunit E1	+	2	3.0	+
Dshi_3066	*atoB*	Acetyl-CoA acetyltransferase	+	2	2.9	+
Dshi_2363	*ureE*	UreE urease accessory domain-containing protein	+	2	2.7	o
Dshi_0432	*arcA*	Arginine deiminase	+	2	2.5	o
Dshi_3590		NADH dehydrogenase (ubiquinone)	+	2	2.1	+
Dshi_0563	*irpA*	Iron-regulated protein	+	2	2.1	+
Dshi_2052		Hypothetical protein	+	2	2.1	o
Dshi_2966	*panB*	3-Methyl-2-oxobutanoate hydroxymethyltransferase	+	2	2.1	o
Dshi_0426		Hypothetical protein	+	2	2.1	o
Dshi_3805	*phaA*	NADH dehydrogenase	+	-	2.0	+
Dshi_3249	*fliE*	Flagellar hook-basal body protein FliE	+	2	1.9	o
Dshi_2965		Hypothetical protein	+	2	1.8	o
Dshi_3553	*Acs*	Acetate--CoA ligase	+	2	1.8	+
Dshi_0540		NnrU family protein	+	2	1.8	+
Dshi_1399	*acsA*	Acetate--CoA ligase	+	2	1.8	+

2.4.5 Molybdopterin cofactor biosynthesis for nitrate reductase formation is essential under anaerobic growth conditions

The nitrate reductase NapAB contains a molybdopterin cofactor (Moco), iron-sulfur clusters and a cytochrome *c* subunit. The nitrate reductase NasA is also an iron-sulfur cluster and Moco containing enzyme (Gates *et al.*, 2011). Consequently, nitrate reductase formation in general requires the biosynthesis of cofactors including molybdopterin, heme and iron sulfur-clusters (Grimaldi *et al.*, 2013; Iobbi-Nivol & Leimkühler, 2013). Therefore, it was not surprising that transposon mutants with defects in *moeB* (Dshi_2974) and *moaB* (Dshi_3089) encoding enzymes of molybdopterin biosynthesis were not able to grow under denitrifying conditions (Table 2.1). However, the expression of both genes was found not induced under anaerobic conditions. The MoeB protein was exclusively observed under anaerobic conditions in the proteome of *D. shibae* suggesting a posttranscriptional control of MoeB formation (Table 2.3). During Moco biosynthesis MoeB catalyzes the adenylation of the MoaD subunit of the molybdopterin synthase MoaDE (Dahl *et al.*, 2011; Zhang *et al.*, 2010). MoaB catalyzes the adenylation of the metal-binding pterin (MPT) to prepare molybdenum insertion (Bevers *et al.*, 2008). How is Moco made in *D. shibae* under anaerobic conditions without MoeB and MoaB? The structural homologue MogA substitutes for MoaB function in other organisms (Bevers *et al.*, 2008). However, the potential *mogA* gene (Dshi_0119) of *D. shibae* encodes rather a Moco binding protein than a real MogA. This leaves the question for the aerobic Moco biosynthesis without MoeB and MoaB open. The unaffected growth of both mutants under aerobic conditions suggested that other yet unknown enzymes of *D. shibae* complement the defect or that *D. shibae* does not have an essential Moco-dependent enzyme under the aerobic growth conditions tested.

2.4.6 Mutants affecting cytochrome *c* and disulfide bond formation

The nitrate reductase NapAB and the nitrite reductase NirS both require cytochrome *c* as cofactor and electron transfer molecule. The nitrate reductase NapAB was shown to be essential for anaerobic growth (see above). Mutants in Dshi_3082 (*dsbC*), plasmid encoded Dshi_3606/3944 (potential *dsbD*) and Dshi_3777/4053 (*ccmH*) carried defects in genes involved in disulfide bond formation and cytochrome *c* formation. The disulfide bond formation machinery is part of cytochrome *c* formation. Mutants in these genes showed a loss of anaerobic growth, two of them without influence on aerobic growth (*dsbC, ccmH*). One

mutant (*dsbD*) was also found to be reduced in aerobic growth. *D. shibae* possesses two identical cytochrome c biosynthesis gene clusters (*ccmFGHI-dsbD*) on the sister plasmids pDSHI01 and pDSHI03. Consequently, the exact localization of the transposon insertion site was not possible by the performed sequencing approach. As a consequence, the employed DNA microarray approach cannot distinguish between the identical *dsbD* and *ccmH* genes. However, neither of the clusters was differentially expressed during aerobic and anaerobic growth. In agreement the protein CcmH was detected under aerobic and under anaerobic denitrifying conditions (Table 2.3). The distinct behaviour of the isolated mutants indicated that only one of the clusters is functional because they obviously were not able to compensate for each other. For the further description of the various systems of disulfide bond and cytochrome *c* formation please consult the Supplemental Material. Multiple mutations in other genes of the cytochrome *c* biogenesis pathway did not result in an aerobic or anaerobic phenotype. Obviously, plasmid encoded *D. shibae ccmH* and most likely *dsbC*/*dsbD* are essential for the formation of the anaerobic cytochrome *c* biogenesis machinery.

2.4.7 Plasmid encoded cytochrome *c* is essential for anaerobic growth in *D. shibae*

One transposon was found integrated in Dshi_3887 localized on plasmid pDSHI02 encoding the class I cytochrome *cccA*. The *cccA* gene expression was found slightly enhanced under anaerobic growth conditions, indicating a role under denitrifying conditions. Class I cytochrome *c* molecules are small soluble cytochromes, which are needed for electron transfer reactions during denitrification in other bacteria (Zumft, 1997). In *Neisseria gonorrhoeae* the *cccA* gene product cytochrome *c2* is essential for the shuttling of electrons towards the denitrification machinery (Hopper *et al.*, 2013). Several other unclassified class I cytochromes of *D. shibae* (Dshi_0508, Dshi_2868) did not influence anaerobic growth. The expression of these genes was found to be down-regulated or unaffected (Table 2.3). Obviously, the transposon has identified an essential cytochrome involved in the initial steps of denitrification.

2.4.8 One of three pyruvate dehydrogenases is essential for anaerobic growth

A transposon mutant in gene *pdh2* (Dshi_2159) encoding the E1 component one of the three pyruvate dehydrogenase complexes displayed decreased growth under aerobic conditions and lacked growth under anaerobic conditions (Table 2.1). In general, pyruvate dehydrogenase converts into acetyl-CoA. *D. shibae* possesses 3 loci for pyruvate dehydrogenase, namely *pdhA2B1C2* (Dshi_0534-Dshi_0536), *aceEFlpdA* (Dshi_1968-1970) and *pdhA1B2C1* (Dshi_2158-2160). In contrast to *pdhB2*, inactivation of *pdhB1* (Dshi_0535) did not influence anaerobic growth. However, both the *pdhA1B2C1*- and *pdhA2B1C2*-operon were not found differentially expressed. Consequently, the functional basis for the observed phenotype remains to be determined.

2.4.9 Sodium-dependent transport processes are essential for anaerobic growth

The identification of the Na^+-dependent NADH dehydrogenase PhaA and Na^+-dependent C4-dicarboxylates TRAP transporters (DctM1 and DctM3), as essential for the anaerobic growth of *D. shibae*, pointed towards an important role of the Na^+ gradient (Table 2.1, in detail described and discussed in the Supplemental Material section). Furthermore, Dshi_0543 encodes a type II Na^+/P_i-cotransporter similar to transporters found in *Methylobacter*, *Campylobacter*, *Helicobacter* species and *Pseudomonas stutzeri* (Lebens *et al.*, 2002; Werner & Kinne, 2001). Finally, the mechanosensitive ion channel encoded by Dshi_2998 showed 33% amino acid sequence identity to *E. coli* YbiO (Malcolm & Maurer, 2012). YbiO of *E. coli* revealed NaCl-induced channel activity (Edwards *et al.*, 2012). Finally, Dshi_3675 encodes a Na^+/H^+ exchange protein. Overall, Na^+-gradient-dependent membrane associated processes are essential for the anaerobic growth of *D. shibae*. This might reflect an adaptation of *D. shibae* to its marine habitat.

2.4.10 Potential genome rearrangement as part of the anaerobic adaptation process

Unexpectedly, several genes encoding phage-related proteins and transposases were found essential for anaerobic growth of *D. shibae*. The gene Dshi_2174 encodes a phage capsid

protein and is part of a large operon from Dshi_2176 to Dshi_2161 encoding a complete HK97 type (pro)phage (Juhala *et al.*, 2000). These phages were described to carry so called morons, DNA elements which increase host fitness (Cumby *et al.*, 2012). A corresponding lambda prophage of *E. coli* increased mammalian host cell binding and resistance to killing (Barondess & Beckwith, 1990, 1995). The *Salmonella* phages Fels-2 and GIFSY-2 carried morons encoding superoxide dismutase which sustained bacterial fitness during host infection (Figueroa-Bossi & Bossi, 1999). Many morons provide resistance to phage superinfections (Uc-Mass *et al.*, 2004; Lu & Henning, 1994; Lu *et al.*, 1993). Inspection of the genes downstream of Dshi_2174 identified genes of unknown function between the classical phage genes, however, without providing an explanation for the observed anaerobic growth phenotype.

Another surprise observation was that the transposon mutants found in Dshi_3356, encoding an ISR1 insertion element protein A3 (Priefer *et al.*, 1989), and in Dshi_3655, which encodes a type IV secretory TRAG-type family protein involved in DNA transfer, were located in the vicinity of numerous genes whose products are predicted to be to be involved in DNA transport function. Similarly, Dshi_3628 and Dshi_3678 are part of inserted transposons. Furthermore, the anaerobically essential gene Dshi_3758 encodes a transposase of an IS4 element. The gene Dshi_2313 encodes a HsdR family type I DNase, as part of a restriction/modification system (Simons & Szczelkun, 2011). In *Mycoplasma* the HsdSMR enzyme system has been shown to be activated by high-frequency gene rearrangements (Dybvig *et al.*, 1998) and the whole system is controlled by proteolysis (Makovets *et al.*, 1999). Overall, genetic mobility and rearrangement, most likely involving the highly conserved areas of the plasmids are an integral part of the adaptation strategy of *D. shibae* to anaerobic conditions.

2.4.11 Anaerobic growth requires proteases, peptide transport, restructuring of the cell envelope, cation efflux proteins and FliK

The residual found transposon mutants are described and discussed in the Supplemental Material.

2.4.12 Adaptation strategy of *D. shibae* to anaerobic growth conditions

Obviously, solely nitrate reductases and the corresponding cofactor formation (Moco, Cyt*c*) are the crucial parts of energy conversation under anaerobic growth conditions. The residual denitrification machinery, which is significantly induced under anaerobic conditions, further sustains anaerobic growth without being essential. Some of the anaerobically essential genes are plasmid-encoded. Clear evidence for the importance of a Na^+-gradient for anaerobic growth of *D. shibae* was found. Another surprise was the essential role of genome restructuring genes localized on phages, transposons and IS elements. The cell envelope has to be restructured and due to the fact that a set of proteases appears to be required to allow anaerobic growth this might suggest they are linked to cell-wall restructuring. Overall, new surprising insights into the adaptation of the marine model bacterium *D. shibae* to oxygen-limiting conditions were obtained.

2.5 Acknowledgement Part I

This work was funded by the transregional Collaborative Research Consortium 51 of the Deutsch Forschungs Gesellschaft. We thank Vanessa Hering and Annika Michel for support.

2.6 Supplemental Material Part I

The network of chromosomal and plasmid encoded genes for the adaptation of the marine bacterium *Dinoroseobacter shibae* to anaerobic conditions.

Matthias Ebert[1§], Sebastian Laaß[1§], Melanie Burghartz[1], Jörn Petersen[2], Sebastian Koßmehl[3], Lars Wöhlbrand[3], Ralf Rabus[3], Christoph Wittmann[4], Petra Tielen[1#], Dieter Jahn[1]

[1]Institute for Microbiology, Technische Universität Braunschweig, D-38106 Braunschweig, Germany
[2]Leibniz-Institut DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Inhoffenstraße 7 B, D-38124 Braunschweig, Germany
[3]Institut für Chemie und Biologie des Meeres, Carl von Ossietzky Universität Oldenburg, Carl-von-Ossietzky Str. 9-11, D-26111 Oldenburg
[4]Institute of Biochemical Engineering, Technische Universität Braunschweig, D-38106 Braunschweig, Germany

[§]Authors contributed equally.

Table S1, dataset for transposon mutants

(Table S1 is deposit according to its size under
http://jb.asm.org/content/195/20/4769/suppl/DCSupplemental)

2.6.1 Establishment of a mariner-based transposon system for *D. shibae*

In the initial step of our investigations it was necessary to define suitable parameters for the transfer of a transposon into the genome of *D. shibae*. First, the plasmid pBT20 encoding a mariner transposon was chosen (Fig. 2.1). It further harbors the C9 mariner transposase necessary for random recombination and transposon integration. The plasmid contains two origins of replication. The *oriT* from the broad host range plasmid pRK2 allows for conjugation into Gram-negative bacteria (O'Toole *et al.*, 1999). With its origin of replication R6Kγ (IncX) the plasmid pBT20 can only be replicated in strains expressing *pir* (Matsumoto-Mashimo *et al.*, 2004). In *pir*-negative recipients like *D. shibae* the plasmid should behave like a suicide vector mediating plasmid loss and selection for integrated transposons as observed for other bacteria (O'Toole *et al.*, 1999; Herrero *et al.*, 1990). A corresponding procedure was established and systematically optimized to finally obtained 9.0 x 10^3 transposon mutants/per 2.5 x 10^8 bacteria. Precultures of *D. shibae* DFL12^T (acceptor strain) and *E. coli* ST18 (donor strain) were incubated under indicated different growth conditions. In the exponential growth phase, co-cultures of both strains were prepared in a volume ratio of 10:1 of donor to acceptor strain. For this purpose *D. shibae* and *E. coli* ST18 cell cultures were mixed and sedimented together for 4 min (4000 x g). The supernatant was discarded and the cell material resuspended in hMB medium. Spots of the co-cultures were incubated for conjugation on hMB-agar plate supplemented with 50 µg/ml aminolevulinic acid for 24 h at 30 °C. The *D. shibae* DFL12^T transposon-mutants were subsequently selected on hMB-agar plates supplemented with 80 µg/ml gentamycin. For this purpose, serial dilutions of the conjugation cultures of 10^{-1}-10^{-7} were plated to maximize the efficiency. Single transposon mutants were isolated and preserved.

2.6.2 Localization of the loci of transposon insertion in the DNA of *D. shibae*

For the localization of the integrated transposons in the chromosome or the plasmids of *D. shibae* an arbitrary PCR approach was used (O'Toole *et al.*, 1999). This method allows the amplification of DNA fragments consisting of 250 bp of the transposon DNA and a random length part from the genome or plasmids of *D. shibae* (Fig. 2.2a). The insertion loci were finally identified via DNA sequence determination of the arbitrary PCR products. Randomly selected mutants showed PCR products from 270 bp up to 2000 bp (Fig. 2.2b). The obtained

DNA sequences for the various transposon integration sites indicated that no hot spots of integration were present.

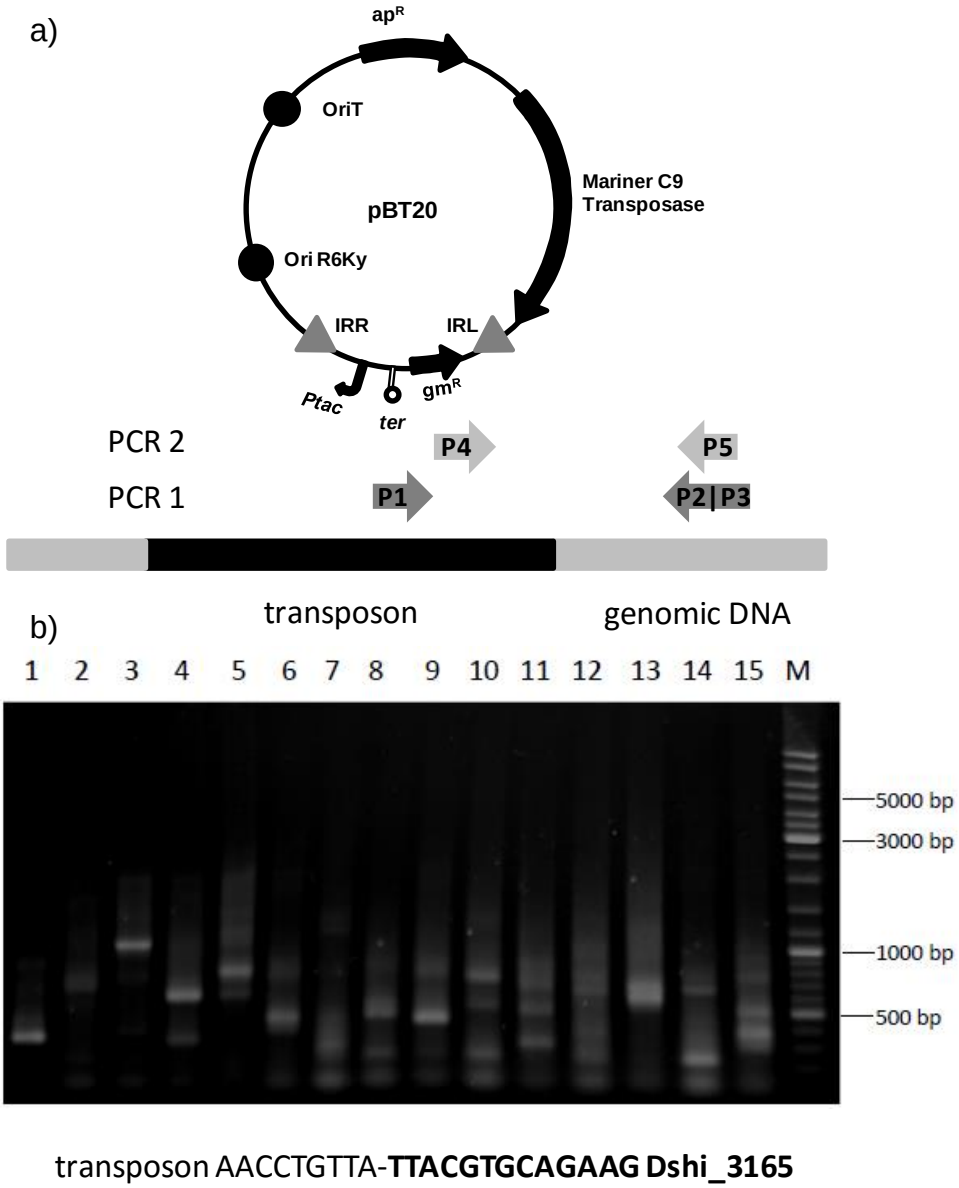


Fig. 2.2: Experimental approach of transposon mutagenesis and insertion site localization. The structure of the employed mariner transposon carrying plasmid pBT20 is depicted (a). Below the strategy of arbitrary PCR approach is shown (b). Arrows represent the annealing location and orientation of the used primers. The first PCR-round contained primers 1, 2 and 3. The second PCR-round included primers 4 and 5 (modified after O'Toole *et al*., 1999). Analysis of arbitrary PCR products. Obtained PCR products were separated by agarose gel electrophoreses and visualized by ethidium bromid staining. Shown are the used marker and lanes 1 to 15 display the PCR products from different *D. shibae* DFL12^T transposon mutants.

2.6.3 Selection of transposon mutants with an anaerobic growth phenotype

The isolated 4500 *D. shibae* transposon mutants were screened for growth defects under anaerobic, denitrifying conditions. For 1580 out of 4500 tested mutants, the loci of integration were identified by DNA sequencing (Table S1). Residual transposon mutants are currently under investigation. Overall, 718 out of 1000 transposon mutants were in different genes. Assuming the presence of approximately 12% essential genes (Jacobs *et al.*, 2003), which do not result in viable transposon mutants upon mutation, a saturation of 82% of the genome can be deducted. From the 4500 tested mutant strains 53 showed a decreased or even loss of growth under tested anaerobic conditions (Table 2.1). This suggests that approximately 1% of the genome of *D. shibae* was found essential or important for anaerobic growth. Besides insertion into the chromosome multiple insertions into the pDSHI01, pDSHI02, pDSHI03 and pDSHI04 were found. In total, *D. shibae* contains 5 plasmids, which are the 191 kb plasmid pDSHI01, the 153 kb plasmid pDSHI02, the 126 kb plasmid pDSHI03, the 86 kb plasmid pDSHI04 and the 72 kb plasmid pDSHI05 (Wagner-Döbler *et al.*, 2010). In figure 1 of the results section the random distribution of transposon integration sites resulting in anaerobic growth defects of corresponding strains is shown. Three genes were hit twice by the transposon – *napA* encoding the nitrate reductase, the promoter region of the transposase gene Dshi_3356 and the plasmid encoded gene Dshi_3678/3874/4083. For eight plasmid encoded genes the final identification of the loci of integration failed, because they exists as multiple copies on the various plasmids of *D. shibae* (Wagner-Döbler *et al.*, 2010). Interestingly, no transposon insertion was found for plasmid pDSHI05 indicating that genes encoded by this plasmid do not play a role in anaerobic growth. As expected, accumulation of transposon integration sites was observed between region 3142258 to 3767137 bp of the *D. shibae* chromosome (Fig. 2.1). This region contains several known genes and operons involved in anaerobic metabolism (Wagner-Döbler *et al.*, 2010).

Table 2.3: Transcriptional profiling of gene classes including essential genes for anaerobic growth. Maximal fold change of gene expression within 2 h of oxygen depletion and presence of cytoplasmic and membrane proteins under anaerobic, denitrifying conditions. (o) not detected, (+) detected

Locus tag	Gene name	Function of the gene product	Fold change/Detection		
			Transcript	Protein	
			anaerob	aerob	anaerob
Denitrification					
Dshi_3161	*napC*	NapC/NirT cytochrome *c* domain-containing protein	2.9	o	+
Dshi_3162	*napB*	Nitrate reductase cytochrome *c*-type subunit (NapB)	2.5	o	+
Dshi_3163	*napH*	Quinol dehydrogenase membrane component	3.2	o	o
Dshi_3164	*napG*	NapG family ferredoxin-type protein	3.0	o	o
Dshi_3165	*napA*	Nitrate reductase catalytic subunit	4.4	+	+
Dshi_3166	*napD*	NapD family protein	3.6	o	o
Dshi_3167	*napF*	Ferredoxin-type protein NapF	1.4	o	o
Dshi_1667	*nasD*	Nitrite reductase (NAD(P)H), large subunit	1.2	o	o
Dshi_1668	*nasE*	Nitrite reductase (NAD(P)H), small subunit	1.1	o	o
Dshi_1669	*nasA*	Molybdopterin oxidoreductase	-1.0	o	o
Dshi_1670		Hypothetical protein	1.0	o	o
Dshi_1671	*cysG*	Uroporphyrin-III C-methyltransferase	1.1	o	o
Dshi_0323		Ferredoxin	-1.3	o	o
Dshi_0540		NnrU family protein	1.8	+	+
Dshi_3180	*nirS*	Nitrite reductase precursor	31.6	o	+
Dshi_3181	*nosR2*	Nitrous oxide reductase regulatory protein NosR	13.0	o	+
Dshi_3192		Hypothetical protein	14.2	o	o
Dshi_3195	*nosD*	Nitrous oxide maturation protein	12.8	o	o
Molybdopterin biosynthesis					
Dshi_2974	*moeB*	Molybdopterin biosynthesis protein	1.1	o	+
Dshi_3089	*moaB*	Molybdopterin binding domain	-1.1	+	+
Dshi_1290	*moaA*	Molybdenum cofactor biosynthesis protein A	-1.4	+	+
Dshi_3482	*modB*	Molybdenum transport system permease protein ModB	-1.1	o	o
Dshi_3483	*modC*	Molybdenum import ATP-binding protein ModC	-1.1	o	o
Cytochromes *c* and its biosynthesis					
Dshi_0508		Cytochrome *c* class I	-1.2	o	o
Dshi_1932		Glutathione S-transferase	-1.8	o	o

Dshi_2081		Putative cytochrome *c*	-2.5	o	o
Dshi_2868		Cytochrome *c*	-1.6	o	o
Dshi_3082	*dsbC*	Putative *C*-type cytochrome biosynthesis protein	-1.2	o	o
Dshi_3407	*dsbD*	Thiol:disulfide interchange protein DsbD	1.4	+	+
Dshi_3606 Dshi_3944		Cytochrome *c* biogenesis protein transmembrane region	-1.0	o	o
Dshi_3620	*dsbA1*	DSBA oxidoreductase	-1.5	+	+
Dshi_3621	*dsbB*	Disulfide bond formation protein	-1.2	o	o
Dshi_3775	*ccmF*	Cytochrome *c*-type biogenesis protein CcmF	-1.2	o	+
Dshi_3776	*ccmG*	Periplasmic protein thiol disulphide oxidoreductase DsbE	1.0	+	+
Dshi_3777 Dshi_4053	*ccmH*	Cytochrome *c* biogenesis protein	-1.1	+	+
Dshi_3778	*ccmI*	TPR repeat-containing protein	-1.1	+	+
Dshi_3779	*dsbD*	Thiol:disulfide interchange protein DsbD precursor	1.3	o	o
Dshi_3887	*cccA*	Cytochrome *c* class I	1.2	o	o
Dshi_3894		Cytochrome *c*	1.2	o	o
Anaerobic electron transport chain					
Dshi_0451	*pqqB*	Coenzyme PQQ biosynthesis protein B	-1.6	o	o
Dshi_0452	*pqqC*	Coenzyme PQQ biosynthesis protein C	-1.6	o	o
Dshi_0473		Alcohol dehydrogenase class III/S-(hydroxymethyl)glutathione dehydrogenase	-1.5	o	o
Dshi_0476	*gcd*	Quinoprotein glucose dehydrogenase	-2.1	+	+
Dshi_0504	*fdnG*	Formate dehydrogenase alpha chain	-1.9	+	+
Dshi_0664	*fixP*	Cytochrome c oxidase	5.7	+	+
Dshi_0728	*mnhA*	NADH dehydrogenase (quinone)	-1.1	o	o
Dshi_0729	*mnhB*	Na^+/H^+ antiporter MnhB subunit-related protein	-1.1	o	o
Dshi_0730	*mnhC*	Putative monovalent cation/H^+ antiporter subunit C	-1.1	o	o
Dshi_0731	*mnhD*	NADH dehydrogenase (quinone)	-1.1	o	o
Dshi_0732	*mnhE*	Cation antiporter	-1.1	o	o
Dshi_0733	*mnhF*	Multiple resistance and pH regulation protein F	-1.2	o	o
Dshi_0734	*mnhG*	Monovalent cation/proton antiporter, MnhG subunit	-1.0	o	o
Dshi_0948	*lldD2*	L-lactate dehydrogenase	1.2	+	o
Dshi_1140		Cytochrome c oxidase subunit II	-4.2	+	+

Dshi_1144	*ctaE*	Cytochrome c oxidase subunit II	-2.9	o	o
Dshi_1281	*fdhB*	Respiratory-chain NADH dehydrogenase domain	1.2	o	o
Dshi_1282	*fdhA*	Complex with *fdhB*, Molybdopterin oxidoreductase, contains Fe-S cluster	1.0	o	o
Dshi_1328	*nuoM*	Proton-translocation NADH-quinone oxidoreductase	1.3	+	+
Dshi_1954		putative short-chain dehydrogenase	-1.1	+	o
Dshi_2278	*dmsA*	Dimethyl sulfoxide reductase precurser	11.7	o	o
Dshi_3324	*dld2*	D-lactate dehydrogenase	1.0	o	o
Dshi_3590		Ubiquinone dependent NADH dehydrogenase	2.1	+	+
Dshi_3805	*phaA*	NADH dehydrogenase	2.0	+	+
Dshi_3806	*phaC*	Putative monovalent cation/H^+ antiporter subunit	1.2	+	+
Dshi_3807	*phaD*	Putative monovalent cation/H^+ antiporter subunit	1.2	+	+
Dshi_3808	*phaE*	Putative monovalent cation/H^+ antiporter subunit	1.1	o	o
Dshi_3809	*phaF*	Multiple resistance and pH regulation protein	1.3	o	+
Dshi_3810	*phaG*	Monovalent cation/proton antiporter, PhaG subunit	1.3	o	o
Photosynthesis					
Dshi_3524	*pufM*	Reaction center protein M chain	-1.1	+	+
Dshi_3525	*pufC*	Photosynthetic reaction center cytochrome c subunit precurser	-1.1	+	+
Dshi_3544	*acsF*	Aerobic magnesium-protoporphirin IX monomethyl ester	1.0	+	+
Fermentation					
Dshi_0432	*arcA*	Arginine deminase	2.5	o	o
Dshi_1825	*pta1*	Phosphate acetyl transferase	1.0	o	o
Dshi_3553	*Acs*	Acetyl-coenzym A synthetase	1.8	+	+
Central metabolism					
Dshi_0535	*pdhB1*	Pyruvate dehydrogenase E1 component subunit beta	-1.5	o	+
Dshi_1227	*glcB*	Malate synthase G	-2.1	o	o
Dshi_1966	*lpdA*	Dihydrolipoyl dehydrogenase	1.3	+	+
Dshi_1968	*aceE*	Pyruvate dehydrogenase E1 component	3.0	o	+
Dshi_2158	*pdhA1*	Pyruvate dehydrogenase (acetyl-transferring)	-1.1	+	+
Dshi_2159	*pdhB2*	Pyruvate dehydrogenase subunit beta	-1.9	+	+
Dshi_2160	*pdhC1*	Branched-chain alpha-keto acid dehydrogenase subunit E2	-2.4	+	+

Dshi_2485	*pyc*	Pyruvate carboxylase	-1.1	+	+
Dshi_2490	*citE1*	Citrate lyase	-1.7	o	o
Dshi_2491	*sucC2*	Succinyl-CoA synthetase	-2.3	o	o
Dshi_2876	*mdh*	Malate dehydrogenase	1.1	+	+
Potential Na^+-dependent membrane processes					
Dshi_0699	*dctM1*	TRAP dicarboxylate transporter, DctM subunit	-1.1	o	o
Dshi_0743	*mcsS*	MscS mechanosensitive ion channel	1.1	o	o
Dshi_1035	*dctP*	TRAP dicarboxylate transporter- DctP subunit	-1.9	o	o
Dshi_1036	*dctQ*	Tripartite ATP-independent periplasmic transporter DctQ	-1.6	+	+
Dshi_1037	*dctM1*	TRAP dicarboxylate transporter, DctM subunit	-1.4	o	o
Dshi_1709	*mscS*	MscS mechanosensitive ion channel	-1.4	+	+
Dshi_1816	*mscS*	MscS mechanosensitive ion channel	1.1	o	+
Dshi_2998	*mscS*	MscS mechanosensitive ion channel	-1.3	+	+
Dshi_3326	*dctP3*	TRAP dicarboxylate transporter- DctP subunit	-2.1	+	+
Dshi_3328	*dctM4*	TRAP dicarboxylate transporter, DctM subunit	-1.4	o	o
Dshi_3395	*dctM3*	TRAP C4-dicarboxylate transport system permease DctM subunit	-1.3	o	o
Dshi_3396	*dctQ*	Tripartite ATP-independent periplasmic transporter DctQ	-1.6	o	+
Dshi_3397	*dctP*	TRAP dicarboxylate transporter- DctP subunit	-1.8	+	+
Dshi_3905	*mscS*	MscS mechanosensitive ion channel	1.2	+	o
Dshi_4182	*mscS*	MscS mechanosensitive ion channel	1.1	o	o
Peptidases and peptide transporters					
Dshi_0655	*oppA*	ABC peptide transporter	-1.1	+	+
Dshi_0658	*oppDF*	ABC peptide transporter	-1.2	+	+
Dshi_0841		Hypothetical protein	-1.3	o	o
Dshi_1223	*pepN*	Aminopeptidase N	1.1	o	o
Dshi_1777		ATP-dependent protease	-1.0	+	+
Dshi_1883		Putative ClpA/ClpB family protein	-1.4	+	+
Dshi_3624 Dshi_3962		Co/Zn/Cd efflux system component	1.1	o	o
Dshi_3626 Dshi_3964		Co/Zn/Cd resistance protein	-1.0	o	o
Dshi_3625 Dshi_3963		Hypothetical protein	-1.1	o	o
Dshi_3796	*oppD*	ABC transporter (importer)	-1.1	o	o

		ATP-binding protein			
Phages, transposons, insertion elements, DNA restructuring enzymes					
Dshi_1643	*recA*	Bacterial DNA recombination	-1.1	+	+
Dshi_2174		Putative phage capsid protein	1.0	+	+
Dshi_2177		Phage portal protein, HK97 family	1.2	o	o
Dshi_3758 Dshi_4034		Transposase	-1.1	o	o
Dshi_3679 Dshi_3875 Dshi_4082		Integrase catalytic region (transposase)	1.2	o	o
Dshi_3678 Dshi_3874 Dshi_4083		ATP-binding protein, putative transposase	1.1	o	o
Dshi_3678 Dshi_3874 Dshi_4083		ATP-binding protein, putative transposase	1.1	o	o
Dshi_4023	*repA*	Regulator protein RepA	-1.4	+	+
Cell envelope					
Dshi_0027	*alkB1*	Fatty acid desaturase	-1.0	o	o
Dshi_0543		Na^+/P_i-cotransporter	3.5	o	o
Dshi_0750		Conserved hypothetical protein	-1.4	+	+
Dshi_0808	*mipA*	Membrane bound transglycosylase and penicillin-binding protein	1.0	+	+
Dshi_1134		3-Oxo acid-CoA-transferase (B subunit)	-1.7	+	+
Dshi_1277		Hypothetical protein	-1.0	o	o
Dshi_1766	*lysM*	Pepidoglycan-binging protein LysM	1.0	+	+
Dshi_2238		Periplasmic binding protein/LacI transcriptional regulator	-1.0	o	o
Dshi_2312		Type I restriction-modification system (R subunit)	1.2	o	o
Dshi_2726		Hypothetical protein	1.0	o	o
Dshi_3168	*apbE*	ApbE family lipoprotein	23.5	o	o
Dshi_3673		Hypothetical protein	1.2	o	o
Dshi_3708		AraC-like ligand binding domain	-1.1	o	o
Dshi_3872		Hemolysin-type calcium-binding protein	1.1	o	o

2.6.4 Genes essential for aerobic and anaerobic growth of *D. shibae*

Table 2.1 provides an overview over the functional categories for the genes for which the 53 transposon mutants were isolated. These categories are described and discussed in the results section and here in the Supplemental Material. Only 5 of the obtained mutants showed a

decreased growth under aerobic conditions indicating a general role for the *D. shibae* life cycle. For example, Dshi_1643 encoding RecA, which is essential for the repair and maintenance of DNA, was disrupted by the transposon close to the end of the gene. Partial activity might be retained. Nevertheless, the significant decrease of growth under aerobic conditions and complete loss of growth under anaerobic conditions showed the general importance of this gene for *D. shibae*. Accordingly, when the *recA* gene was deleted in *E. coli* a growth rate decrease by 50 % was observed under anaerobic conditions compared to the wildtype (Kouzminova *et al.*, 2004).

A similar phenotype was observed for disrupted gene Dshi_1932, encoding a putative glutathione-S-transferase. Glutathione S-transferase catalyzes the conjugation of the reduced tripeptide glutathione via the sulfhydryl groups to electrophilic substrates. In eukaryotes substrates are made soluble and accessible to detoxification this way. Multiple families of the enzyme catalyzing a broad variety of reactions were described (Board & Menon, 2013). In contrast glutathione and the glutathione-S-transferase possess various controversially discussed functions in bacteria (Vuilleumier, 1997). They are involved in the protection against oxidative stress, in the maturation of proteins, in the metabolism of aromatic compounds and in antibiotic resistance (Allocati *et al.*, 2012). Interestingly, the enzyme was also found in the periplasm contributing to redox processes, including disulfide bond formation (see results and below) and cytochrome c formation (Eser *et al.*, 2009). Our findings underscore the importance of the enzyme for *D. shibae*, especially for anaerobic growth.

2.6.5 Transcriptome and proteome of aerobically and anaerobically grown *D. shibae*

To identify anaerobically induced genes, transcriptome and proteome analyses were performed. For this purpose *D. shibae* DFL12^T was cultivated in a chemostat using salt water medium (SWM) supplemented with 25 mM nitrate to sustain denitrification when oxygen became limited. After 20 h *D. shibae* reached the steady state with a constant cell density of OD_{578} = 0.5 +/- 0.04. After 40 h of growth the aeration was switched off and the oxygen concentration in the culture decreased within 20 min to 0.05 µM indicating microaerobic to anaerobic conditions. The corresponding transcriptome dataset revealed 474 genes which were differentially expressed by at least 1.74-fold when denitrifying and aerobic growth conditions were compared. Out of the 474 genes 207 were found induced and 267 showed a

decreased expression. Proteome profiles were obtained via shot-gun analyses or inspection of the membrane protein-enriched fraction (both by means of nanoLC-ESI MS). The analyses detected 878 different proteins in the whole cell shot-gun approach and 1215 different proteins in the membrane fraction, which covered nearly 25 % of the predicted proteins of *D. shibae*. Results were compared with the results of the transposon mutagenesis (Table 2.3).

2.6.6 General aspects of cytochrome *c* and disulfide bond formation

Disulfide bond formation in bacteria occurs in the periplasm. Corresponding target proteins are secreted via the Sec-system into the periplasm. The disulfide bridges are then formed by the disulfide bond protein A (DsbA). Recycling of DsbA is performed by the inner membrane protein DsbB, which in turn transfers the electrons to various aerobic and anaerobic electron transport chains of energy generation (Depuydt *et al.*, 2011). DsbC (Dshi_3082) is a protein disulfide isomerase, which corrects DsbA misfolds or introduces non conservative disulfides in periplasmic and outer membrane proteins like LptD (Berkmen *et al.*, 2005; Hiniker & Bardwell, 2004; Vertommen *et al.*, 2008; Denoncin *et al.*, 2010). To fullfill its task DsbC is kept reduced in the periplasm by DsbD, an integral membrane protein of the inner membrane. Our study identified chromosomal *dsbC* and a plasmid encoded *dsbD* gene as essential for anaerobic growth. Both DsbC and DsbD were linked to cytochrome *c* biosynthesis and anaerobic metabolism before (Stirnimann *et al.*, 2005; Metheringham *et al.*, 1996; Kumar *et al.*, 2011). In *E. coli* DsbA, DsbB and DsbD were found essential for anaerobic nitrate and nitrite respiration (Metheringham *et al.*, 1996). In *Xanthomonas oryzae* DsbC was found essential for a pathogenesis in rice (Guo *et al.*, 2012). In *Xylella*, DsbC is required for biofilm formation (Santos *et al.*, 2012).

During cytochrome *c* maturation iron protoporphyrin IX is exported via the Ccm-system through the cytoplasmic membrane into the periplasm and covalently linked via disulfide bridges to an apoprotein (Sanders *et al.*, 2010). Three different machineries for cytochrome *c* formation (system I, II, III) are known. In *D. shibae* most likely analogously to *Rhodobacter capsulatus* (Ekici *et al.*, 2012) the apocytochrome protein gets translocated into periplasm via the Sec-system. Subsequently, DsbA/DsbB, most likely in cooperation with DsbC/DsbD catalyzes the thio-oxireduction of the apocytochrome *c*. The Ccm machinery (CcmABCDEFGH) transports, chaperones, delivers and ligates the heme to the apocytochrome *c* (Richard-Fogal *et al.*, 2012). In this context, a *ccmH* (Dshi_3777/4053) mutant abolished anaerobic growth of *D. shibae*. The CcmH protein is part of the CcmFHI heme ligation complex which forms the stereo-specific thioether bonds between the vinyl

groups of the Fe-protoporphyrin IX and the thiol group of the apocytochrome *c* (Verissimo *et al.*, 2011; Richard-Fogal *et al.*, 2009). Interestingly, mutations of cysteine residues in the active site of *E. coli* CcmH inactivated the protein under aerobic but not anaerobic conditions (Robertson *et al.*, 2008). Clearly, different modes of cytochrome *c* generation exist for anaerobic and aerobic growth conditions.

D. shibae possesses *fixNOQP*- and *cycHJKL*-operons encoding cbb_3-type cytochrome oxidases. Cbb_3-type cytochrome oxidases have a high O_2-affinity and are important for energy generation under microaerobic conditions (Williams *et al.*, 2007). In *P. aeruginosa* it was shown that all of the here outlined cytochrome oxidases are essential for anaerobic growth. The isoforms fulfilled specialized roles under different oxygen tensions. They cannot complement for each other (Comolli & Donohue, 2004). However, in *D. shibae* mutation of *fixP* did not lead to an anaerobic phenotype. As expected the mutant with defect in the aerobic caa_3-type cytochrome *c* oxidase subunit II encoding gene Dshi_1140 was found without anaerobic growth phenotype. Accordingly, the expression of this gene was found decreased under anaerobic conditions (Table 2.3).

2.6.7 Electron donating systems for respiratory energy generation under anaerobic conditions

Membrane localized NADH dehydrogenases serve as primary dehydrogenase of many electron transport chains. Different types of NADH dehydrogenases are known including type I proton translocating (Nuo), type II-non-ion translocating (Ndh) and type III-Na^+-translocating. *D. shibae* possesses genes for all three types of NADH dehydrogenases. The operon encoding the main proton-translocating NADH dehydrogenase I *nuoABCDEFGHIJKLMN* is encoded by the genes Dshi_1307-Dshi_1329. A mutant defect in *nuoM* (Dshi_1328) showed no anaerobic growth defect (Table 2.3) indicating a minor role of the proton-translocation NADH dehydrogenase Nuo for anaerobic energy generation. Accordingly, the transcription of *nuoM* was found uneffected by the switch from aerobic to anaerobic conditions (Table A1, appendix). The genes Dshi_1390 and Dshi_3590 encode two potential type II NADH dehydrogenases (Ndh). Expression of both genes was not influenced by oxygen tension. The *mnhABCDEFG* operon encodes the potential type III NADH dehydrogenase (Dshi_0728-Dshi_0734). The expression of the *mnhABCDEFG*-operon was found slightly decreased under conditions of oxygen depletion (Table 2.3). A second type III NADH dehydrogenase operon *phaACDEF* is located on the plasmid pDSHI02. The gene

phaA (Dshi_3805) was found essential for the anaerobic growth of *D. shibae* (Table 2.1). The gene is part of the *phaACDEF* operon (Dshi_3805-Dshi_3810) encoding a Na^+-translocating type III NADH dehydrogenase (NADH:quinone oxidoreductase). In accordance with its function the expression of the *phaACDEF* gene cluster was found enhanced under conditions of oxygen depletion. Currently, almost nothing is known about the function of the Pha-type NADH dehydrogenase. However, its essential anaerobic functions raises the question for the importance of Na^+-dependent processes under anaerobic conditions in *D. shibae.*

Mutations in other established primary dehydrogenases like glucose dehydrogenase (*gcd*, Dshi_0476), formate dehydrogenase (*fdnG*, Dshi_0504, *fdhD*, Dshi_3282) and lactate dehydrogenase (*lldD2*, Dshi_0948) did not yield an anaerobic phenotype (Table 2.3). Consequently these primary dehydrogenases are not essential for anaerobic growth.

A mutant carrying a defect in gene Dshi_0323, annotated to encode ferredoxin, with amino acid sequence homology to NapF was found unable to grow under oxygen limitation (Table 2.1). Ferredoxins (EC 1.7.7.2) are iron-sulfur proteins that mediate electron transfer for a wide range of metabolic reactions. In several bacteria reduced ferredoxins function as electron donors during the reduction of nitrate to nitrite (Moreno-Vivián *et al.*, 1999) or for the assimilatory reduction of nitrate to ammonium (Jepson *et al.*, 2004; Fujinaga *et al.*, 1999). In agreement, only nitrate reduction was found essential for anaerobic growth. Here we add a Na^+- translocating NADH dehydrogenase and a NapF-like ferredoxin to the essential components of the anaerobic electron transport chains.

2.6.8 Adaptation of the central metabolism to anaerobic growth

The Dshi_1134 gene encodes 3-oxoacid CoA-transferase subunit B, which catalyzes the reaction of 3-oxoacids with succinyl-CoA to obtain activated 3-oxoacyl-CoA. Its exact function for anaerobic growth remains to be determined.

The two C_4-dicarboxylate transporter genes *dctM1* (Dshi_1037) and *dctM3* (Dshi_3395) and a TRAP transporter solute receptor (Dshi_1195) were inactivated during transposon mutagenesis, causing an anaerobic growth phenotype. The first two genes are forming potential operons with *dctP*- and *dctQ*-type genes. Clearly, two tripartite ATP-independent periplasmic (TRAP) transporters for the uptake of succinate, the major carbon source of the used SWM medium, were hit (Forward *et al.*, 1997). However, both potential operons were not found oxygen tension-regulated. Corresponding proteins were detected in our proteome analysis for aerobic and anaerobic growth conditions. In *P. aeruginosa dctPQM* was subject

to catabolite repression via the *crc*-system (Valentini & Lapouge, 2013). Their contribution to the anaerobic metabolism of *D. shibae* remains to be determined. The transposon mutant of Dshi_3708 hit a gene encoding an AraC, helix-turn-helix domain containing, transcriptional regulator. The gene is localized downstream of the *dctPQM*-operon encoded by Dshi_3711-3709. It was proposed that these transporters are high-affinity, Na^+-dependent unidirectional secondary transporters (Mulligan *et al.*, 2011; Mulligan *et al.*, 2009), again pointing towards an important function of Na^+-dependent transport processes for anaerobic growth.

Surprisingly, only few enzymes of the central metabolism were found essential for anaerobic growth. Many enzymes of the citric cycle and fermentation can be eliminated by transposon mutagenesis without major consequences for aerobic or anaerobic growth. Other enzymes might be important for both life styles and therefore not be traceable via the mutagenesis approach. Only one of the pyruvate dehydrogenases was found essential for anaerobic growth. Again, evidence for the importance of Na^+ gradient-dependent processes was obtained.

2.6.9 Proteases are involved in anaerobic growth of *D. shibae*

Four protease encoding genes for aminopeptidase N (Dshi_1223), DNA binding, ATP-depending protease Lon (Dshi_1777), the potential AAA-ATPase subunit of a Clp-type protease (Dshi_1883) and a hemolysin type RTX (repeats-in-toxin) protein (Dshi_3872) were identified with the transposon mutagenesis approach to be essential for anaerobic denitrifying growth (Table 2.1).

The gene Dshi_1223 encodes the aminopeptidase PepN, which is involved in the degradation of the intracellular peptides generated by protein breakdown during the normal growth or in response to nutrient starvation and temperature stress (Bhosale *et al.*, 2013; Chandu & Nandi, 2003). PepN is also a negative regulator of sodium-salicylate-induced stress (Chandu & Nandi, 2003). Interestingly, *Vibrio fisheri* aminopeptidase N is essential for the colonization of the squid *Euprymna scolopes* (Fidopiastis *et al.*, 2012). Analogously, *D. shibae* colonizes dinoflagellates.

The gene Dshi_1883 encodes a putative ClpA/ClpB family protein. This type of ATP-dependent proteases plays a major role in the degradation of misfolded proteins and is induced in response to heat shock and many other stress signals (Fu *et al.*, 1997; van Melderen & Aertsen, 2009; Gottesman, 2003). The gene Dshi_1777 encodes the Lon protease. Lon proteases degrade short-lived regulatory and abnormal proteins in presence of ATP (Fu *et al.*, 1997). Lon proteases negatively control the acid resistance genes of *E. coli*

(Heuveling *et al.*, 2008), bacterial communication via quorum sensing (Bertani *et al.*, 2007; Takaya *et al.*, 2008), motility via flagellar structures (Claret & Hughes, 2000; Tomoyasu *et al.*, 2003), the SOS response to DNA damage (Mizusawa & Gottesman, 1983; Goodman, 2000) and heme biosynthesis (Wang *et al.*, 1999). The mutation of *lon* confers reduced pathogenicity/virulence to many bacteria, for example via regulation of type III secretion system (Butler *et al.*, 2006; Losada & Hutcheson, 2005). Lon proteases activity is controlled by phospholipids, especially cardiolipin (Minami *et al.*, 2011). Finally, Lon protease is essential for the anaerobic survival of *E. coli* during glucose starvation (Luo *et al.*, 2008).
The gene Dshi_3872 encodes a hemolysin-type calcium-binding region protein belonging to the RTX exoprotein family with similarity to the peptidase serralysin (Linhartová *et al.*, 2010). These proteins are exported across the bacterial envelope via a type I secretion system and contain glycine and aspartate rich repeats for Ca^{2+} binding. The target of this protein, maybe the dinoflagellate, remains to be determined. A hemolysin-type transporter is cotranscribed with Dshi_3873. The clear measurable decrease of growth of these mutants under anaerobic conditions compared to the wildtype indicated an important regulatory and restructuring effect of these proteases for the adaptation to anaerobiosis.

2.6.10 Peptide transport is necessary for anaerobic growth

The gene Dshi_3796 encodes the ATP-binding protein OppD of an oligopeptide ABC transporter. The gene is obviously necessary for anaerobic growth of *D. shibae*. The *oppD* gene was not found differently expressed between aerobic and anaerobic conditions (Table 2.1 and Table 2.3). Clearly, no peptides or amino acids are provided by the SWM medium. The Opp transporter was shown to be involved in the transport of small external signal peptides involved in cell-cell communication and intracellular regulation in *Enterococcus faecalis* and other Gram-positive bacteria (Lazazzera, 2001). The use of signal peptides in Gram-negative bacteria is currently discussed. Their essential function to anaerobic growth in *D. shibae* remains to be determined.

2.6.11 Restructuring of the cell envelope during anaerobic growth

Several genes encoding enzymes involved in the restructuring of the cytoplasmic membrane, the cell wall and the lipopolysaccharide layer (LPS) of the outer membrane were found essential for anaerobic growth. The *alkB2* gene (Dshi_0027) encodes an alkane-1-monooxygenase. It is an integral membrane di-iron enzyme which oxidases C_{12} up to C_{20} *n*-

alkanes using molecular oxygen. Acyl lipid desaturases are members of this enzyme family. Differential gene expression for *alkB1* and *alkB2* genes from *P. aeruginosa* in dependence of the growth phase was described (Marín *et al.*, 2003).

The *fadK* gene (Dshi_3403) encodes a short chain acyl-CoA synthetase, which activates fatty acids via the ATP-dependent formation of a fatty acyl-CoA. The acyl-CoAs are central intermediates for fatty acid transport, β-oxidation or phospholipid biosynthesis. The *E. coli fadK* is maximally expressed under anaerobic conditions and repressed in the presence of oxygen (Morgan-Kiss & Cronan, 2004). However, the expression of its *D. shibae fadK* counterpart was not respondinig to oxygen tension. One general explanation of our observations is the proven existence of two distinct pathways for the β-oxidation of lipids under aerobic and anaerobic conditions in bacteria.

The gene Dshi_0808 encodes MipA, a scaffolding protein essential to murein biosynthesis (Vollmer *et al.*, 1999). Several proteins of cell wall formation are coordinated in their function via MipA interaction. The MipA protein was found essential for biofilm formation in *E. coli* and *Salmonella* (Rivas *et al.*, 2008; Giaouris *et al.*, 2013). The expression of the *mipA* gene in *E. coli* responded to the glucose concentration in the medium (Yang *et al.*, 2011a). Interestingly, the *mipA* gene of *E. coli* is regulated by NO via a cascade including the NO sensor NsrR, the alternative sigma factor E and the small RNA RybB (Thompson *et al.*, 2007) indicating its essential function in nitrate respiration. However, no differential *mipA* expression was observed for *D. shibae*.

The gene Dshi_1766 encodes a LysM domain protein. The LysM domain is a binding motif for peptidoglycan (Buist *et al.*, 2008). Obviously, this protein involved in the cell wall metabolism is essential for anaerobically growing *D. shibae*.

Finally, the glycosyl transferse gene Dshi_3576 is forming at its genomic locus an operon with various genes involved in LPS biosynthesis. Changes in the LPS structure in response to anaerobic growth have been reported before (Landini & Zehnder, 2002; Davies *et al.*, 1992).

Obviously, the cell envelope composed of the inner membrane, the cell wall and the outer membrane with its LPS have to adapt to anaerobic growth conditions. Most likely we identified some of the essential players involved in these processes.

2.6.12 Cation efflux proteins sustain anaerobic growth delay

Transition metals are known to cause toxicity under anoxic conditions (Bird *et al.*, 2013). The gene Dshi_3624 encodes the cation efflux system CzcD. It was found induced under

anaerobic conditions in *P. stutzeri* (Yang *et al.*, 2011b). It is known that transition metals interfere with the anaerobic metabolism and must be exported.

2.6.13 The flagellar hook-length control protein FliK and nitrogen regulation

The Dshi_3364 gene encodes the flagellar hook-length control protein FliK. Besides its function in flagellar biosynthesis, the gene was important for biofilm development in *Shewanella oneidensis* (Thormann *et al.*, 2004). For *Campylobacter jejuni* modulation of the sigma 54-dependent regulon by the *fliK* locus was observed, including the regulation of the *nuo* genes for NADH dehydrogenase (Kamal *et al.*, 2007). Similar observations were made for *Heliobacter pylori*. Here, the FliK influenced the transcription of genes for a ferredoxin and thioredoxin (Douillard *et al.*, 2009). Obviously, the FliK protein mediates multiple regulatory functions besides its structural function during flagella formation. One of these functions is essential for anaerobic growth of *D. shibae* under anaerobic conditions.

3 Part II: Gene Regulatory and Metabolic Adaptation Processes of *Dinoroseobacter shibae* DFL12T during Oxygen Depletion

Sebastian Laass[1*], Sarah Kleist[2*], Nelli Bill[2], Katharina Drüppel[3], Sebastian Kossmehl[3], Lars Wöhlbrand[3], Ralf Rabus[3], Johannes Klein[1], Manfred Rohde[5], Annekathrin Bartsch[4], Christoph Wittmann[4], Kerstin Schmidt-Hohagen[2], Petra Tielen[1], Dieter Jahn[1] and Dietmar Schomburg[2#]

[1]Institute of Microbiology, Technische Universität Braunschweig, D-38106 Braunschweig, Germany
[2]Institute for Biochemistry, Biotechnology and Bioinformatics, Technische Universität Braunschweig, D-38106 Braunschweig, Germany
[3]Institute for Chemistry and Biology of the Marine Environment, General and Molecular Microbiology, Carl von Ossietzky University Oldenburg, D-26111 Oldenburg, Germany
[4]Institute of Biochemical Engineering, Technische Universität Braunschweig, D-38106 Braunschweig, Germany
[5]Department of Medical Microbiology, Helmholtz-Centre for Infection Research (HZI), D-38106 Braunschweig, Germany

* Authors contributed equally.

corresponding author:
Prof. Dr. Dietmar Schomburg
E-mail: d.schomburg@tu-bs.de
Tel.: 49-531-391-8300; Fax: 49-531-391-8302

My contribution: design of experiments (with D.S., D.J., S.K., K.S-H and P.T.); establishment of continuously cultivation of *D. shibae* in a chemostate; experimental procedure of transcriptome analyses and sampling for proteome analysis; PHB verification (with A.B., M.R.) analysis of transcriptome and proteome data; first draft of manuscript (with S.K.)

3.1 Capsule

Background: The bacterium *Dinoroseobacter shibae* was exposed to environmental anoxia.
Results: Systems biology analyses showed the time-resolved cellular adaptation processes of *D. shibae* during oxygen depletion.
Conclusion: Oxygen depletion led to a metabolic crisis due to the missing regeneration of ATP and reduction equivalents, until denitrification was established.
Significance: Here we have elucidated the adaptation processes of marine bacteria to anoxic respiration.

3.2 Abstract Part II

Metabolic flexibility is the key to the ecological success of the marine *Roseobacter* clade bacteria. We investigated the metabolic adaptation and the underlying changes in gene expression of *Dinoroseobacter shibae* DFL12^T to anoxic life by a combination of metabolome, proteome, and transcriptome analyses. Time-resolved studies during continuous oxygen depletion were performed in a chemostat using nitrate as the terminal electron acceptor. Formation of the denitrification machinery was found enhanced on the transcriptional and proteome level, indicating that *D. shibae* DFL12^T established nitrate respiration to compensate for the depletion of the electron acceptor oxygen. In parallel, arginine fermentation was induced. During the transition state, growth and ATP concentration were found to be reduced, as reflected by a decrease of A_{578} values and viable cell counts. In parallel, the central metabolism, including gluconeogenesis, protein biosynthesis, and purine/pyrimidine synthesis was found transiently reduced in agreement with the decreased demand for cellular building blocks. Surprisingly, an accumulation of poly-3-hydroxybutanoate was observed during prolonged incubation under anoxic conditions. One possible explanation is the storage of accumulated metabolites and the regeneration of $NADP^+$ from NADPH during poly-3-hydroxybutanoate synthesis (NADPH sink). Although *D. shibae* DFL12^T was cultivated in the dark, biosynthesis of bacteriochlorophyll was increased, possibly to prepare for additional energy generation via aerobic anoxygenic photophosphorylation. Overall, oxygen depletion led to a metabolic crisis with partly blocked pathways and the accumulation of metabolites. In response, major energy-consuming processes were reduced until the alternative respiratory denitrification machinery was operative.

3.3 Introduction Part II

Dinoroseobacter shibae DFL12^T belongs to the family of *Rhodobacteriaceae* within the Alphaproteobacteria (Biebl *et al.*, 2005; Wagner-Döbler & Biebl, 2006). The Gram-negative *D. shibae* DFL12^T is a member of the *Roseobacter* clade, which is highly abundant in marine habitats (Wagner-Döbler & Biebl, 2006; Brinkhoff *et al.*, 2008). This heterogeneous group of bacteria exhibits a wide potential of metabolic capacities (Wagner-Döbler & Biebl, 2006). Therefore, they play a major role in the remineralization of the oceans and thus in the global carbon cycle (Azam *et al.*, 1983). The mixotrophic *D. shibae* DFL12^T can utilize a relatively small range of carbon sources like carboxylic acids, glucose, and glycerol. However, it is not able to grow with butanoate, ethanol, or methanol (Biebl *et al.*, 2005; Rex *et al.*, 2013). Because a phosphofructokinase activity is missing, *D. shibae* DFL12^T uses the Entner-Doudoroff pathway instead of the standard glycolysis pathway (Fürch *et al.*, 2009). Moreover, *D. shibae* DFL12^T is able to perform aerobic anoxygenic photophosphorylation to gain additional energy (Biebl *et al.*, 2005). Recently, the anaerobic growth of *D. shibae* DFL12^T using nitrate as a terminal electron acceptor was shown (Piekarski *et al.*, 2009). Indeed, the 4.4-Mb genome of *D. shibae* DFL12^T contains genes encoding enzymes of the denitrification pathway (Wagner-Döbler *et al.*, 2010). Denitrification is the reduction of nitrate in four sequential steps into dinitrogen by the concomitant generation of a proton-motive force, which fuels ATP synthesis via ATPase (Zumft, 1997). Interestingly, the bacterium possesses a *nap* operon encoding the periplasmic nitrate reductase NapA (EC 1.7.99.4) catalyzing the reduction of NO_3^- to NO_2^- instead of a cytoplasmic NarG nitrate reductase (EC 1.7.99.4) as known from other denitrifying bacteria (Zumft, 1997). The *nir* operon encoding the periplasmic nitrite reductase NirS (EC 1.7.2.1) that catalyzes the reduction of NO_2^- to NO, the *nor* operon encoding the nitric oxide reductase NorB (EC: 1.7.2.5) that reduces NO to N_2O, and the *nos* operon encoding the nitrous oxide reductase NosZ (EC: 1.7.2.4) that converts N_2O to N_2 are also present in the genome of *D. shibae* DFL12^T (Wagner-Döbler *et al.*, 2010; Zumft, 1997). Furthermore, *D. shibae* DFL12^T possesses genes for the assimilatory nitrate reductase NasA (EC 1.7.99.4) and the two subunits of the assimilatory nitrite reductase NasDE (EC 1.7.1.4). Additionally, genes for high affinity *cbb*$_3$-type cytochrome *c* oxidases and alternative oxygen-independent NADH dehydrogenases necessary for energy generation via anaerobic respiration were identified in the genome of *D. shibae* DFL12^T (Zumft, 1997; Wagner-Döbler *et al.*, 2010). This gene cluster (*ccoGHI*, *NOQS*) is widespread in bacteria of the *Roseobacter* clade but was not found as a gene cluster in 30 other analyzed bacteria; no

orthologues are found in other bacteria, only a few orthologues concerning the enzyme activity.

Genes encoding enzymes of fermentative pathways are also present in the genome of *D. shibae* DFL12^T (Wagner-Döbler *et al.*, 2010). The *arcABC* operon encodes enzymes mediating the conversion of arginine to ornithine with the concomitant production of one ATP under anoxic conditions (Schobert & Tielen, 2010). Moreover, genes necessary for mixed acid fermentation were identified in the genome of *D. shibae* DFL12^T (Wagner-Döbler *et al.*, 2010). With its genetic equipment, *D. shibae* DFL12^T should be able to convert pyruvate to acetate and ethanol. However, experimental details of its regulatory and metabolic response to lack of oxygen are still missing.

Recently, a transposon mutagenesis study using *D. shibae* DFL12^T identified nitrate reductase and corresponding cofactor-synthesizing enzyme-encoding genes as essential for anaerobic growth (Ebert & Laaß, 2013). Surprisingly, chromosomal and plasmid-encoded genes involved in membrane-localized sodium gradient-dependent processes, genomic rearrangements, and cellular envelope restructuring were indispensable for growth without oxygen (Ebert & Laaß, 2013). Until now, our knowledge about the details of the metabolic processes in *Roseobacter* clade members has been rather limited. Recently, first systems biology-oriented studies with *Phaeobacter inhibens* DSM 17395 (formerly deposited as *Phaeobacter gallaeciensis* DSM 17395) (Buddruhs *et al.*, 2013) were published covering the analysis of the proteomic and metabolic response to rich medium and amino acid-containing medium (Zech *et al.*, 2013b; Zech *et al.*, 2013a). In comparison with *D. shibae* DFL12^T, *P. inhibens* DSM 17395 is able to degrade a wide range of carbon sources. It shows a preference for amino acids as carbon sources related to its habitat (Drüppel *et al.*, 2014). This underlines the need for systematic investigations of this group of bacteria as a precondition to unravel the survival strategies of *Roseobacter* clade bacteria in the marine environment.

Here, we present a systematic investigation using transcriptome, proteome, and metabolome analysis to unravel the metabolic adaptation of *D. shibae* DFL12^T to oxygen depletion with nitrate as the terminal electron acceptor.

3.4 Experimental Procedures Part II

3.4.1 Chemostat Cultivation of *D. shibae* DFL12^T

Continuous cultivation of *D. shibae* DFL12^T was performed in salt water minimal medium with 5 mm succinate as a carbon source and 25 mm nitrate as an alternative electron acceptor in an Inforce HT Multifors 2 reactor (Infors, Bottmingen, Switzerland) at 30 °C, pH 8.0, with aeration of 0.7 liter of air/min and a stirring speed of 150 rpm. The working volume of the reactor was 1 liter. The chemostat was protected from light by covering with aluminum foil to avoid aerobic anoxygenic photosynthesis of *D. shibae* DFL12^T. Inoculation, starting of the continuous cultivation, and the anaerobic shift were done as described before (Ebert & Laaß, 2013). Nitrate at a concentration of 25 mm was continuously supplemented to the culture. Fig. 3.1 shows the consumption of the residual oxygen and the slightly decreasing cell, optical density, and time points of sampling for the observation of the adaptation.

3.4.2 Determination of Nitrate and Nitrite

For determination of the nitrate concentration, a 2-ml sample of a *D. shibae* DFL12^T culture was heated for 20 min at 80 °C and centrifuged for 3 min at 10,000 × *g*, and the supernatant was sterilized using a cellulose-acetate filter with a pore size of 0.2 μm (Sarstedt, Nümbrecht, Germany). The investigated time points were prior to the anaerobic shift (0 min) and 15, 30, 60, 120, and 240 min after the oxygen supply was switched off. The determination of nitrate and nitrite was performed using the nitrite/nitrate colorimetric test (Roche Applied Science) according to the manufacturer's instructions.

3.4.3 Microarray Experiment and Data Analysis

A whole genome microarray of *D. shibae* DFL12^T from Agilent (8 × 15K format; Agilent, Santa Clara, CA) was used as described before (Tomasch *et al.*, 2011). Time-resolved transcriptome analyses were performed with three technical and three biological replicates. Pairwise comparisons of obtained expression rates for different time points after the shift to anoxic conditions with data obtained prior to anaerobic shift (0 min) were made. The investigated time points were 5, 10, 15, 20, 30, 60, and 120 min after the oxygen supply was switched off (Fig. 3.1). Cell harvesting, RNA isolation, and DNA arrays were processed as described before (Ebert & Laaß, 2013). The data discussed here have been deposited in the

NCBI Gene Expression Omnibus (Edgar *et al.*, 2002) and are accessible through GEO Series accession number GSE47445. Genes were considered to be differently transcribed with a - fold change above 1.7)

Table 3.1: Fold changes of proteins displaying significantly changed abundances relative to aerobic growth as determined by 2D-DIGE. Shading corresponds to an abundance change ≥ 1.5 (light gray) or ≤ 1.5 (dark gray).

Locus Tag	Gene name	Description	Fold changes over time [min]				
			15	30	60	120	240
Dshi_3180	*nirS*	nitrite reductase precursor	1.8	1.6	6.9	23.7	46.5
Dshi_0216	*eftA*	electron transfer flavoprotein alpha subunit	1.0	2.5	4.4	9.0	17.7
Dshi_2232		hypothetical protein	1.7	2.1	3.6	6.4	11.3
Dshi_2220		conserved hypothetical protein	-1.3	1.0	1.7	3.3	5.5
Dshi_2213		putative UspA Domain protein	1.5	1.8	2.4	3.5	4.3
Dshi_2673	*exaA*	quinoprotein ethanol dehydrogenase precursor	-1.1	-1.2	1.1	2.3	4.1
Dshi_3917		conserved hypothetical protein	-1.1	1.1	2.0	2.2	2.4
Dshi_0596	*leuA*	2-isopropylmalate synthase	1.3	1.4	1.4	1.4	2.2
Dshi_1693	*cobB*	cobyrinic acid A,C-diamide synthase	1.0	1.0	-1.1	1.1	2.2
Dshi_0541	*hemN1*	oxygen-independent coproporphyrinogen III oxidase	-1.1	1.3	1.5	1.8	2.0
Dshi_3165	*napA*	periplasmic nitrate reductase NapA	1.5	1.8	1.5	2.7	1.8
Dshi_3066	*atoB*	acetyl-CoA acetyltransferase	1.1	1.1	1.2	1.4	1.8
Dshi_2886	*lpd*	dihydrolipoyl dehydrogenase	1.1	1.1	1.0	1.4	1.7
Dshi_0212		two component transcriptional regulator	1.1	-1.1	1.3	1.5	1.6
Dshi_1740	*gap2*	glyceraldehyde-3-phosphate dehydrogenase	1.1	1.2	1.3	1.4	1.6
Dshi_2937	*atpH*	ATP synthase delta chain	1.5	1.5	1.7	1.5	1.6
Dshi_0701		methyltransferase domain protein	1.1	1.2	1.2	1.3	1.6
Dshi_3067	*fabG1*	acetoacetyl-CoA reductase	1.2	1.2	1.4	1.5	1.5
Dshi_2188	*rplI*	ribosomal protein L9	1.1	1.1	1.4	1.8	1.5
Dshi_3681	*thiC*	thiamine biosynthesis protein	-1.1	-1.1	-1.4	-1.6	-1.2
Dshi_2836	*trpS*	tryptophanyl-tRNA synthetase	-1.2	-1.2	-1.1	-1.7	-1.3
Dshi_1738	*tktA*	transketolase 1	-1.0	-1.1	-1.4	-1.6	-1.3
Dshi_1195		TRAP transporter solute receptor	-1.1	-1.1	-1.1	-1.3	-1.7

3.4.4 Shotgun Proteome Analysis by Nanoliquid Chromatography-Electrospray Ionization Tandem Mass Spectrometry (Nano-LC-ESI-MS/MS)

The investigated time points were 15, 30, 60, 120, and 240 min after the oxygen supply was switched off (Fig. 3.1 and Table 3.1). Cell pellets of ~50 mg wet weight were resuspended in 200 µl of lysis buffer, and cells were disrupted using the PlusOne grinding kit (GE Healthcare) as described before (Zech *et al.*, 2013b). Protein concentration was determined according to a method described previously (Bradford, 1976). Following reduction and alkylation of 50 µg of total cellular protein, proteolytic digest was performed overnight with 0.5 µg of trypsin GOLD (Promega, Mannheim, Germany). Finally, 1 µg of total digested

protein was separated applying a 215-min gradient of increasing acetonitrile concentration using an UltiMate 3000 nano-LC (Thermo Scientific, Bremen, Germany) online-coupled to an electrospray-ionization ion trap mass spectrometer (amaZon ETD, Bruker Daltonik GmbH, Bremen, Germany) operated as described before (Zech *et al.*, 2013b). Three biological replicates were analyzed.

Protein identification was performed with ProteinScape (version 3.0; Bruker Daltonik GmbH) on a Mascot server (version 2.3; Matrix Science Ltd., London, UK) searching against a genomic database of *D. shibae* DFL12^T translated into amino acid sequences, including a target-decoy strategy. A single missed cleavage was allowed for tryptic peptides. Furthermore, carbamidomethylation (cysteine) as a fixed modification and oxidation of methionine as a variable modification as well as a mass tolerance (monoisotopic) of 0.4 Da for MS and MS/MS were chosen. Searching was restricted to doubly and triply charged peptides. The instrument type was ESI-TRAP. A false discovery rate of <1.0% was set. The significance threshold was $p < 0.05$, and only peptides with a Mascot score of >25 were considered for protein identification.

3.4.5 Analysis of the Membrane Protein-enriched Fraction by Nano-LC-ESI-MS/MS

The investigated time points were 15, 30, 60, 120, and 240 min after the oxygen supply was switched off (Fig. 3.1). Preparation and SDS-PAGE separation of the membrane protein-enriched fraction was performed as described recently (Zech *et al.*, 2013b). For each sample, one gel lane was cut into 11 slices that were further cut into smaller pieces for washing, reduction, alkylation, and tryptic digest as described before (Zech *et al.*, 2013b). Separation of generated peptides was performed with an UltiMate 3000 nano-LC (Thermo Scientific) applying a 95-min linear gradient of increasing acetonitrile concentration (Zech *et al.*, 2013b). Mass spectrometric analysis of the nano-LC eluent was performed with an online-coupled ion trap mass spectrometer (amaZon ETD; Bruker Daltonics GmbH) operated as described before (Zech *et al.*, 2013b). Protein identification was performed as outlined above.

3.4.6 Analysis of Soluble Proteins by Two-dimensional Difference Gel Electrophoresis (2D-DIGE) and Protein Identification by MALDI-TOF-MS/MS

Time-resolved proteome analysis was performed with three biological replicates. Pairwise comparisons with data obtained prior to anaerobic shift (0 min) were made. The investigated time points were 15, 30, 60, 120, and 240 min after the oxygen supply was switched off (Fig. 3.1). 40 ml of culture were harvested and centrifuged for 5 min (4 °C, 10,000 × *g*), and the cell pellet was washed with 1 ml of 100 mm Tris-HCl (pH 7.5) supplemented with 5 mm $MgCl_2$ and centrifuged for 3 min (4 °C, 13,400 rpm, Minispin, Eppendorf, Hamburg, Germany) to yield 50 mg wet weight. Resuspension of cells and cell breakage were performed as described recently (Zech *et al.*, 2013b). Subsequent protein content determination was done according to the method described previously (Bradford, 1976), and pre-electrophoretic labeling was carried out as described before (Gade *et al.*, 2003). Protein extracts of cells grown under oxic conditions (0 min) served as reference state and were labeled with Cy5. Protein extracts of cells harvested after shutdown of the oxygen supply served as test states and were each labeled with Cy3. The internal standard was composed of equal amounts of all test states and the reference state and was labeled with Cy2. Isoelectric focusing (pH range of 3.0–5.6 and 3–11 non-linear) and second dimension separation were performed as described previously (Zech *et al.*, 2013b). Spots fulfilling the following criteria were considered to have significantly different abundances: -fold change of ≤ -1.5 or ≥ 1.5 (Zech *et al.*, 2011), an analysis of variance p value of <0.05, t test value of $<10^{-4}$, and matched in at least 75% of the analyzed gel images.

For protein identification, the 2D-DIGE gels were stained with colloidal Coomassie Brilliant Blue as described before (Buddruhs *et al.*, 2013), and spots of interest were robotically excised using the EXQuest spot cutter (Bio-Rad). In-gel digest, sample spotting, and acquisition of mass spectra by MALDI-TOF-MS with an UltrafleXtreme MALDI-TOF/TOF mass spectrometer (Bruker Daltonik GmbH) as well as protein identification with a mass tolerance of 50 ppm (MS) and 100 ppm (MS/MS) were performed as reported before (Zech *et al.*, 2013b).

3.4.7 Poly-3-hydroxybutanoate (PHB) Determination

Time-resolved analysis of PHB concentration was performed in three biological replicates. The investigated time points were 0 min (before stopping the aeration), 15, 30, 60, 120, and 240 min after oxygen supply was switched off.

2 ml of the chemostat culture were harvested and centrifuged for 5 min at 10,000 × *g* and 4 °C. The cells were hydrolyzed with 2 m NaOH as described previously (Don *et al.*, 1994). In parallel, standards with pure PHB (Sigma-Aldrich) were hydrolyzed in the same way. PHB was then quantified by HPLC (La Chrome EliteR HPLC, HWR-Hitachi International HPLC, Darmstadt, Germany) using an Aminex HPX-87H column (300 mm × 7.8 mm; Bio-Rad) at 45 °C with 12 mm H2SO4 as mobile phase with a flow rate of 0.5 ml min−1 and UV detection at 210 nm.

3.4.8 Metabolome Analysis

Cultures were harvested and washed as described previously (Börner *et al.*, 2007) with the exception of using 3.5% (w/v) sodium chloride solution for washing; centrifugation was performed at 8819 × *g* for 3 min. Pairwise comparisons with data obtained prior to anaerobic shift (0 min) were made. The investigated time points were 15, 30, 60, 120, and 240 min after the oxygen supply was switched off (Fig. 3.1). Intracellular metabolites were extracted as described previously (Zech *et al.*, 2009) with the exceptions of using 0.75 ml of ethanol, containing 15 µl of a 0.2 mg/ml ribitol solution, for resuspension and 0.75 ml of iced water for further extraction. After chloroform extraction, 0.75 ml of the polar phase were withdrawn and dried in a vacuum concentrator overnight. The two-step derivatization reaction was performed as described recently (Zech *et al.*, 2013a). Gas chromatography (GC) was performed with a 7890 Agilent GC chromatograph, equipped with a ZB-5MS column (30 m × 0.25-mm inner diameter, 25-µm particle size; Phenomenex, Aschaffenburg, Germany). MS analysis of intracellular metabolites was performed as described recently (Zech *et al.*, 2013b; Zech *et al.*, 2013a) using a Leco Pegasus 4D GCxGC-TOF-MS (Leco Instrumente, Mönchengladbach, Germany) operated in GC-TOF mode and equipped with an MPS 2 XL autosampler (Gerstel, Mühlheim an der Ruhr, Germany); full-scan mass spectra were collected from *m*/*z* 45 to 600 at 4 scans/s, and the re-equilibration time at 330 °C was shortened from 8 to 3 min.

Data analysis was done with the Metabolite Detector software (Hiller *et al.*, 2009) as described recently (Zech *et al.*, 2013a). Data were normalized by cell mass (7 mg cell dry weight), the internal standard ribitol, and finally by central normalization. Changes in metabolite concentrations extending a threshold of 1.5 were analyzed (Table A2).

3.4.9 Cultivation for ATP Measurement

For the ATP measurement *D. shibae* DFL12^T was cultivated in darkness in salt water minimal medium at 30 °C and a stirring speed of 150 rpm, supplying 16.9 mm succinate as a carbon source and 25 mm nitrate as an alternative electron acceptor. After the culture reached an optical density A_{600} of 0.9, the culture was converted into 50-ml falcons and transferred to an anaerobic chamber, and the stirring was stopped.

3.4.10 Measurement of ATP

For determination of the ATP content, about 500 µl of culture were quick-frozen by using liquid nitrogen. Afterward, the samples were diluted (5-fold; only reference was diluted 20-fold). In the following, ATP levels were determined by the BacTiter-Glo Microbial Cell Viability Assay (Promega, Germany) following the manufacturer's instructions, using a sample volume of 50 µl. ATP content was determined using a calibration curve (range 1.25–20 pmol). The investigated time points were 0, 15, 30, 60, 120, 180, 240, 300, and 360 min after oxygen shutdown. Data were normalized by cell mass.

3.4.11 Transmission Electron Microscopy

One ml of cell culture was taken from the chemostat after 0, 15, 30, 60, 120, and 240 min. Samples were centrifuged (5 min, 15,000 × *g*, 4 °C), the supernatant was discarded, and cell pellets were stored at −80 °C until further processing. Cells were fixed with 2% glutaraldehyde, 5% formaldehyde in cacodylate buffer for 1 h on ice, washed with buffer, and further fixed with 1% aqueous osmium for 1 h at room temperature. Samples were then dehydrated with a graded series of acetone (10, 30, 50%). At the 70% dehydration step, samples were left overnight in 70% acetone containing 2% uranylacetate and further dehydrated with 90 and 100% acetone. Samples were then embedded in the epoxy resin Spurr according to procedures described previously (Spurr, 1969). Ultrathin sections were cut with a diamond knife, picked up with Butvar-coated grids, counterstained with uranyl acetate and

lead citrate, and examined in a TEM910 transmission electron microscope (Carl Zeiss) at an acceleration voltage of 80 kV. Images were recorded digitally at calibrated magnifications of ×5000 (×4000 for the 15 min image) with a Slow-Scan CCD camera (ProScan, 1024 × 1024, Scheuring, Germany) with ITEM software (Olympus Soft Imaging Solutions, Münster, Germany). Contrast and brightness were adjusted with Adobe Photoshop CS3.

3.5 Results and Discussion Part II

3.5.1 Physiological Adaptation of *D. shibae* DFL12^T to Oxygen Depletion

A combination of transcriptome, proteome, and metabolome analyses served to investigate the dynamic metabolic adaptation of *D. shibae* DFL12^T to oxygen limitation. For this purpose, *D. shibae* DFL12^T was cultivated in an aerated chemostat at steady state. After two reactor residence time periods, the aeration was switched off, and the oxygen concentration in the culture decreased within 20 min to 0.05 µm (Fig. 3.1), establishing microoxic to anoxic conditions.

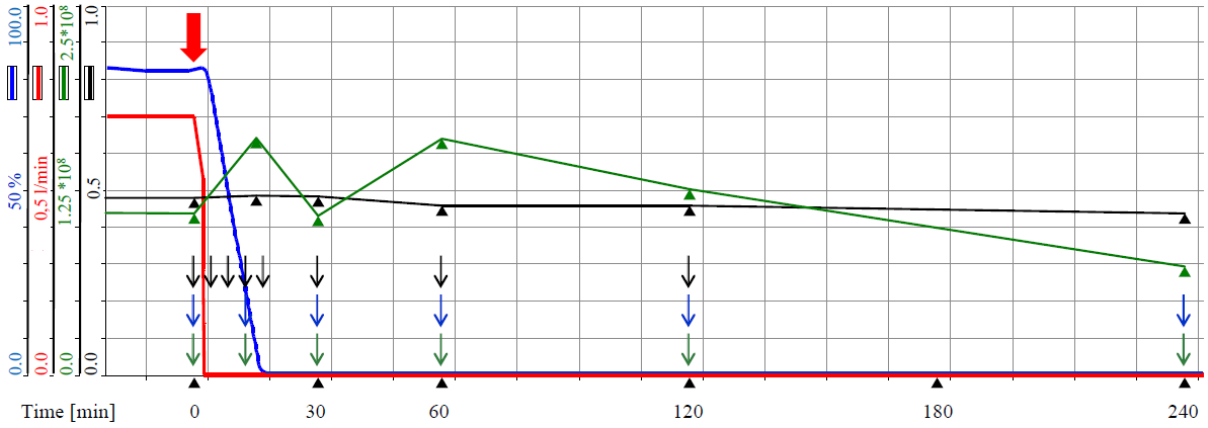


Fig. 3.1: **Continuous cultivation of *D. shibae* DFL12T under oxygen-depleted conditions.** *D. shibae* DFL12T was grown under continuous aerated conditions in salt water minimal medium supplemented with 25mM nitrate to the steady state. Shown are aeration (*red line*), the oxygen partial pressure (*blue line*), colony-forming units (*green line*), and the cell density *A*578 (*black line*). The *red arrow* indicates the time point when the oxygen supply (*red line*) was switched off. *Black arrows* indicate sampling time points for transcriptome analyses, *green arrows* indicate proteome sampling time points, and *blue arrows* indicate sampling time points for metabolome analyses.

The A_{578} slightly decreased from 0.5 to 0.45, and the viable cell count decreased from 1.1 × 10^8 to 7.2 × 10^7 cfu/ml within the first 60 min after the oxygen shutdown (Fig. 3.1). Electron microscopy analyses of the culture at different time points revealed a constant cell size but an accumulation of strongly refractive intracellular granula (see below). Nitrate at a concentration of 25 mM was continuously supplemented to the culture. During prolonged time of anoxic cultivation, the nitrate concentration in the effluent of the reactor was found constant at 20 mm, indicating that *D. shibae* DFL12^T utilized the supplied nitrate. Because the medium also contained a 4.7 mm concentration of the preferred, already reduced nitrogen source ammonium chloride and the concentration of the toxic reduction product nitrite was below the detection limit in the effluent at all sample time points, a complete reduction of nitrate to dinitrogen via denitrification was concluded.

We intended to systematically determine the cellular dynamics during adaptation of *D. shibae* DFL12^T to oxygen limitation to identify key enzymes and metabolic pathways used by this bacterium during oxygen depletion. Time-resolved studies exhibited 792 genes differently transcribed over a prolonged time of oxygen depletion, indicating a complex adaptation process of *D. shibae* DFL12^T (Table 3.2). The strongest transcriptional response was reached 30 min after oxygen shutdown (Table 3.3). The adaptation of the proteome was much slower where the maximal difference compared with aerobic growth was observed 240 min after oxygen shutdown (Table 3.1 and Table 3.3). In total, 875 different proteins were identified by shotgun analysis, and 1210 were identified in the membrane protein-enriched fraction. Interestingly, 2D-DIGE analysis revealed only 23 (of 1325 separated protein spots) differentially formed proteins upon oxygen limitation, 19 of which had increased and 4 of which had decreased abundance (Table 3.1). Apparently, the observed strong transcriptional adaptation is not completely translated into an adaptation on the proteome level as observed for other adaptation processes (Taniguchi *et al.*, 2010). Moreover, the production of metabolically active enzymes is controlled by substrate availability rather than by oxygen concentration (Gray *et al.*, 1966; Nam *et al.*, 2005).

Table 3.2: Numbers of transcripts, proteins and metabolites of *D. shibae* DFL12^T with differential abundances upon prolonged time of oxygen depletion.

	Increased	Reduced	Total
Transcripts	314	478	792
Proteins[a)]	19	4	23
Metabolites	48	32	89

a) here only 2D-DIGE results are shown

Table 3.3: Mean absolute fold changes between the pairwise compared cellular states over all differently expressed genes, proteins and all metabolites. n.d. not determined

	Mean fold-changes							
Time (min)	**5**	**10**	**15**	**20**	**30**	**60**	**120**	**240**
Transcriptome	1.91	1.17	1.37	1.75	4.16	3.06	2.54	n.d.
Proteome[a)]	n.d.	n.d.	1.22	n.d.	1.33	1.87	3.27	5.14
Metabolome	n.d.	n.d.	1.4	n.d.	2.71	3.37	2.60	1.83

[a)] differently abundant proteins detected by 2D-DIGE were considered

The concentration of 80 identified metabolites changed over time, with 48 metabolites showing increased and 32 showing decreased concentrations. The hierarchical cluster analysis over all metabolites revealed the first clear differences from the aerobic situation 30 min after

oxygen shutdown, followed by a major shift between 30 and 60 min (Table 3.2 and Table 3.3). The results from the transcriptome, proteome, and metabolome analyses were combined to unravel the metabolic networks involved in the adaptation of *D. shibae* DFL12^T to anoxic, nitrate-reducing conditions.

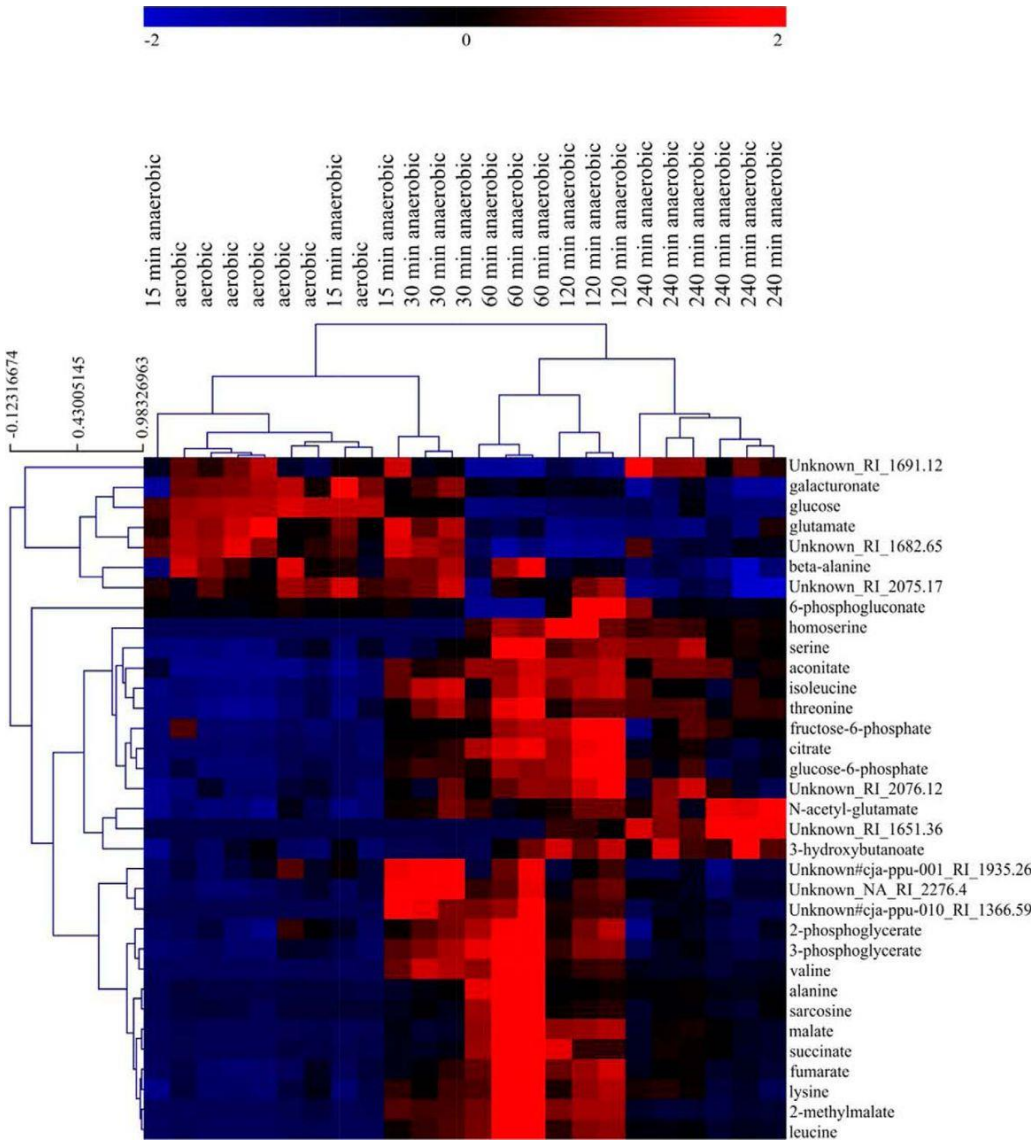


Fig. 3.2: Hierarchical Cluster Analysis (HCL) of metabolome data. HCL of metabolome data was done with TIGRMeV4 (Saeed *et al.*, 2003) using a critical p-value of 0.05 and the adjusted Bonferroni correction.

3.5.2 The Denitrification Machinery Substitutes for Oxygen Respiration

The transcription of genes and the abundances of corresponding enzymes of the denitrification pathway were found significantly induced starting 20 min after oxygen shutdown (supplemental Table S4 and Fig. 3.3). Because sufficient nitrogen in the reduced form was present in the growth medium, nitrate assimilation (NasA, NasDE) was not influenced by the change in oxygen tension.

The *nap* operon (Dshi_3161-Dshi_3167) encoding the periplasmic nitrate reductase Nap (EC 1.7.99.4), which catalyzes the first step of denitrification, was only slightly induced (*e.g. napA* 4.4-fold, 30 min after oxygen shutdown; Fig. 3.3, *a* and *b*). Furthermore, the NapA protein was also found in significant amounts under oxic conditions in the proteome (Fig. 3.3*c* and Table 3.1 and supplemental Table S3.1–2). Accordingly, the Nap proteins of other denitrifying bacteria are known to be synthesized and active under oxic as well as under anoxic conditions (Zumft, 1997). This allows for an immediate transition from oxygen respiration to nitrate reduction when oxygen becomes limited (Zumft, 1997). *D. shibae* DFL12^T possesses only the periplasmic nitrate reductase Nap (EC 1.7.99.4) and not the membrane-bound nitrate reductase NarG, which is the main nitrate reductase of many other species (Wagner-Döbler *et al.*, 2010; Zumft, 1997). It was shown for Nar-negative bacteria, that Nap is involved in the formation of a proton-motive force efficient for energy generation based on the additional proton translocation mediated by the ferrodoxins NapG and NapH (González *et al.*, 2006). The corresponding genes *napGH* are part of the *nap* operon of *D. shibae* DFL12^T.

Transcripts of the *nir* operon, encoding the respiratory nitrite reductase (NirS) and enzymes for cofactor biosynthesis, showed a progressive increase in abundance beginning 20 min after oxygen shutdown and reaching a maximum after 30 min (*e.g. nirS* >30-fold; Fig. 3.3*b* and supplemental Table S4). Accordingly, the nitrite reductase (NirS) displayed a steady increase in abundance beginning 60 min after the shift with a maximum of 46-fold after 240 min (Fig. 3.3, *c* and *d*). Similar transcript and protein profiles were observed for the *nor* operon, encoding NO reductase (NorB; EC 1.7.2.5), and the *nos* operon, encoding N_2O reductase (NosZ; EC 1.7.2.4). They showed a concomitant abundance increase beginning 20 min after oxygen shutdown and a maximum after 30 min (supplemental Table S4). Correspondingly, NorCBQ and NosZY proteins were detected 30–60 min after the shift (supplemental Table S4). This abundance pattern suggests a fine-tuned regulatory network with (i) nitrite formed by Nap most likely triggering *nir* gene expression and (ii) the nitrite reduction product NO

initiating expression of *nor* and *nos* genes as described for *P. aeroginosa* (Tielen *et al.*, 2013). Furthermore, direct reduction of nitrite prevents its intermediary accumulation, thereby avoiding accumulation of toxic nitrite levels.

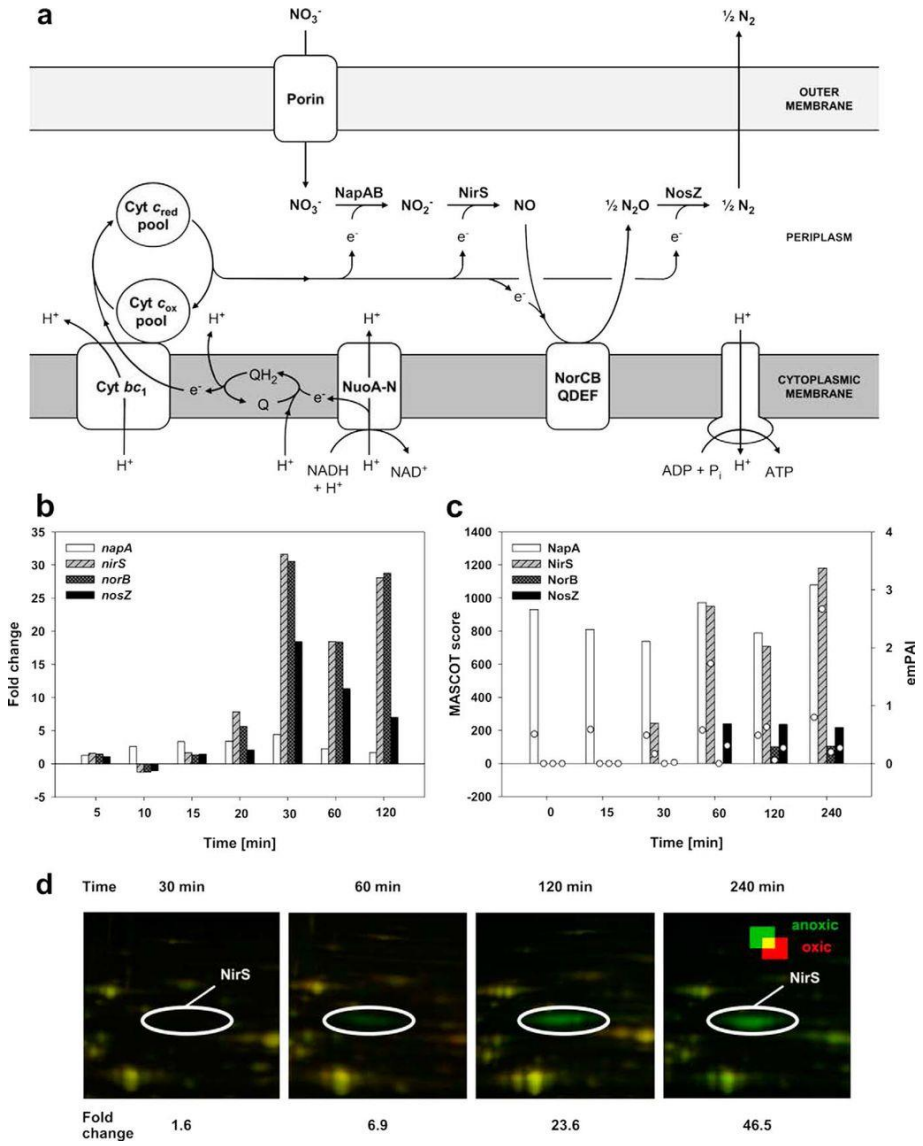


Fig. 3.3: Electron transport and energy generation in *D. shibae* DFL12^T grown under anoxic, nitrate-reducing conditions. *a*) schematic representation of the denitrification apparatus present in *D. shibae* DFL12^T. Shown are periplasmic nitrate reductase (*NapA*), nitrite reductase (*NirS*), nitric oxide reductase (*NorB*), nitrous oxide reductase (*NosZ*), ATPase, NADH dehydrogenase (*NuoA-N*), quinone pool (*Q*), electrons (e^-), cytochrome *c* (*Cyt c*), and cytochrome bc_1 (*Cyt* bc_1). b) expression dynamics of genes encoding the enzymes involved in denitrification: *napA*, *nirS*, *norB*, and *nosZ. c*) protein abundance as detected via membrane proteome and shotgun analyses: NapA, NirS, NorB, and NosZ. *d)* time-dependent abundance increase of NirS (marked by a *white circle*) as detected by 2D-DIGE.

3.5.3 Adaptation of the Electron Transfer Chains to Anoxic Conditions

In *D. shibae* DFL12^T, respiratory energy generation employs various primary dehydrogenases for electron abstraction from different substrates (NADH, glucose, gluconate, lactate, glycerol 3-phosphate, and succinate) to shuttle them via ubiquinone to terminal reductases and oxidases. The latter mediate the reduction of oxygen, *N*-oxides (see above), and dimethyl sulfoxide (Wagner-Döbler *et al.*, 2010). The generated proton gradient is used for ATP generation.

However, most of the mentioned primary dehydrogenases were not differentially produced under oxygen limitation. Only the transcription of *nuoH*, *nuoI*, and *nuoK* encoding NADH dehydrogenase I (EC 1.6.99.5), Dshi_1390 encoding an alternative NADH dehydrogenase (EC 1.6.5.3 and 1.6.99.3), and *sdhAB* encoding the succinate dehydrogenase (EC 1.3.99.1) were found slightly enhanced under anoxic conditions (Table A1 and S4). The corresponding proteins were detected under oxic as well as anoxic conditions by proteome analyses (Tables S3.1–2 and S4). As expected, most primary dehydrogenases were employed during aerobic as well as anaerobic respiration.

The terminal reductases of cbb_3-type cytochrome oxidase type are characterized by their high O_2 affinity and are often found to be essential for growth and survival under microoxic conditions (Schobert & Tielen, 2010; Williams *et al.*, 2007). *D. shibae* DFL12^T exhibits two gene clusters encoding cbb_3-type cytochrome oxidases: the *fixNOQPGHIS*- (Dshi_0661-0668) and the cytochrome *c* oxidase operon (Dshi_3891–Dshi_3894). The transcription of the *fix* operon was significantly induced 10 min after oxygen shutdown, and seven of eight Fix proteins were detected in the membrane protein-enriched fraction (supplemental Table S4). In contrast, transcription of the associated transcriptional regulator FNR (*fixK*, Dshi_0660) was slightly decreased at those time points where the highest transcription of the other fix genes was observed. The cytochrome *c* oxidase operon remained unaffected. Obviously, the *fix* operon encodes the *cbb*3-type cytochrome for the transition from oxic to anoxic conditions, whereas the cytochrome *c* oxidase operon encodes the enzyme for oxic conditions. In *Pseudomonas aeruginosa*, similar observations were made under low oxygen conditions. *P. aeruginosa* possesses two cbb_3 oxidases encoded by the *cco1* and *cco2* operons. The *cco1* genes were constitutively expressed, whereas the transcription of the *cco2* genes was induced under low oxygen conditions (Arai, 2011). As expected, transcription of the oxygen-dependent aa_3-type cytochrome oxidases encoded by *ctaCBGE* (Dshi_1140–Dshi_1144) and *ctaD* (Dshi_2383) was reduced in response to oxygen depletion (Table A1 and S4). However,

CtaDC proteins were detected in the membrane protein-enriched fraction across the entire time span, with rather constant abundances indicating a long lifetime (supplemental Tables S3.2 and S4).

Finally, the *D. shibae* DFL12^T genome contains two gene clusters encoding F_0F_1-ATP synthases (Dshi_0435–Dshi_0445 and Dshi_2933–Dshi_2937/Dshi_3027–Dshi_3031). The first operon was not differently transcribed. Interestingly, the expression of the second gene cluster was reduced 60 min after oxygen shutdown but normalized to aerobic levels after 240 min (supplemental Table S4), whereas protein detection remained constant. (The changes of the ATP concentration during the shift from oxic to anoxic conditions are discussed below.) With the onset of denitrification and the formation of its various terminal reductases, the residual terminal reductase portfolio of *D. shibae* DFL12^T becomes systematically adapted. In contrast, no major adjustments at the level of the primary dehydrogenases were observed.

The genome of *D. shibae* DFL12^T contains the *arcABC* operon for arginine fermentation (Wagner-Döbler *et al.*, 2010) and for mixed acid fermentation using pyruvate as substrate. Genes encoding enzymes converting pyruvate to acetoin (Dshi_4158), 2,3-butanediol (Dshi_4158), ethanol (AdhA), or acetate (Pta and AckA) are present in the genome of *D. shibae* DFL12^T (Wagner-Döbler *et al.*, 2010). For both fermentation types, only small increases of transcription at some time points was observed, but the proteins were not found (supplemental Table S4).

3.5.4 Metabolic Crisis I; Transient Adaptation of the TCA Cycle during Decreasing Oxygen Tension

Metabolome analyses detected interesting concentration changes of metabolites from the central metabolism. Apart from oxaloacetate and succinyl-CoA, all intermediates of the TCA cycle were detected. Interestingly, except for 2-oxoglutarate, these metabolites showed an almost identical concentration pattern over time. Their concentration increased between 15 and 30 min after oxygen shutdown and reached a maximum after 60 min. This was followed by a decrease in metabolite concentration, reaching a level similar to oxic conditions after 240 min.

The determination of the ATP concentration showed a fast decline of ATP by 60% after oxygen shutdown. After 2 h, the ATP concentration increased again, but it reached only two-thirds of the original value at the end of the experiment (Fig. 3.4). A similar observation was found for *S. cerevisiae* (Gonzalez *et al.*, 2000). This is in accordance with expectations, with

the ATP formation being impaired due to the lack of oxygen. Nitrate can only replace oxygen as electron acceptor after the alternative respiration apparatus has been formed. Because the respiratory chain is inhibited, no NAD^+ can be regenerated in this way. Hence, the discussed concentration patterns are a direct response to the highly decreased redox potential present in the cell during adaptation to anoxic conditions.

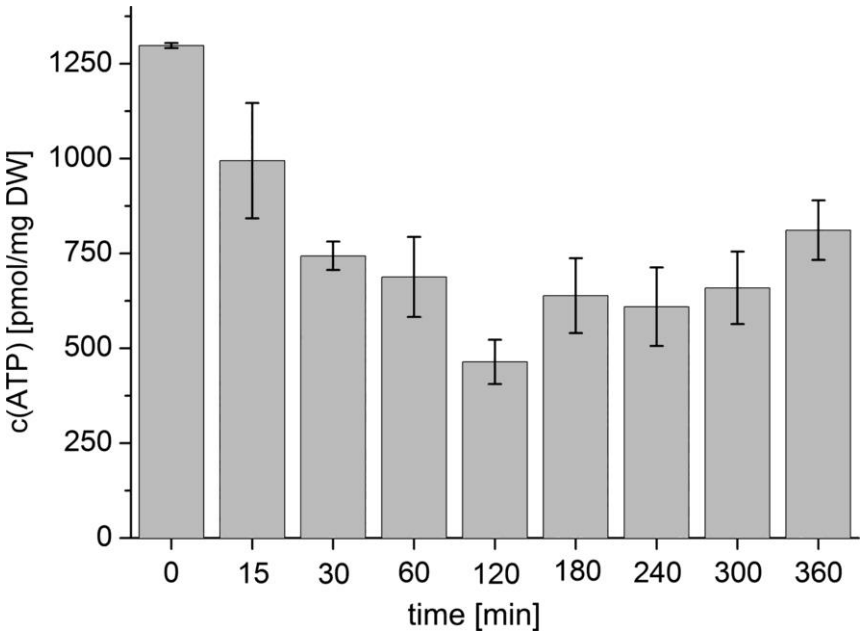


Fig. 3.4: ATP concentration over time (oxic (0 min) to 360 min of anoxia) of batch cultures (*n* = 4) shifted from oxic to anoxic conditions. *DW*, dry weight. *Error bars*, S.D.

Aconitate and citrate accumulated during the first 30–60 min probably as a consequence of the inhibition of isocitrate dehydrogenase by NADPH due to missing $NADP^+$ regeneration during respiration (Lebedeva *et al.*, 2002; Pardo *et al.*, 1999). The subsequent intermediates of the TCA cycle (succinate, fumarate, and malate) also showed the described characteristic concentration pattern (Table A2). Again, succinate dehydrogenase as part of the electron transport chain suffers from the missing terminal electron acceptor in the transition state between 15 and 30 min. It appears that the TCA cycle during this period lost its function in energy metabolism and is rather used for biosynthesis only.

The transcriptional response mirrored the compensation for the observed metabolic changes. Transcriptional changes were observed for genes encoding aconitate hydratase (*acnB*, Dshi_2060) and isocitrate dehydrogenase (*icd*, Dshi_1986), both decreased after 30 min. The genes encoding enzymes mediating the next steps in the TCA cycle, the ATP-generating conversion of succinyl-CoA to succinate, were found significantly up-regulated in the transcriptome after 20–30 min (*sucA*, Dshi_2883; *sucB*, Dshi_2884; Dshi_2866; Dshi_2867;

sucC, Dshi_2878; *sucD*, Dshi_2882). One gene encoding succinate dehydrogenase was also slightly up-regulated after 30 min (*sdhA*, Dshi_2865).

3.5.5 Metabolic Crisis II; Transient Adaptation of Gluconeogenesis and Pentose Phosphate Pathway

Growth on succinate necessitates gluconeogenesis for the formation of C5 bodies, including the sugar moiety of nucleotides. Interestingly, a significant increase of transcription of the phosphoenolpyruvate carboxykinase (*pckA*, Dshi_0213) catalyzing the conversion of oxaloacetate to phosphoenolpyruvate, the entry step into gluconeogenesis from the TCA cycle, was detected 30 min after oxygen shutdown. In the proteome, only the abundance of glyceraldehyde-3-phosphate dehydrogenase (Gap2, Dshi_1740) started to increase 60 min after oxygen shutdown and increased significantly up to 240 min (Table 3.1 and supplemental Table S4). On the metabolic level, a significant increase of phosphoenolpyruvate (4.19-fold change) was detected 60 min after oxygen shutdown. This was also observed for 2- and 3-phosphoglycerate (Fig. 3.5 and Table A2).

Dihydroxyacetone phosphate, which is almost exclusively formed during gluconeogenesis, is significantly decreased with a minimum at 60 min (0.51-fold change) after the oxygen shutdown. Its balanced tautomer glyceraldehyde 3-phosphate was not detected via GC-MS analysis. These observations suggest that formation of glyceraldehyde 3-phosphate/dihydroxyacetone phosphate from 3-phosphoglycerate was impaired due to their dependence on ATP. Beyond glyceraldehyde 3-phosphate/dihydroxyacetone, reactions in the pentose phosphate pathway are needed to produce C5 carbohydrates. However, the transcript for transketolase and the enzyme concentration (TktA, Dshi_1738) decreased up to −3.5-fold and −1.56-fold, 60 min after oxygen shutdown, respectively. The transketolase catalyzes several balanced reactions of the non-oxidative pentose phosphate pathway. The two detected pentose phosphate pathway intermediates xylulose 5-phosphate and ribose (possible decomposition product of ribose 5-phosphate during sample processing or product of the ribokinase-catalyzed conversion) showed a minimum concentration 60 min after oxygen shutdown. Clearly, the flux into and through the pentose phosphate pathway is reduced by the metabolic changes induced by oxygen limitation, which in addition indicates a reduced formation of nucleotides (see below). As a further consequence, the concentrations of glucose 6-phosphate and fructose 6-phosphate increased up to 120 min (4.79- and 4.36-fold change), due to a lack of electron acceptors after oxygen shutdown. The flow through the Entner-

Doudoroff pathway should be reduced due to the inhibition of glucose-6-phosphate dehydrogenase by accumulated NADPH (Hansen *et al.*, 2002; Lessmann *et al.*, 1975; Schaeffer & Stanier, 1978).

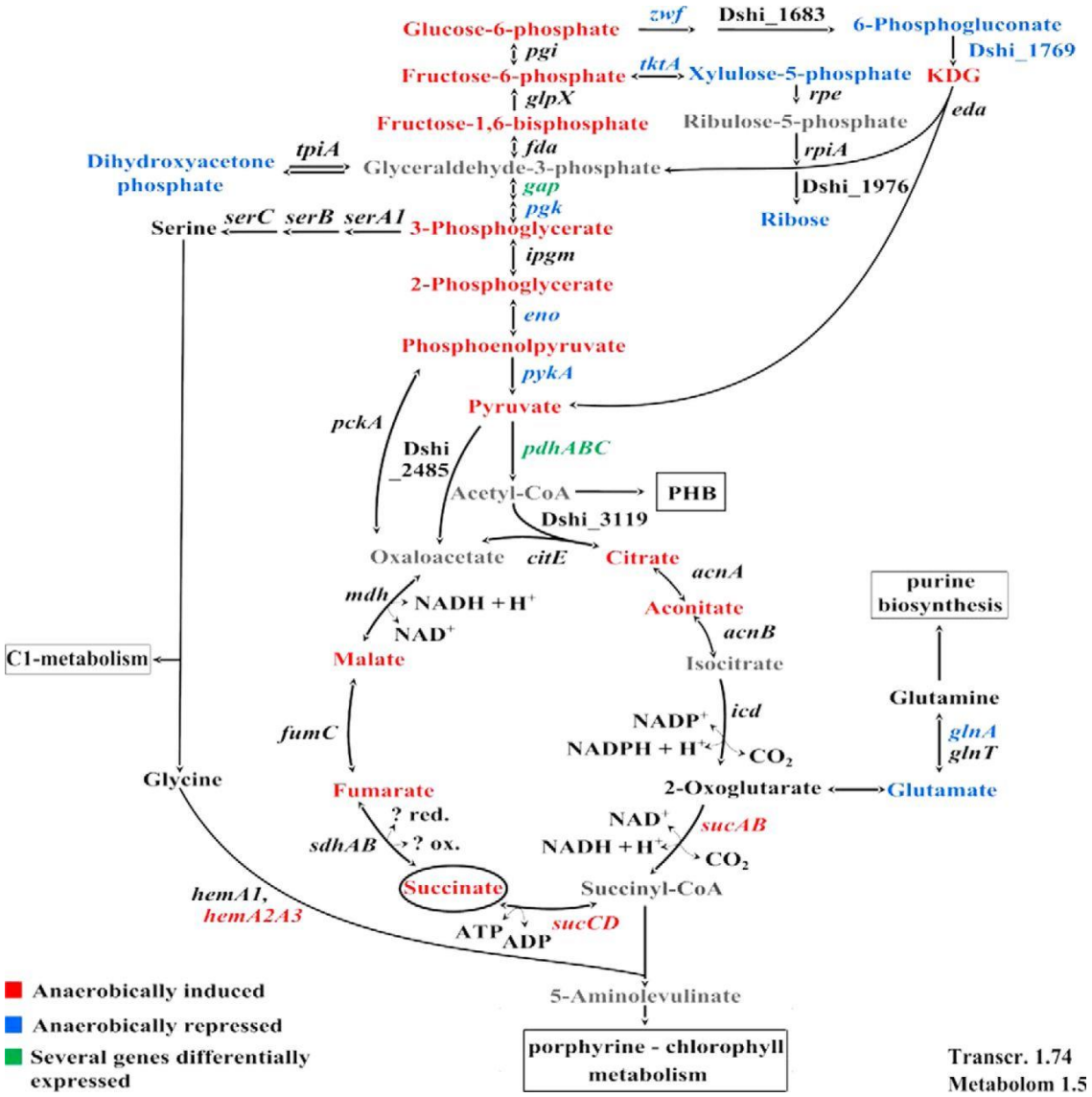


Fig. 3.5: Central metabolism. Schematic representation of the central metabolism. Expression of genes and concentration of metabolites found induced (*red*), reduced (*blue*), not differently expressed (*black*), or not detected (gray) in *D. shibae* DFL12^T 60 min after oxygen shutdown. For transcriptomics, a -fold change cut-off of 1.7 and a *p* value of <0.05 and for metabolites, a -fold change cut-off of 1.5 was applied.

In agreement, the intermediate 6-phosphogluconate, which decreased in concentration until 60 min after oxygen shutdown, revealed a high increase in concentration after 120 min, before its concentration reverted to amounts similar to what was found for *D. shibae* DFL12^T grown under oxic conditions after 240 min. This indicates that the Entner-Doudoroff pathway only plays a minor role under succinate feeding conditions.

In general, the results show an early metabolic response due to the missing oxygen and a not yet fully compensating denitrification apparatus (Fig. 3.3). In consequence, the hampered respiration causes a severe disruption of the oxidative phosphorylation, which leads to an impaired energy balance and, as shown by Watanabe *et al.* (Watanabe *et al.*, 2011) and Gonzalez *et al.* (Gonzalez *et al.*, 2000) to an accumulation of reduced reduction equivalents in the cell. Therefore, the observed metabolic regulation is caused by metabolic feedback systems, missing substrates and oxidized cofactors. All changes described above begin to revert 60 min after oxygen shutdown, indicating the regeneration of the metabolism. This corresponds to the establishment of the completely functional denitrification apparatus on the proteome level (Fig. 3.3), enabling the use of nitrate as an alternative electron acceptor (see above). This leads to the oxidation of the earlier accumulated reduction equivalents and consequently to a re-establishment of a functional energy metabolism.

3.5.6 Metabolic Crisis Management I; PHB Production

The transcription of genes involved in PHB synthesis, poly-β-hydroxybutyrate polymerase (Dshi_2233), and the preceding genes Dshi_2231 and Dshi_2232, showing a certain homology to polyhydroxyalkanoate-associated proteins (*e.g.* in *Jannaschia* sp. Jann_1118), was induced 30 min after oxygen shutdown, reaching a maximum after 120 min (~3-fold change) (supplemental Table S4). The corresponding proteins were only found after oxygen shutdown (supplemental Table S4). The transcription of the related polyhydroxyalkanoate synthesis repressor, PhaR (Dshi_2230) and of Dshi_2234, encoding polyhydroxyalkanoate depolymerase, was not significantly affected.

Polyhydroxybutanoate is produced by numerous microorganisms in response to an imbalanced nutrient supply (Madison & Huisman, 1999; Xiao & Jiao, 2011) or, as suggested by Trautwein *et al.* (Trautwein *et al.*, 2008), during impaired denitrification. The polymer is usually employed by microorganisms as a form of energy storage molecule. Biosynthesis of PHB starts with the condensation of two molecules of acetyl-CoA to acetoacetyl-CoA, which is subsequently reduced to (*R*)-3-hydroxybutanoyl-CoA. This latter compound is then polymerized to PHB (Reusch, 2013). In agreement with the initial observations, metabolome analyses detected a constant increase of the PHB intermediate 3-hydroxybutanoate over time (Table A2). Electron micrographs show the growth of PHB granules over time after oxygen shutdown (Fig. 3.6), and HPLC analysis shows a 10-fold increase of PHB concentration.

Apparently, *D. shibae* DFL12^T uses the formation of PHB under nitrate-reducing conditions for balancing the disturbed central metabolism (see above) and the regeneration of electron acceptors as shown in previous studies (Xiao & Jiao, 2011; Senior & Dawes, 1971). Because NADPH is used in the second step of PHB formation for the reduction to (*R*)-3-hydroxybutanoyl-CoA, $NADP^+$ becomes again available for other oxidation reactions.

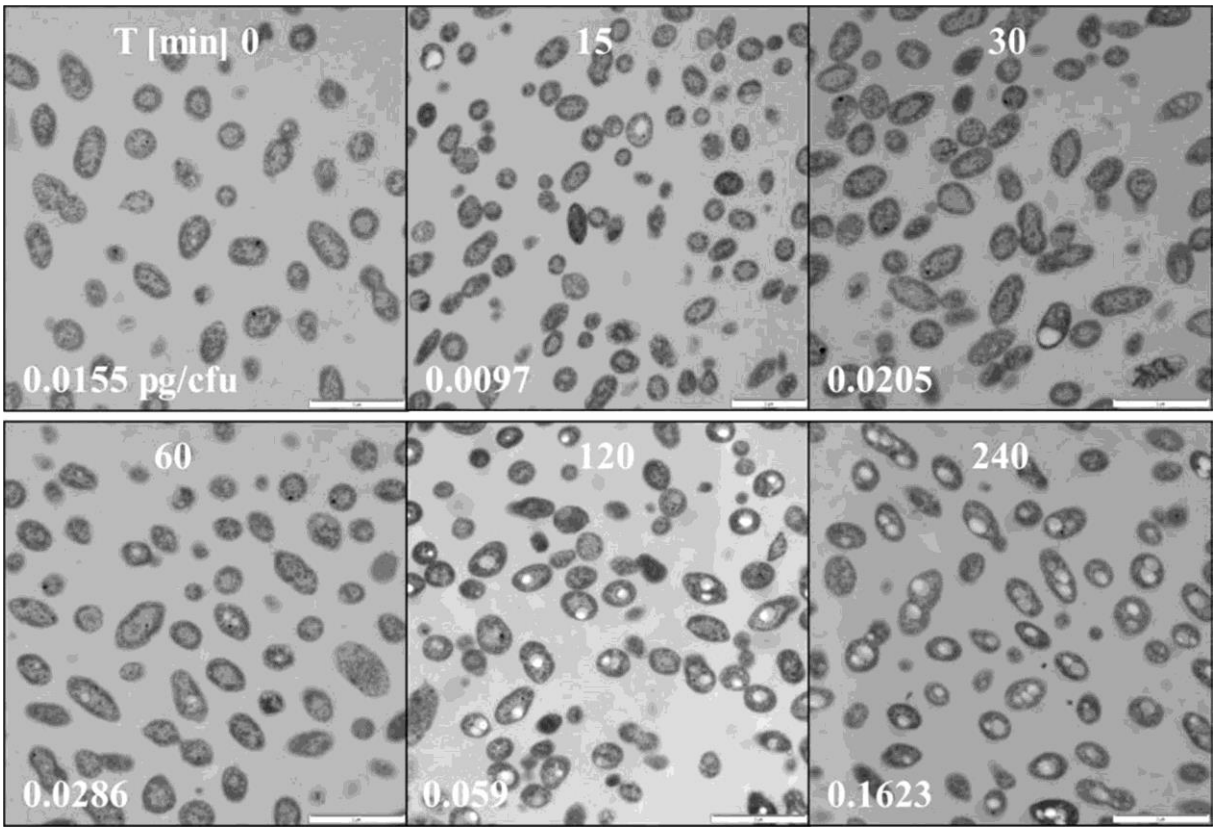


Fig. 3.6: PHB granula formation under anoxic nitrate-reducing conditions (indicated as *light spots* in the cells). Transmission electron microscopy of *D. shibae* DFL12^T shifted from oxic to anoxic conditions. *Top*, time of sampling in min; *bottom left*, concentration of PHB/cfu in pg. PHB concentration was measured via HPLC analysis of hydrolyzed cell samples.

3.5.7 Metabolic Crisis Management II; Reduction of Amino Acid and Protein Biosynthesis

Protein biosynthesis from amino acids consumes a large share of the ATP produced by the cell. As observed in the transcriptome data, protein biosynthesis is down-regulated about 20–30 min after oxygen shutdown (supplemental Table S4). Several aminoacyl-tRNA synthetases (among others, LeuS, PheT, and ThrS) were detected only under oxic conditions, or their concentrations were found strongly diminished after oxygen shutdown. Even more extreme

was the effect on transcription of genes encoding ribosomal proteins, which decreased already 15 min after oxygen shutdown by a factor of 7.9 after 60 min.

As expected, most amino acids accumulated in the intracellular metabolome after 60 min as a result of the decreased protein biosynthesis during the transition phase (). Especially the branched-chain amino acids (Leu, Ile, Val, and related intermediates) were highly increased in abundance, whereas the aromatic amino acids were decreased. As the synthesis of branched-chain amino acids consumes excess NADPH (ketol-acid reductoisomerase), production is increased as an electron sink, and consumption for protein biosynthesis is decreased. Furthermore, serine and glycine were found increased up to 5.03-fold, indicating a channeling of accumulated 3-phosphoglycerate (see above) into glycine and serine metabolism as an alternative to the hindered gluconeogenesis (see above).

60 min after oxygen shutdown, amino acid concentrations started to decrease again, whereas the expression of genes involved in protein biosynthesis and amino acid metabolism increased. Taken together, the results show that protein biosynthesis in *D. shibae* DFL12^{T} is reduced during the metabolic crisis after oxygen shutdown due to an excess of reduced reducing equivalents, metabolite accumulation, and a disturbed energy balance. However, after the outlined adaptation for the management of the crisis, protein biosynthesis restarts.

3.5.8 Metabolic Crisis Management III; Reduction of Purine and Pyrimidine Metabolism

In general, down-regulation of many genes encoding enzymes involved in purine and pyrimidine metabolism began after 20 min and showed a minimum of transcription 60 min (up to −3-fold changes) after oxygen shutdown (supplemental Table S4). In agreement, for some metabolic intermediates, a decreased abundance was detected in the metabolome. Clearly, reduced nucleotide formation inhibits DNA and RNA formation, being one of the reasons for the reduced growth of *D. shibae* DFL12^{T}. However, after metabolic crisis management (see above), these transcriptional processes resume their activity.

3.5.9 Metabolic Crisis Management IV; Adaptation of Bacteriochlorophyll Biosynthesis

Interestingly, although the chemostat was protected from light to avoid aerobic anoxygenic photophosphorylation, many genes encoding enzymes for bacteriochlorophyll synthesis were

found up-regulated, some of them immediately after interruption of the oxygen supply with -fold changes of up to 17.7. Others started to increase after 30 min with lower -fold changes of up to 2.1 (Fig. 3.7 and supplemental Table S4). The transcriptional changes were also mirrored in the proteome at 120 min after oxygen shutdown because oxygen-independent coproporphyrinogen III dehydrogenase (HemN1, Dshi_0541; 2D-DIGE) catalyzing the protoporphyrinogen IX formation showed an increased concentration (up to 2.02-fold change).

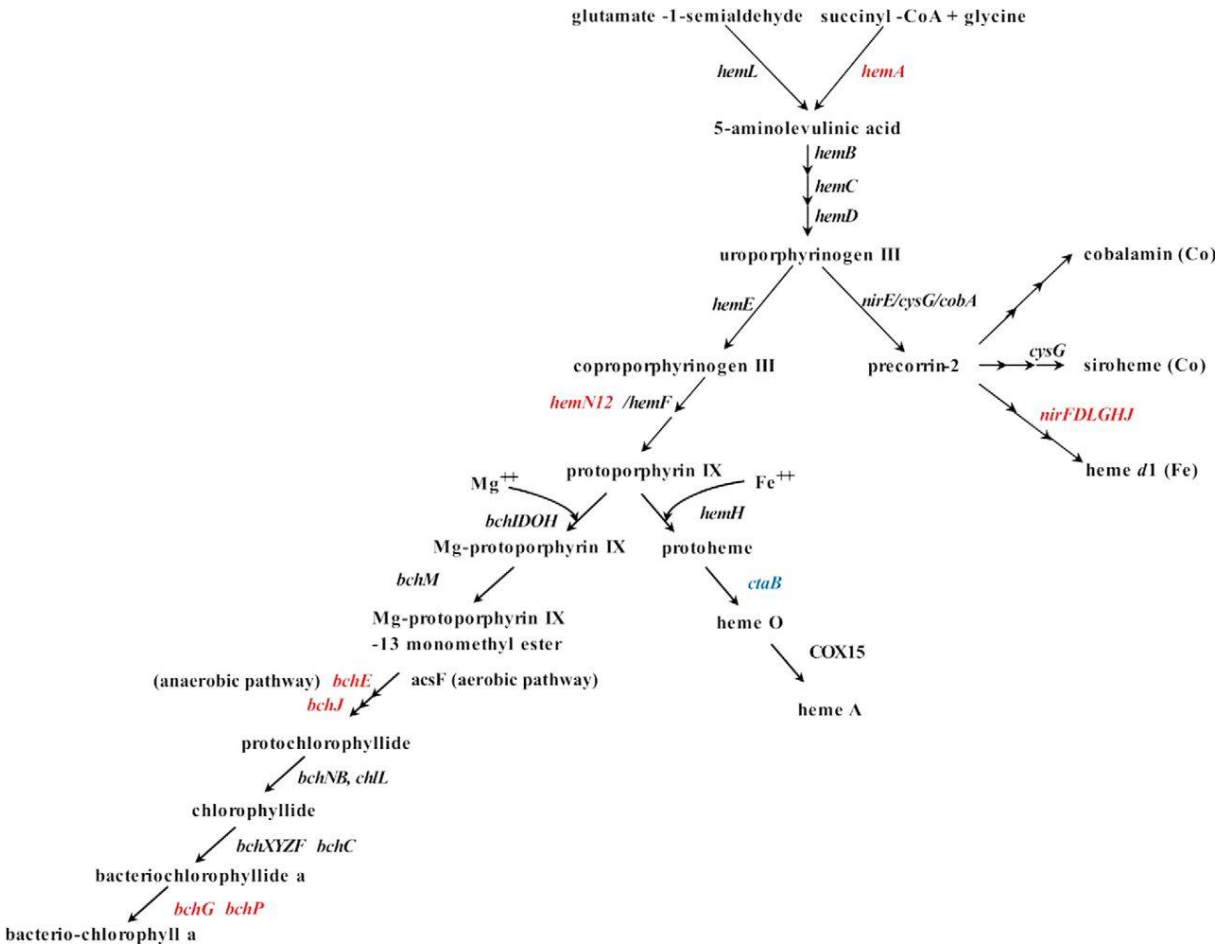


Fig. 3.7: Schematic view of bacteriochlorophyll biosynthesis in *D. shibae* DFL12^{T}. Shown is expression of genes found induced (*red*), reduced (*blue*), or not differently expressed (*black*) 60 min after oxygen shutdown. A -fold change cut-off of 1.7 was applied.

One of the steps in the enzyme of the bacteriochlorophyll biosynthesis can be catalyzed by an oxygen-dependent or an oxygen-independent protoporphyrin monomethyl ester cyclase (Ouchane *et al.*, 2004). The transcript for the *bchE* gene (Dshi_2637) encoding the proposed oxygen-independent Mg-protoporphyrin monomethyl ester cyclase increased after 5 min with

a maximum 30 min after oxygen shutdown (up to 17.7-fold change). The oxygen-dependent cyclase gene showed no changes in expression.

The increase of bacteriochlorophyll *a* during starvation in darkness was already observed before (Biebl *et al.*, 2005; Wagner-Döbler & Biebl, 2006). As an alternative energy source, the up-regulation of genes involved in anoxygenic photosynthesis is an efficient rescue strategy for the bacteria under oxygen-depleted conditions.

3.6 Conclusion Part II

The combination of transcriptome, proteome, and metabolome analysis allowed a detailed time-resolved characterization of the cellular processes of *D. shibae* DFL12^T during the adaptation to oxygen depletion. A fast response in transcription and metabolism 15–30 min after oxygen shutdown is followed by significant changes in the cellular protein inventory after 120–240 min. Overall, oxygen depletion led to a metabolic crisis, where central metabolic processes were blocked due to the missing regeneration of NAD^+/$NADP^+$ and lower ATP supply. The transient accumulation of metabolites and a resulting gene regulatory response were observed. Energy-consuming processes, including cell division with corresponding nucleotide and protein biosynthesis, were significantly down-regulated. Interestingly, PHB biosynthesis was induced, most likely for the recovery of accumulated metabolites and the reduction of the pool size of NAD(P)H. After 60 min, the metabolic crisis caused by the oxygen deficiency of *D. shibae* DFL12^T to anoxic conditions was resolved to a large degree, reflected by a changed enzyme repertoire and a relaxed metabolome and transcriptome.

3.7 Acknowledgment Part II

We gratefully acknowledge the assistance of Marcus Ulbrich with enzyme function prediction.

3.8 Footnotes Part II

This work was supported by Deutsche Forschungsgemeinschaft Transregio SFB TRR 51.

4 Part III: Characterization of dissimilative nitrate respiration regulators (Dnr) of *D. shibae*

4.1 Introduction Part III

Nitric oxide (NO) is an intermediate of the reduction from nitrate to dinitrogen in denitrifying bacteria (Zumft, 1997). A fine tuned regulation of the enzymes involved in denitrification is required to avoid accumulation of these toxic intermediates also including nitrite (NO_2^-) and nitrous oxide (N_2O). Crp/Fnr-like transcription factors (cAMP receptor protein, fumarate and nitrate reductase regulator) are known to be involved in corresponding regulatory networks. The global transcription factor Fnr (e.g. *E. coli*) or one of the Fnr-like factors Anr, FnrA, FnrL or FnrP belonging to the same regulatory family are known for their oxygen tension mediated transcriptional regulation (Zumft, 1997). In *P. aeruginosa* a second Crp/Fnr-like regulator, Dnr, is involved in the regulation of the *nirS*, *norCB*, and *nosR* promoters (Arai *et al.*, 1995; Arai *et al.*, 2003). *P. stutzeri* possesses four *fnr*-like genes, *fnrA*, *dnrD*, *dnrE* and *dnrS*, all co-expressed under denitrifying conditions (Vollack *et al.*, 1999). Despite their low amino acid sequence identity of 25 %, this group of transcription factors share common structural features. All homodimers contain an N-terminal sensor domain, a dimerization helix and a C-terminal DNA binding domain with a Helix-Turn-Helix (HTH) motif. A conformational change of the homodimer induced by the binding of an effector molecule to the sensor domain leads to the active conformation and appropriate binding of the corresponding DNA sequence (Körner *et al.*, 2003; Giardina *et al.*, 2011).

In *D. shibae*, 7 Crp/Fnr-like regulators are described (Dshi_0660, Dshi_3189, Dshi_3191, Dshi_0447, Dshi_2521, Dshi_2528, Dshi_3270). However, only Dshi_0660 carries the cysteine residues for iron sulfer cluster formation (Wagner-Döbler *et al.*, 2010).

In time resolved transcriptome and proteome analyses of a *D. shibae* continuous culture shifted from aerobic to nitrate respiration conditions only three Crp/Fnr-like genes (*dnrD* Dshi_3189, *dnrE* Dshi_3191 and *dnrF* Dshi_3270) showed an increased transcription and proteinformation (Laass *et al.*, 2014). A computational analysis for the classification of the *D. shibae* Crp/Fnr-like regulators was performed according to the phylogenetic tree generated by Körner *et al.*, in 2003 (Körner *et al.*, 2003). To define the role of the DnrF transcription factor a *D. shibae* DFL12^T *dnrF* (Dshi_3270) regulator deletion mutant was created and DNA microarray experiments were performed. Furthermore, protein production of recombinant DnrD, DnrE and DnrF was established for a biochemical protein characterization.

4.2 Materials and Methods Part III

4.2.1 Bacterial strains & media

All bacterial strains used in this work are listed in Table 4.1.

Table 4.1: Bacterial strains

Bacterial strain	Description	Reference.
Dinoroseobacter shibae		
D. shibae DFL12^T	Wildtype, type strain	Biebl *et al.*, 2005
D. shibae ΔdnrF	*ΔdnrF*, Gm^R	This work
Escherichia coli		
E. coli ST18	*E. coli* S17-1*ΔhemA thi pro hsdR*-M-chromosomal integrated [RP4-2 Tc::Mu:Km^r::Tn7, Tra$^+$ Tri^r Str^r]	Thoma and Schobert, 2009
E. coli DH10b	*F- endA1 recA1 galE15 galK16 nupG rpsL ΔlacX74 Φ80lacZΔM15 araD139 Δ(ara,leu)7697 mcrA Δ(mrr-hsdRMS-mcrBC) λ-*	Invitrogen
E. coli BL21 (DE3) pLysS	*F- ompT gal dcm lon hsdSB(rB- mB-) λ(DE3) pLysS(cmR)*	Stratagene

4.2.2 Construction of a *D. shibae* DFL12^T*dnrF* (Dshi_3270) regulator deletion mutant

To obtain a *dnr* gene deletion mutants from *D. shibae* DFL12^T the gene deletion vector pEX18Δ*dnrF*::Gm^R was constructed by cloning the *SacI*-digested **Ω**-gentamicin resistance cassette of pPS858 (Hoang *et al.*, 1998) between two PCR fragments of the upstream and downstream region of the *dnrF* gene (Dshi_3270) in the multiple cloning site of the suicide vector pEX18Ap (Hoang *et al.*, 1998) (See Table 4.2 for plasmids used in this work). A 686-bp fragment containing the upstream promoter region of Dshi_3270 was amplified using primer oPT146 (primers are listed in Table 4.3), which contains a *KpnI* restriction site at the 5´end, and oPT147, containing a *SacI* restriction site. The primers oPT148, containing a *SacI* restriction site, and oPT149, which contains a *HindIII* restriction site, were used to amplify 541 bp of the corresponding downstream region of Dshi_3270. For the plasmid transfer via conjugation *E. coli* ST18, a Δ*hemA* mutant of *E. coli* ST17-1 (Thoma & Schobert, 2009), was used as donor strain as described before (Piekarski *et al.*, 2009). The strain was transformed with the new suicide vector pEX18Δ*dnrF*::Gm^R. Luria Bertani (LB) medium (Roth,

Karlsruhe, Germany) supplemented with 50 µg/ml aminolevulinic acid (ALA) and 100 µg/ml of ampicillin was used for the cultivation of *E. coli* ST18 carrying pEX18Δ*dnrF*::Gm^R, The conjugation process was performed in half-concentrated MB (hMB) also supplemented with 50 µg/ml ALA. For selection of the *D. shibae* $DFL12^T$ *dnrF* regulator deletion mutant, the maiting was plated on hMB supplemented with 80 µg/ml of gentamicin. To confirm homologous recombination PCR analysis was performed.

Table 4.2: Plasmids used in this work

Plasmid	Description	Reference
pEX18AP	ApR; *oriT*$^+$ *sacB*$^+$, gene replacement vector with MCS	(Hoang *et al.*, 1998)
pPS858	Ap^R, Gm^R, *gfp*, vector with Gm*R* selectable FRT cassette	(Hoang *et al.*, 1998)
pEX18Δ*dnrF*::Gm^R	Suicide vector for gene replacement of *dnrF* and Gm^R	This work
pET14b	pET system expression vector	Novagen
pET14b*dnrD*	*dnrD* cloned into NdeI and BamHIII site of pET14b	This work
pET14b*dnrE*	*dnrE* cloned into NdeI and BamHIII site of pET14b	This work
pET14b*dnrF*	*dnrF* cloned into NdeI and BamHIII site of pET14b	This work

Table 4.3: Oligonucleotides used in this work

Name	Sequence	Funktion
oPT146	GACGGTACCCTGATGACGGGCGAGAAC	Upstream Dshi_3270 fw, (KpnI)
oPT147	GACGAGCTCCATCCTTGATCTGTGCCA	Upstream Dshi_3270 rev, (SacI)
oPT148	GACGAGCTCGGAGAGGCACATGACACCT	Downstream Dshi_3270 fw, (SacI)
oPT149	GACAAGCTTGTAAAGGCCGGTGACGATG	Downstream Dshi_3270 rev, (HindIII)
oPT159	CAGCCATATGGCTTTATCGCATCTC	*dnrD* fw (NdeI)
oPT160	CATGGATCCCGCTACATCATGCGCTGG	*dnrD* rev, (BamHI)
oPT161	CGTCATATGACCTTGAACGATAGCG	*dnrE* fw (NdeI)
oPT162	GTAGGATCCACCTCAGCGGACACGGTTG	*dnrE* rev, (BamHI)
oPT163	GTCGCATATGGCACAGATCAAGGATG	*dnrF* fw (NdeI)
oPT164	CATAGGATCCATCAGGCGACGCGGCG	*dnrF* rev, (BamHI)

The type strain *D. shibae* $DFL12^T$ as well as the *D. shibae* $DFL12^T$ *dnrF* regulator deletion mutant were cultured in Marine Bouillon (MB; Roth, Karlsruhe, Germany) at 30°C in bottle

flasks in the dark shaking at 200 rpm. If cultured with the addition of an antibiotic half concentrated Marine Bouillon was used.

4.2.3 Construction of vectors for recombinant protein production

The gene *dnrF* (Dshi_3270) encoding a potential transcription factor involved in expression of genes under nitrate respiratory conditions from *D. shibae* DFL12^T was PCR amplified using the primers oPT163 and oPT164 containing *NdeI* and *BamHI* restriction sites and cloned into a cut pET14b vector (Novagen, Darmstadt, Germany) to generate pET14_dnrF. The vectors pET14_dnrD and pET14_dnrE were generated using the primers oPT159 and oPT160 for *dnrD* and oPT161 and oPT162 for *dnrE*, respectively. Genomic DNA from *D. shibae* DFL12^T was used as template for the corresponding PCR reaction. *E. coli* DH10B was used as a host for construction of production vectors.

4.2.4 Production and purification of recombinant produced proteins

E. coli strain BL21 (DE3) pLysS was used for production of the recombinant proteins. For protein production, *E. coli* BL21 (DE3) pLysS carrying the vector pET14_dnrD, pET14_dnrE and pET14_dnrF, respectively, were grown in 500 ml LB-medium containing 100 µg/ml of ampicillin and 34 µg/ml of chloramphenicol at 37°C and 200 rpm. The medium was inoculated to a starting OD_{578} of 0.05 with an over night pre-culture. At an OD_{578} of 0.6 isopropyl-*β*-D-thiogalactopyranosid (IPTG) was added to the culture to a final concentration of 50 µM for induction of protein production. For protein production the cultures were shifted at 17°C and 200 rpm for 16 hours. The cells were harvested by centrifugation and resulting cell pellets were stored at -20°C.

Precipitated cells were resuspended in 10 ml binding buffer (50 mM Tris-HCl pH 7.5, 300 mM NaCl, 20 mM imidazole). For cell disruption a French press (1200 p.s.i.) was used and a soluble protein fraction was obtained by ultracentrifugation (40000 x g, 65 min, 4 °C). The supernatant was transferred to 1 mL of Ni Sepharose Fast Flow (GE Healthcare, Solingen, Germany). The column was washed two times with 10 ml of washing buffer (50 mM Tris-HCl pH 7.5, 300 mM NaCl, 30 mM imidazole). The bound proteins were eluted with elution buffer (50 mM Tris-HCl pH 7.5, 300 mM NaCl, 300 mM imidazole). The purified recombinant proteins were stored at 4 °C.

Protein fractions were analyzed by SDS-polyacrylamide gel electrophoresis (SDS-PAGE) as described before by (Laemmli, 1970; Righetti, 1990). Protein concentrations were determined

by using the Bradford Reagent (Sigma-Aldrich, St. Louis, USA) according to the manufacturer`s instructions.
For removal of the His-Tag from the various fusion proteins, the Thrombin restriction grade kit (Merck, Darmstadt, Germany) was used according to the manufacturer`s manual.

4.2.5 DNA microarray experiments and data analysis

For the comparative transcriptome analyses *D. shibae* DFL12^T and the *dnrF* deletion mutant were cultured in artificial salt water medium (SWM; 4.0 g $NaSO_4$, 0.2 g KH_2PO_4, 0.25 g NH_4Cl, 20.0 g NaCl, 3.0 g $MgCl_2 \cdot 6\ H_2O$, 0.5 g KCl and 0.15 g $CaCl_2 \cdot 2\ H_2O$, 0.19 g $NaHCO_3$, 0.02 g biotin, 0.2 g nicotinic acid and 0.08 g 4-aminobenzoic acid 5.9 g succinic acid and 1 ml trace solution per liter). The trace element solution contained 2.1 g Fe $(SO_4) \cdot 7\ H_2O$, 13 ml 25 % (v/v) HCl, 5.2 g $Na_2EDTA \cdot 2\ H_2O$, 30 mg H_3BO_3, 0.1 g $MnCl_2 \cdot 4\ H_2O$, 0.19 g $CoCl_2 \cdot 6\ H_2O$, 2 mg $CuCl_2 \cdot 2\ H_2O$, 0.144 g $ZnSO_4 \cdot 7\ H_2O$ and 36 mg $Na_2MoO_4 \cdot 2\ H_2O$ per liter. Bottle flasks were inoculated to a starting OD_{578} of 0.02 with an appropriate preculture and cultivated aerobically at 30 °C in the dark and shaking at 200 rpm. After reaching an OD_{578} of 0.5, the culture was shifted to anaerobic conditions in anaerobic bottles. The oxygen concentration was determined with a sensor spot O2 (PreSence, Regensburg, Germany). Three biological replicates were performed.
A customized whole-genome DNA microarray (8x15 k format; Agilent, Santa Clara, CA) containing three different 60-nucleotide oligonucleotides per gene, covering 96% of the genes of *D. shibae* DFL12^T was designed with the eArray platform from Agilent and used as described before (Tomasch *et al.*, 2011). The investigated time points were before and 60 min after shifting to an anaerobic bottle. Three biological and one technical replicates were performed. Two micrograms of isolated total cellular RNA was labeled with either Cy3 or Cy5 with the ULS fluorescent labeling kit for Agilent arrays (Kreatech, Amsterdam, the Netherlands) according to the manufacturer's manual. Subsequently, 300 ng labeled RNA of the wild-type sample and 300 ng RNA of the mutant gene sample were fragmented and hybridized according to the "two-color microarray" protocol from Agilent. The DNA microarrays were scanned with an Agilent C scanner with the Agilent scan control 8.4.1 software and the feature extraction 10.7.3.1 software. Data processing was performed in the R environment (http://www.cran.r-project.org/) with the limma package, the BioBASE package, and the gplots package of Bioconductor project q (http://www.bioconductor.org/) (Smyth *et al.*, 2005; Miller & Alachi, 1996). The median was calculated and only genes with a

logarithmic change change of > 0.8 in their expression between aerobic (0 min) and anaerobic (60 min) conditions and a *P* value of < 0.05 were considered in subsequent analyses.

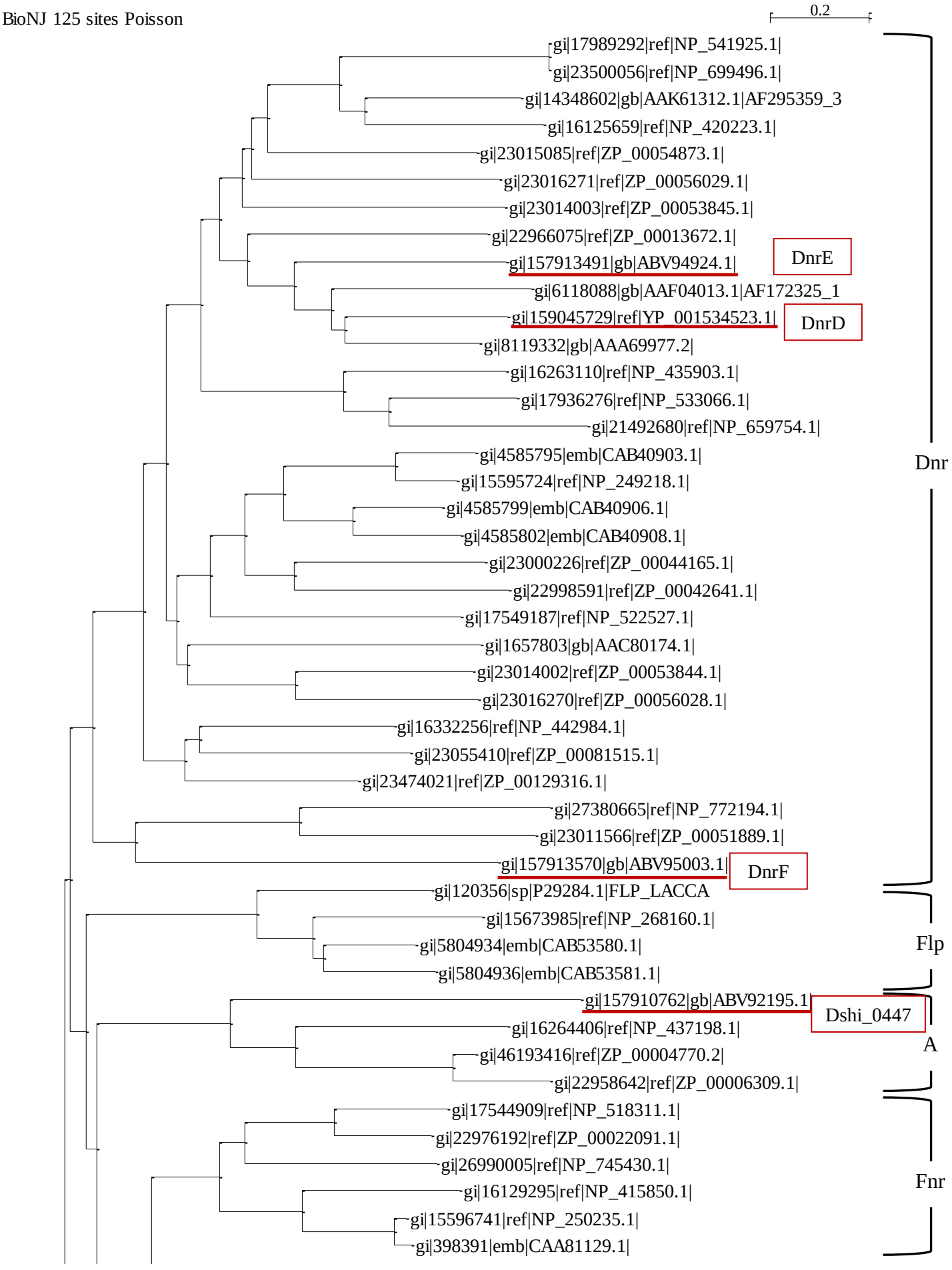
4.2.6 Phylogenetic affiliation of Crp/Fnr-like transcriptional regulators

The Crp/Fnr-like transcription regulators were choosen according to the phylogenetic investigation of Körner *et al*., (Körner *et al.*, 2003). At least two members of every subgroup were selected. All necessary DNA sequences were taken from the NCBI homepage. Table A2 (appendix) lists the NCBI access data and data referred to Körner *et al*, 2003, including the NCBI sequence identification numbers (GI numbers), reference numbers and versions, locus tags and encoded proteins, related proteins (Crp/Fnr group), and the name of the host bacterium. The multiple sequence alignments in FASTA format were processed by the Clustal OMEGA program (Clustal OMEGA). Based on these analyses, a neighbor-joining tree was calculated and displayed by the Seaview software (SEAview).

4.3 Results and Discussion Part III

4.3.1 Computational analysis of Crp/Fnr-like regulators of *D. shibae*

The phylogenetic affiliation of the 7 Crp/Fnr-like regulators of *D. shibae* classifies the analyzed regulators in several branches of the superfamily according to the classification of Körner *et al*. in 2003 (Fig 4.1). The [4Fe-4S] cluster protein FnrL (Dshi_0660) of *D. shibae* clusters as expected in the FnrL subgroup when compared to 84 sequences from the branches of the unrooted neighbor-joining tree. Both regulators DnrD (Dshi_3189) and DnrE (Dshi_3191) localized on the chromosome between the genes coding for enzymes of the denitrification pathway are found integrated in the Dnr branch. Interestingly, a third *D. shibae* protein DnrF (Dshi_3270) is classified as a member of the Dnr-like transcriptional regulators. The predicted Dnr-like protein located at Dshi_0447 is classified into the A subgroup and therefore probably not involved in the regulation of the denitrification pathway, which is supported by the transcriptome analysis described below. The postulated regulators encoded by Dshi_2521 and Dshi_2528 also do not seem to be involved in this regulatory network due to their classification into subgroup B and the described transcriptome analyses (Laass *et al.*, 2014). In addition to the phylogenetic approach, functional predictions can sometimes be derived by genome comparison and analysis of the genomic context (Körner *et al.*, 2003). However, the genome comparison as well as the analysis of the genomic context did not provide information for the possible function of Dshi_2521 and Dshi_2528. Both genes are surrounded by genes coding for hypothetical proteins in the genome of *D. shibae*. The regulator Dshi_0447 is located downstream of genes encoding a F0F1 ATP synthase, which was not differently transcribed under anaerobic conditions (Laass *et al.*, 2014). However, the genomic context of DnrD and DnrE supports the phylogenetic approach due to their location between genes encoding enzymes of the denitrification pathway. On the other hand, the *dnrF* gene is localized upstream of a gene encoding an L-carnitin dehydratase, which does not provide further insights into its function.


BioNJ 125 sites Poisson
0.2
gi|17989292|ref|NP_541925.1|
gi|23500056|ref|NP_699496.1|
gi|14348602|gb|AAK61312.1|AF295359_3
gi|16125659|ref|NP_420223.1|
gi|23015085|ref|ZP_00054873.1|
gi|23016271|ref|ZP_00056029.1|
gi|23014003|ref|ZP_00053845.1|
gi|22966075|ref|ZP_00013672.1|
gi|157913491|gb|ABV94924.1|
DnrE
gi|6118088|gb|AAF04013.1|AF172325_1
gi|159045729|ref|YP_001534523.1|
DnrD
gi|8119332|gb|AAA69977.2|
gi|16263110|ref|NP_435903.1|
gi|17936276|ref|NP_533066.1|
gi|21492680|ref|NP_659754.1|
gi|4585795|emb|CAB40903.1|
gi|15595724|ref|NP_249218.1|
gi|4585799|emb|CAB40906.1|
gi|4585802|emb|CAB40908.1|
gi|23000226|ref|ZP_00044165.1|
gi|22998591|ref|ZP_00042641.1|
gi|17549187|ref|NP_522527.1|
gi|1657803|gb|AAC80174.1|
gi|23014002|ref|ZP_00053844.1|
gi|23016270|ref|ZP_00056028.1|
gi|16332256|ref|NP_442984.1|
gi|23055410|ref|ZP_00081515.1|
gi|23474021|ref|ZP_00129316.1|
gi|27380665|ref|NP_772194.1|
gi|23011566|ref|ZP_00051889.1|
gi|157913570|gb|ABV95003.1|
DnrF
Dnr
gi|120356|sp|P29284.1|FLP_LACCA
gi|15673985|ref|NP_268160.1|
gi|5804934|emb|CAB53580.1|
gi|5804936|emb|CAB53581.1|
Flp
gi|157910762|gb|ABV92195.1|
Dshi_0447
gi|16264406|ref|NP_437198.1|
gi|46193416|ref|ZP_00004770.2|
gi|22958642|ref|ZP_00006309.1|
A
gi|17544909|ref|NP_518311.1|
gi|22976192|ref|ZP_00022091.1|
gi|26990005|ref|NP_745430.1|
gi|16129295|ref|NP_415850.1|
gi|15596741|ref|NP_250235.1|
gi|398391|emb|CAA81129.1|
Fnr

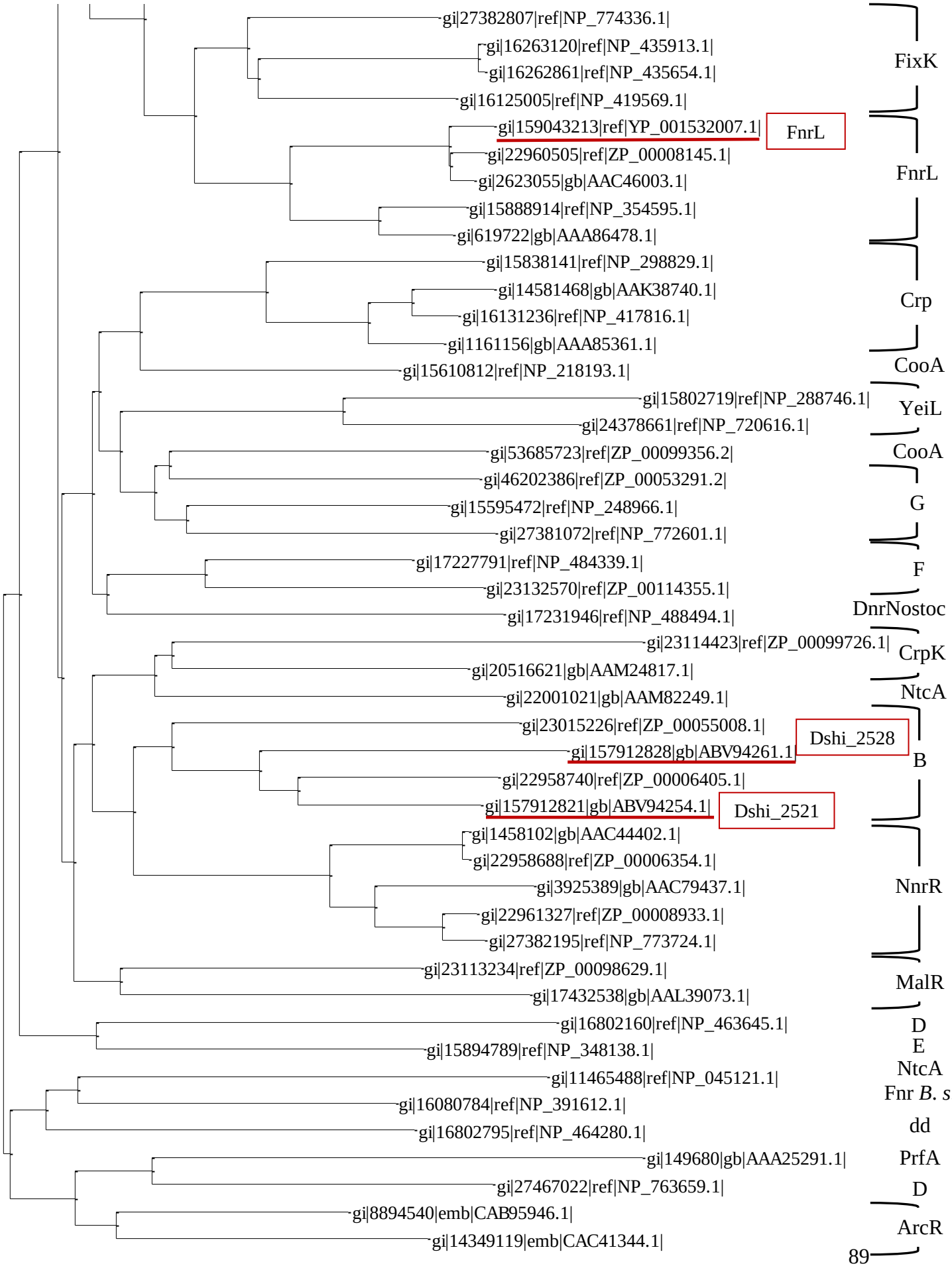

gi|27382807|ref|NP_774336.1|
gi|16263120|ref|NP_435913.1|
gi|16262861|ref|NP_435654.1|
gi|16125005|ref|NP_419569.1|
gi|159043213|ref|YP_001532007.1|
FnrL
gi|22960505|ref|ZP_00008145.1|
gi|2623055|gb|AAC46003.1|
gi|15888914|ref|NP_354595.1|
gi|619722|gb|AAA86478.1|
gi|15838141|ref|NP_298829.1|
gi|14581468|gb|AAK38740.1|
gi|16131236|ref|NP_417816.1|
gi|1161156|gb|AAA85361.1|
gi|15610812|ref|NP_218193.1|
gi|15802719|ref|NP_288746.1|
gi|24378661|ref|NP_720616.1|
gi|53685723|ref|ZP_00099356.2|
gi|46202386|ref|ZP_00053291.2|
gi|15595472|ref|NP_248966.1|
gi|27381072|ref|NP_772601.1|
gi|17227791|ref|NP_484339.1|
gi|23132570|ref|ZP_00114355.1|
gi|17231946|ref|NP_488494.1|
gi|23114423|ref|ZP_00099726.1|
gi|20516621|gb|AAM24817.1|
gi|22001021|gb|AAM82249.1|
gi|23015226|ref|ZP_00055008.1|
gi|157912828|gb|ABV94261.1|
Dshi_2528
gi|22958740|ref|ZP_00006405.1|
gi|157912821|gb|ABV94254.1|
Dshi_2521
gi|1458102|gb|AAC44402.1|
gi|22958688|ref|ZP_00006354.1|
gi|3925389|gb|AAC79437.1|
gi|22961327|ref|ZP_00008933.1|
gi|27382195|ref|NP_773724.1|
gi|23113234|ref|ZP_00098629.1|
gi|17432538|gb|AAL39073.1|
gi|16802160|ref|NP_463645.1|
gi|15894789|ref|NP_348138.1|
gi|11465488|ref|NP_045121.1|
gi|16080784|ref|NP_391612.1|
gi|16802795|ref|NP_464280.1|
gi|149680|gb|AAA25291.1|
gi|27467022|ref|NP_763659.1|
gi|8894540|emb|CAB95946.1|
gi|14349119|emb|CAC41344.1|
FixK
FnrL
Crp
CooA
YeiL
CooA
G
F
DnrNostoc
CrpK
NtcA
B
NnrR
MalR
D
E
NtcA
Fnr *B. s.*
dd
PrfA
D
ArcR
89

Fig. 4.1: Phylogenetic affiliations of Crp/Fnr-like regulators of *D. shibae* into the Crp/Fnr regulators according to Körner *et al.*2003. The unrooted neighbor joining tree shows *D. shibae* Crp/Fnr like regulators underlined (red) in the subgroups Dnr, A, FnrL and B. The members of the tree are identified by their NCBI sequence identification number (GI number). A table of assignment from GI and bacteria species is given in the appendix (**Table A3**).

4.3.2 Transcription profiles of *D. shibae* DFL12^T*dnrF* deletion mutant in comparison to *D. shibae* wild-type under aerobic and nitrate reducing conditions

To investigate the role of DnrF in the regulatory network in *D. shibae*, a *D. shibae* DFL12^{T}Δ*dnrF* (Dshi_3270) deletion mutant was constructed. Furthermore, whole genome microarray analyses were performed to define the influence of DnrF as transcription regulator on the formation of the denitrification apparatus. The *D. shibae* DFL12^{T}Δ*dnrF* (Dshi_3270) deletion mutant and the *D. shibae* wildtype were cultured in three biological replicates aerobically in 150 mL salt water medium with 25 mM nitrate added at an optical density at 578 nm of 0.5. For the aerobic sampling 2 mL were retrieved for RNA isolation. Afterwards, the cultures were shifted to denitrifying conditions in 140 mL in anaerobic bottles and cultivated for an additional hour and 2 mL samples were taken for RNA isolation. The oxygen tension continuously dropped down to the detection limit of 1 ppb after 5 min. Two colour dye swap microarray experiments with samples taken for the deletion mutant in comparison to the wildtype were performed in three biological and one technical replicate. In total, 106 genes were found differently transcribed with a $\log_2$ fold change of ≥ 0.8. Table 4.4 gives an overview of the results.

Table 4.4: Overview of genes differentially transcribed in *D. shibae* DFL12^{T}Δ*dnrF* deletion mutant in comparison to *D. shibae* wild-type under aerobic and anaerobic growth conditions. Overall, samples for three biological and one technical replicates are analyzed.

	overall	induced	repressed
overall	106	59	47
aerobic	83	45	38
only aerobic	38	18	20
anaerobic	68	41	27
only anaerobic	23	14	9
both conditions	45	27	18

Under aerobic growth conditions the expression of 45 genes was found induced and of 38 repressed in the *D. shibae* 12^{T}Δ*dnrF* mutant strain. The expression of 41 genes was found induced and of 27 repressed under denitrifying growth conditions. 38 of all regulated genes

were only detected under aerobic growth conditions and 23 only under denitrifying growth conditions. Under both tested conditions, 45 genes were found differently transcribed, 27 genes were found induced and 18 genes repressed. The DnrF transcriptional regulator seems to be involved in regulatory networks under aerobic and anaerobic growth conditions. Table 4.5 shows the loci, which were differently transcribed in the mutant strain in comparison to the *D. shibae* wildtype.

Table 4.5: Fold changes of genes in gene expression in *D. shibae* DFL12^{T}Δ*dnrF* deletion mutant and the corresponding wildtype under aerobic and anaerobic conditions.

Systematic Name	Gene Name	Description	Fc aerobic	Fc anaerobic
Dshi_0001	*gltD*	glutamate synthase, small subunit		2.27
Dshi_0048		putative transposase		-1.98
Dshi_0107		rubrerythrin		1.89
Dshi_0123		LysR family transcriptional regulator		-2.28
Dshi_0377		hypothetical protein	-2.10	-2.66
Dshi_0450	*pqqA*	coenzyme PQQ biosynthesis protein A	3.14	2.02
Dshi_0457		hypothetical protein	1.94	
Dshi_0468		hypothetical protein	1.85	
Dshi_0472		hypothetical protein	1.90	1.86
Dshi_0473	*adhC*	alcohol dehydrogenase class III/S-(hydroxymethyl)glutathione dehydrogenase	5.07	2.45
Dshi_0474	*fghA*	S-formylglutathione hydrolase	3.58	
Dshi_0475	*cytC*	cytochrome c class I	2.42	
Dshi_0476	*gcd*	quinoprotein glucose dehydrogenase	2.90	
Dshi_0477	*cccA*	cytochrome c protein	2.33	
Dshi_0478		extracellular solute-binding protein	2.12	
Dshi_0482		hypothetical protein	2.13	
Dshi_0561	*fhuD/fecB/ fepB/btuF*	ABC-type cobalamin/Fe3+-siderophores transport system protein		-1.79
Dshi_0685	*apbE*	ApbE family lipoprotein	3.26	
Dshi_0686	*nosR*	regulator of nitric oxide reductase transcription	4.18	2.03
Dshi_0687		binding-protein-dependent transport systems inner membrane component	2.34	
Dshi_0750		hypothetical protein		-1.76
Dshi_0975		LacI family transcription regulator		1.83
Dshi_1094		Fis family transcriptional regulator	7.10	2.89
Dshi_1095		aldehyde dehydrogenase	10.85	3.36
Dshi_1102		hypothetical protein		-1.98
Dshi_1130	*cpaB*	Flp pilus assembly protein CpaB; SAF domain-containing protein	2.34	-2.70
Dshi_1131		hypothetical protein	-2.42	-2.55
Dshi_1132		hypothetical protein	-2.42	-2.57
Dshi_1159		hypothetical protein	-2.17	-2.61
Dshi_1335		hypothetical protein IMG_id: 2500131358	-1.96	-2.55
Dshi_1399	*acsA*	acetate-CoA ligasehypothetical protein; acetyl-coenzyme A synthetase	2.33	
Dshi_1401		ABC transporter related	-1.89	
Dshi_1402		inner-membrane translocator	-2.24	

Table 4.5 (continued)

Systematic Name	*Gene Name*	Description	Fc aerob	Fc anaerob
Dshi_1404		branched-chain amino acid ABC transporter, periplasmic binding protein, putative	-4.08	-2.61
Dshi_1483		hypothetical protein	-2.57	-2.79
Dshi_1507		hypothetical protein	-1.98	
Dshi_1584		hypothetical protein	1.98	2.00
Dshi_1621		ribokinase-like domain-containing protein	-1.93	-1.80
Dshi_1622		hypothetical protein	-2.33	-2.31
Dshi_1633	*iscR*	BadM/Rrf2 family transcriptional regulator		2.37
Dshi_1684	*zwf*	glucose-6-phosphate 1-dehydrogenase	-1.74	
Dshi_1762		putative indolepyruvate oxidoreductase		1.81
Dshi_1845	*fliG*	flagellar motor switch protein FliG		1.86
Dshi_1892		hypothetical protein		2.00
Dshi_2060	*acnB*	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase		1.91
Dshi_2364		hypothetical protein		-2.70
Dshi_2388		glycosyl transferase family protein		1.88
Dshi_2396	*ilvC*	ketol-acid reductoisomerase		2.08
Dshi_2571		RNA methyltransferase, TrmH family, group 3	1.86	
Dshi_2634		hypothetical protein	9.61	3.05
Dshi_2635		pentapeptide repeat-containing protein	3.64	1.88
Dshi_2638		hypothetical protein	-1.82	-1.83
Dshi_2647		hypothetical protein	-2.04	-1.95
Dshi_2658	*coxM*	molybdopterin dehydrogenase FAD-binding	3.22	2.09
Dshi_2659	*coxL1*	carbon monoxide dehydrogenase	3.38	2.50
Dshi_2660	*coxS*	2Fe-2S iron-sulfur cluster binding domain-containing protein	3.02	2.13
Dshi_2661	*coxG*	carbon monoxide dehydrogenase subunit G	2.86	2.28
Dshi_2662		extracellular solute-binding protein	4.85	2.41
Dshi_2663	*exaB*	cytochrome c550, putative	19.01	8.38
Dshi_2664		hypothetical protein	6.66	2.37
Dshi_2665		YVTN beta-propeller repeat-containing protein	12.56	3.72
Dshi_2666		hypothetical protein/ Copper binding protein	20.44	9.41
Dshi_2667		ABC transporter related	5.55	1.87
Dshi_2668		ABC-2 type transporter	1.74	
Dshi_2670		ABC transporter related	6.88	2.48
Dshi_2671		putative ABC transporter periplasmic solute-binding protein	6.23	2.84
Dshi_2672		cytochrome c class I	3.08	
Dshi_2673	*exaA*	quinoprotein ethanol dehydrogenase	15.79	9.27
Dshi_2674		two component LuxR family transcriptional regulator	4.31	2.72
Dshi_2675		hypothetical protein	2.62	1.77
Dshi_2780		hypothetical protein	-1.87	-2.54
Dshi_3096		hypothetical protein	-2.11	-2.47
Dshi_3165	*napA*	nitrate reductase catalytic subunit		1.95
Dshi_3166	*napD*	NapD family protein		2.00
Dshi_3168	*apbE*	ApbE family lipoprotein		-2.38
Dshi_3190	*hemA*	5-aminolevulinate synthase		-1.78
Dshi_3191	*dnrE*	Crp/FNR family transcriptional regulator		-1.93
Dshi_3235		hypothetical protein	-1.78	
Dshi_3269		L-carnitine dehydratase/bile acid-inducible protein F		1.86

Table 4.5 (continued)

Systematic Name	*Gene Name*	Description	Fc aerob	Fc anaerob
Dshi_3270	*dnrF*	CRP/FNR family transcriptional regulator	-15.21	-15.53
Dshi_3359	*flbT*	flagellar biosynthesis repressor FlbT	-1.94	
Dshi_3360	*flaF*	flagellar biosynthesis regulatory protein FlaF	-1.89	
Dshi_3361	*fliC*	flagellin domain-containing protein	-1.91	
Dshi_3380	*motB*	flagellar motor protein-like protein	-2.20	-1.79
Dshi_3433		PAS domain-containing protein		1.88
Dshi_3557		putative CBS domain and cyclic nucleotide-regulated nucleotidyltransferase	3.22	1.84
Dshi_3558		hypothetical protein	2.83	
Dshi_3591		prenyl protease-related	-1.83	
Dshi_3592		Cna B domain-containing protein	-2.00	
Dshi_3698		phage integrase	-1.86	
Dshi_3831		sucrose-6F-phosphate phosphohydrolase	1.75	
Dshi_3832		glucosylglycerol-phosphate synthase	1.81	
Dshi_3841	*gdhA*	glutamate dehydrogenase	1.88	
Dshi_3871		hemolysin-type calcium-binding repeat protein	-2.76	-2.42
Dshi_4071		parallel beta-helix repeat-containing protein; calcium-binding repeat family protein	-2.15	-1.84
Dshi_4114		dTDP-4-dehydrorhamnose 3,5-epimerase	-1.84	
Dshi_4118		glucose-1-phosphate thymidylyltransferase	-1.75	
Dshi_4125		hypothetical protein	-1.75	
Dshi_4130		parallel beta-helix repeat-containing protein	-2.12	
Dshi_4137		hypothetical protein	-1.87	
Dshi_4138		hypothetical protein	-1.94	
Dshi_4139	*gmd*	GDP-mannose 4,6-dehydratase	-1.95	
Dshi_4141		hypothetical protein	-1.76	
Dshi_4144	*wcaG*	hexapaptide repeat-containing transferase	-1.75	
Dshi_4154		beta-lactamase domain-containing protein	5.06	2.65
Dshi_4155		hypothetical protein	7.24	3.85

4.3.3 Definition of the DnrF regulon

Alternative energy generation systems

The comparison of the *D. shibae* wildtype transcriptome with that of the *D. shibae* DFL12^{T}Δ*dnrF* deletion mutant revealed an influence of DnrF on diverse alternative energy generation systems under aerobic as well as under anaerobic growth conditions.

The transcription of the genes *napA* and *napD* encoding the periplasmatic nitrate reductase NapAD were found increased 1.95 and 2.0 fold under anoxic conditions in the *D. shibae* dnrF mutant compared to the wildtype. According to the previous transcriptome analysis of the *D. shibae* wildtype (Laass *et al.*, 2014) with a maximum anaerobic induction of 4.4 and 3.6, DnrF seems to be involved (directly or indirectly) in the repression of the *napAD* expression. A possible DNA binding site according to the Dnr binding site consensus sequence

TTGATN$_4$ATCAA (Körner *et al.*, 2003) was found 97.5 bp downstream of the *napD* open reading frame.

The transcription of the carbon monoxide dehydrogenase (CODH) operon *coxML1SG* (Dshi_2658-Dshi_2661) was found (aerobically 3.22, 3.38, 3.02, 2.86 fold and anaerobically 2.09, 2.50, 2.13 and 2.28 fold, respectively) induced under both tested growth conditions in the mutant strain. This observation indicates repressor function for DnrF. The functional CODH enzyme consists of the small CoxS subunit, which possesses two [2Fe-2S] clusters, the medium subunit CoxM, containing FAD as cofactor and the large subunit CoxL that possesses a molybdenum center. Carbon monoxide is oxidized to carbon dioxide by the CODH yielding in two reducing equivalents, which are passed to the electron transport chain and are used for energy generation (Schübel *et al.*, 1995; Wilcoxen *et al.*, 2011).

Furthermore, the transcription of genes, encoding alternative primary dehydrogenases were found induced in the mutant strain. The transcription of Dshi_0472, homologous to *flhA*, encoding a glutathione-dependent formaldehyde dehydrogenase and Dshi_0473 encoding an alcohol dehydrogenase class III/S-(hydroxymethyl) glutathione dehydrogenase (AdhC) were found induced 1.9 and 5.07 fold aerobically and 1.86 and 2.45 fold under nitrate reducing growth conditions in the *dnrF* mutant. The aerobically enhanced transcription of *fghA* (Dshi_0474) (3.58 fold), encoding the S-formylglutathione hydrolase FghA and of *cytC* (Dshi_0475) (2.42 fold), encoding a class I cytochrome c further indicates *dnrF* repressor function. The spontaneously formed S-(hydroxymethyl) glutathione by glutathione and formaldehyde is hydrolyzed by FghA with the production of $NADH^+ + H^+$ as energy source. Glutathione metabolism is involved in protection against oxygen stress but seemed to be involved in anaerobic sulfide metabolism as well. Furthermore, glutathione S-transferases ensure correct folding, synthesis, regulation and degradation of enzymes (Ras *et al.*, 1995; Vuilleumier, 1997; Roca *et al.*, 2008).

Furthermore, the transcription of several PQQ-dependent dehydrogenases genes was found induced under aerobic conditions in the *dnrF* mutant. The PQQ-containing quinoprotein glucose dehydrogenase (Gcd) encoded by Dshi_0476 catalyzes the oxidation of D-glucose to D-glucono-1,5-lactone and transfers electrons via a specific cytochrome *c* to (Yamada *et al.*, 1993). Downstream of *gcd*, the gene encoding a cytochrome *c* (*cccA*, Dshi_0477) is located. The expression of *cccA* was found 2.9 and 2.13 fold enhanced in the transcriptome analysis under aerobic growth conditions in the *dnrF* mutant.

In addition, the transcription of the quinoprotein ethanol dehydrogenase (QEDH) encoded by the *exaA* gene (Dshi_2673) was found induced 15.79 fold aerobically and 9.27 anaerobically,

respectively. The transcription of the *exaB* gene, encoding a cytochrome c_{550} (Dshi_2663), which accepts the electrons from the QEDH and a gene encoding an aldehyde dehydrogenase with homologies to the *P. aeruginosa exaC* gene (Dshi_1095) were also found 19.01 and 10.85 fold aerobically and 8.38 and 3.36 fold anaerobically induced. Furthermore, the transcription of a gene, encoding an extracellular binding protein (Dshi_2662), which is localized next to *exaB* in *R. capsulatus* SB 1003 and *P. stutzeri* ATCC 17588, was found 4.85 and 2.41 fold enhanced. A transposon mutagenesis by Görisch *et al.*, identified *exaA*, *exaB*, *exaC*, *pqqB*, *pqqC* and *acsA* as essential for growth on ethanol. The *pqqB* and *pqqC* genes encode enzymes involved in PQQ-synthesis. The *acsA* gene encodes an acetyl-CoA synthetase (Görisch, 2003). However, in *D. shibae* the *pqqB* and *pqqC* genes were not found induced. Only the transcription of the *pqqA* gene (Dshi_0450), coding for the coenzyme PQQ biosynthesis protein A (PqqA) was found induced 3.14 fold aerobically and 2.02 fold under denitrifying growth conditions. The transcription of the *acsA* gene (Dshi_1399) was only found 2.33 fold induced under aerobic growth conditions. Furthermore, the transcription of the gene Dshi_2674, encoding a LuxR family transcriptional regulator, which shows amino acid sequence similarities to the two component response regulator ExaE of *P. aeruginosa*, was found enhanced under aerobic (4.31 fold) and anaerobic (2.72 fold) growth conditions. In *P. aeruginosa* ExaE together with the sensor histidine kinase ExaD controls the expression of the *exaA* and *exaBC* genes (Schobert & Görisch, 2001). Interestingly, a virtual footprint analysis revealed an Anr-DNA binding site at position + 220.5 downstream of the exaE start codon indicating a possible repressor role of DnrF for the *exaE* gene (Fig. 4.2; (Münch *et al.*, 2005)).

Promoter Sequence:

```
     1  ATGACCTCGC CAGTCGCATT CCGAAGCGCG ATGATCGTGG ACGATCATCC CCTCTTTCTC GATGCGCTCT CCATGACCTT     80
    81  GCGAACGGTC TCCGACATCG ACGAGATCGC GACTGCGGAC ACGATGGAAT CCGCTCTGTC CCAACTGGAT GGCGCCACAC    160
   161  CGGATGTGAT CGTGCTCGAC CTGAACCTGC CGGACGTGAA CGGGCTCGAC GGGTTGATCC GGCTCAAGAC CGCTGTCCCC    240
   241  TCCACCCCGG TGGTGGTCGT CTCGTCCATG GCCGACAACC GGATGATCAC CTCGACCCTG CGCGTGGGCG CCTCGGGCTT    320
   321  CGTGCCCAAG CACTCCAAGC GCGAAGTCTT CCGCGAAGCC TTCGACGCGA TCCAGAACGG CACGGTCTTC ACCCCCGAGA    400
   401  ACTACGTGCC CAACACCGAT GCCGACAGCC CCCAGAACAA CGCCGAGGAA GCGCTCGCAC GGCTCGGCCT GCTGACCAAG    480
   481  CAGCAGGCCC GCATCCTGCA GCTGATCTGC GCCGGCAAGC TGAACAAGCA GATCGCCTAT GACCTGTCCA TCGCCGAGAC    560
   561  GACCGTGAAG GCCCATGTCA CCGCGATCAT GCGCAAGCTG GGGGTCCAGA GCCGGACGCA GGCGGTTTTG ATTGCACAGG    640
   641  AGGCGAATTT CGCCAATTTT GTGGCGAGCG ACAATACGTT GGCCTGA
```

PWM (species)	Start Position	End Position	Strand	Score	Sequence
Anr | Pseudomonas aeruginosa (strain ATCC 15692 / PAO1)	214	227	-	14.27	TTGAGCCGGATCAA
Anr | Pseudomonas aeruginosa (strain ATCC 15692 / PAO1)	214	227	+	13.99	TTGATCCGGCTCAA

Fig. 4.2: Virtual Footprint analysis of the *D. shibae exaE* gene. The computational analysis predict a possible Anr binding site (red) with the start position +214 to end position 227.

However, in *D. shibae* no ORF homologous to *exaD* was identified. Moreover, the genome organization of the *exa* operon in *D. shibae* is different to that of *P. aeruginosa*. In *P. aeruginosa*, both genes of the *exaBC* operon are cotranscribed from the *exaB* promoter, *exaA* is orientated divergently (Schobert & Görisch, 1999). In *D. shibae exaA* and *exaBC* are not clustered. Four genes encoding ABC transporter associated proteins (Dshi_2667 - Dshi_2671), which were found induced aerobically 5.55, 1.74, 6.88 and 6.23 fold, respectively, and 1.87, 2.48 and 2.84 fold under denitrifying conditions (no fold change was observed for Dshi_2668 under this condition). A gene, ecoding a membrane bound YVTN beta propeller protein (Dshi_2665) was found aerobically induced 12.56 fold and 3.72 fold under anaerobic, denitrifying conditions. The gene, encoding a copper binding protein (Dshi_2666) showed the highest fold change of the approach with 20.44 fold aerobically and 9.41 fold under nitrate reducing conditions. Furthermore, under aerobic conditions the gene Dshi_2672, encoding a cytochrome c class I was found induced 3.08 fold. The expression of the gene Dshi_2664, encoding a hypothetical protein also was found induced 6.66 and 2.37 fold, respectively.

The aerobically -1.89, -2.24 and -4.08 fold reduced transcription of the genes (Dshi_1401, Dshi_1402 and Dshi_1404), encoding a branched chain amino acid ABC transporter suggested a minor role of amino acid utilization. The transcription of the gene *gdhA* (Dshi_3841), encoding a $NADP^+$ specific glutamate dehydrogenase was found 1.88 fold enhanced aerobically. GdhA catalyzes the amination of 2-oxoglutarate to L-glutamate with the concomitant production of $NADP^+$. Interestingly, the transcription of the glutamate synthase small subunit gene *gltD* (Dshi_0001) was found induced 2.27 fold under anaerobic conditions.

The induction of several dehydrogenases genes in the *dnrF* mutant indicated a repressing impact of the *D. shibae* DnrF protein on the regulation of the utilization of various substrates as additional energy sources under aerobic and anaerobic conditions.

Transcriptional regulators

The deletion of the *dnrF* gene also showed an influence on the transcription of the genes of other transcriptional regulators. Under anaerobic growth conditions the transcription of Dshi_0123, encoding a LysR family transcriptional regulator and *dnrE*, encoding the Crp/Fnr

family transcriptional regulator (Dshi_3191) were found decreased in the *dnrF* mutant with a fold change of -2.28 and -1.93, respectively, indicating a positive control by DnrF. In contrast the transcription of Dshi_0975, encoding a LacI family transcriptional regulator and *iscR*, encoding a BadM/Rrf2 family transcriptional regulator (Dshi_1633), were found 1.83 and 2.37 fold increased. Furthermore, the transcription of *nosR1*, encoding the regulator of the nitric oxide reductase (Dshi_0686), Dshi_1094, encoding a Fis family transcription regulator and Dshi_2674, encoding a two component LuxR transcriptional regulator showed an inducted transcription under aerobic conditions of 4.18, 7.1 and 4.31 fold, respectively and under anaerobic growth conditions of 2.03, 2.89 and 2.72 fold, respectively. These findings suggested an influence of DnrF on other transcriptional regulators under aerobic as well as under anaerobic conditions.

Iron-sulfur cluster biogenesis

D. shibae possesses two *apbE* genes (*apbE2* [Dshi_0685], *apbE1* [Dshi_3168]) and a homologous *nosX* (Dshi_3199). The *apbE* gene encodes a membrane-associated lipoprotein and is required in the synthesis of 4-amino-5-hydroxymethyl-2-methyl pyrimidine (HMP) in *Salmonella typhimurium* (Beck & Downs, 1998). The lack of the *apbE* gene results in impaired iron-sulfur cluster metabolism in *Salmonella enterica* and was shown to be zinc and selenium sensitive (Skovran *et al.*, 2004). The homologous *nosX* gene was shown to be essential for nitrous oxide reductase activity in *Paracoccus denitrificans* (Saunders *et al.*, 2000) and *Rhizobium (Sinorhizobium) meliloti* (Chan *et al.*, 1997). A mutation in the *apbE* gene results in a phenotype similar to that of lesions in the *isc* locus in *S. enterica*. ApbE has a role in the assembly and/or the repair of Fe-S clusters (Skovran & Downs, 2003). Fe-S clusters are necessary for enzymes involved in denitrification, cofactor biosynthesis and as oxygen sensor in the global anaerobic regulator FnrL. Therefore, the assembly of Fe-S cluster is essential for the adaptation of *D. shibae* to nitrate respiratory conditions. Interestingly, the transcription of the *apbE1* gene, located in the genome region between the *nap*- and *nir*-operon was found -2.38 fold decreased under anaerobic growth conditions. The *apbE2* gene is found downstream of the gene *nosR1* encoding the nitrous oxide reductase regulator NosR2 (Dshi_0686). Both showed an increased (3.26 and 4.18 fold) transcription under aerobic growth conditions, while under anaerobic growth conditions only the latter was found to have a 2.03 fold increased expression. However, the transcription of the *iscR* (Dshi_1633) gene was found 2.37 fold increased under anaerobic growth conditions. IscR, with a bound Fe-S

cluster acts as a repressor for the *isc* operon under Fe-S cluster sufficient conditions. Under low iron or oxygen stress conditions no Fe-S cluster is formed in the IscR protein and the apo-IscR acts, besides other regulators, as an activator for the transcription of the *suf* operon, which is responsible for Fe-S cluster assembly in this case (Crack *et al.*, 2012). However, DnrF seems to play a direct or indirect role for Fe-S cluster biogenesis under aerobic and under anaerobic conditions.

Flagella biosynthesis

The deletion of the transcription factor DnrF influenced directly or indirectly the flagella biosynthesis and consequently, the motility of *D. shibae*. Under aerobic growth conditions the transcript level of the regulator genes *flbT* (Dshi_3359), *flaF* (Dshi_3360) and *fliC* (Dshi_3360) were found -1.94, -1.89 and 1.91 fold decreased in the mutant under aerobic growth conditions (Table 4.5). Furthermore, the transcription of the flagella motor protein gene *motB* (Dshi_3380) was found decreased under aerobic (-2.20 fold) and under nitrate respiration conditions (-1.79 fold). Interestingly, the gene *fliG* (Dshi_1845), encoding the flagella motor switch protein FliG was found induced 1.86 fold under nitrate respiration conditions. FlbT and FlaF play an important role in the regulation of the *fliC* gene, which encodes a flagellin domain-containing protein. FlbT activates the *fliC* expression, whereas an overexpression of *flaF* in *Brucella melitensis* fails to produce FliC (Ferooz *et al.*, 2011). Moreover, FlaF seems to be involved in filament assembly and is essential for translation of the *fljK* mRNA in *Caulobacter crescentus* (Llewellyn *et al.*, 2005). MotB, together with MotA, forms the stator of the flagella motor, which is driven by the membrane gradient of protons or sodium ions (Kojima & Blair, 2004). The FliG, FliM and FliN proteins belong to the flagella switch and are responsible for direction and rotation of the flagella (Irikura *et al.*, 1993).

Additionally, the transcription of the *cpaB* gene (Dshi_1130) encoding the pilus assembly protein CpaB, which was shown to be homologous to FlgA, a protein involved in the assembly of the P-ring, was found decreased -2.34 fold aerobically and -2.70 fold under nitrate respiration conditions (Pallen & Matzke, 2006). The genes upstream of *cpaB* Dshi_1131 and Dshi_1132 encoding hypothetical proteins, showed also a decrease in transcription (aerobically both -2.42and anaerobically -2.55 fold and -2.57, respectively). In a multiple genome map comparison these two genes were also found upstream of the *cpaB* gene in other members of the Rhodobacterales (MBGD, Microbial Genome Database,

http://mbgd.genome.ad.jp/) (Uchiyama, 2003). Furthermore, the Dshi_2638 gene, a homologous of Dshi_1131 and Dshi_1132 was found to be -1.82 fold and -1.83 fold less expressed under both conditions.
These findings suggest an influence of DnrF on the biosynthesis of the flagella in *D. shibae*.

Hypothetical proteins

Overall 32 genes annotated as hypothetical proteins showed differential transcription profiles in the *D. shibae* DFL12^{T}*dnrF* deletion mutant in comparison to the wild type. Eleven genes were found induced with a maximum fold change of 20.44 (Dshi_2666, putative copper binding protein) and 19 repressed with a maximum fold change of 2.79 (Dshi_1483). However, 10 genes were only detected under aerobic and 4 genes under anaerobic growth conditions.

4.3.4 Recombinant protein production of the *D. shibae* DnrD, DnrE and DnrF protein in *E. coli* BL21 (DE3)

The *dnrF* gene was amplified from *D. shibae* chromosomal DNA with restriction sites for cloning into appropriate expression vectors as described in the Materials and Methods. Afterwards the digested and purified gene was cloned into the digested pET14b expression vector encoding a T7 promoter, an N-terminal His-Tag, a thrombin restriction site and a T7 terminator (Fig. 4.3). The same procedure was applied to *dnrD* and *dnrE*.

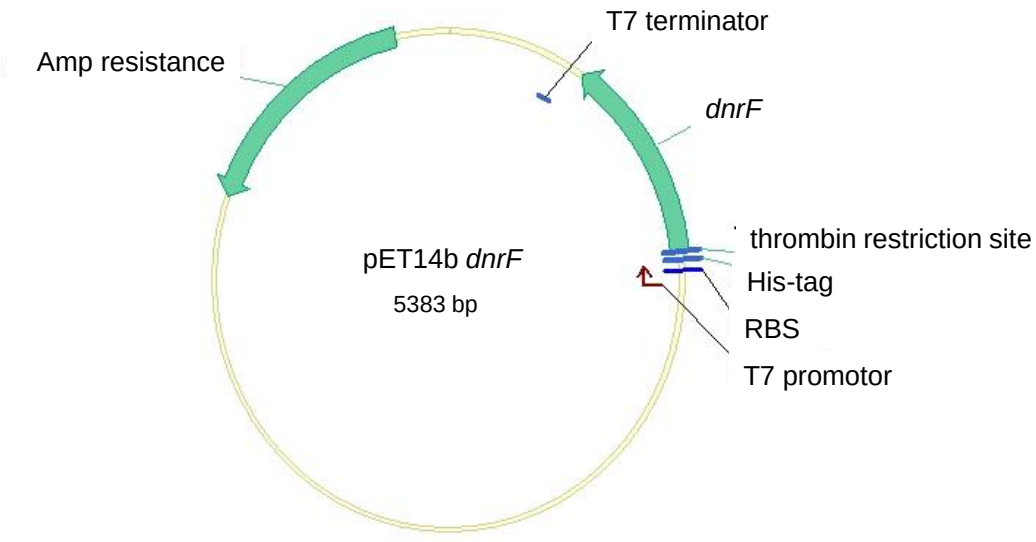


Fig. 4.3: Vector map of pET14b*dnrF*. The *dnrF* gene is cloned into the *NdeI* - *BamHIII* restriction sites

The recombinant protein production of DnrD, DnrE and DnrF in *E. coli* BL12 (DE3) using the plasmids pET14b*dnrD*, pET14b*dnrE* and pET14b*dnrF* was performed as outlined in the Materials and Methods section. Purification of the recombinantly produced proteins was performed using nickel sepharose fast flow affinity chromatography. A temperature of 25°C for DnrD, in comparison to 17°C for DnrE and DnrF, was determined as the optimal according to the weaker background observed in SDS PAGE analysis. Fig. 4.4 provides documentation of the purification procedure. Same results were found for the production of DnrE and DnrF (Data not shown).

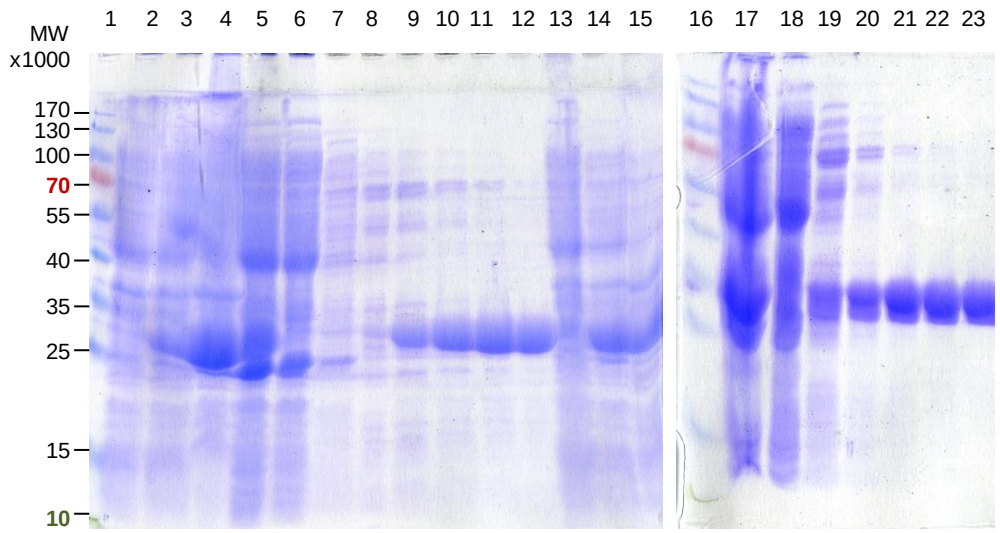


Fig. 4.4: Production and purification of recombinant *D. shibae* DnrD. Proteins were separated by 12 % SDS Page and visualized by Coomassie blue staining. Lane 1 and 16: PageRuler^{TM} Prestained Protein Ladder, lane 2 - 12: production temperature 17°C, lane 13 – 23: production temperature 25°C, lane 2 (13) and 3 (14): *E. coli* BL21 (DE3) cell carrying pET14b*dnrD* before (lane 2/13) and 4 h after induction with 50 µM IPTG (lane 3/14), lane 4 (15) and 5 (17): pellet (lane 4/15) and soluble fraction (lane 5/17) after ultracentrifugation, lane 6 (18): flow through, lane 7: wash fraction, lane 8 – 12 (19 – 23): eluate fraction 1 – 5.

SDS PAGE analysis of the purified protein (lane 22 - 23) resulted in a major band corresponding to a protein with a Mr of 27 000 +/- 5000, which correlates with the calculated DnrD molecular mass of 27,965 kDa. About 40 mg of purified DnrD were obtained per liter cell culture. The purification of DnrE and DnrF yielded in 50 mg and 34 mg per liter cell culture respectively.

5 Summary

Dinoroseobacter shibae is a marine bacterium and belongs to the ubiquitously found Roseobacter clade. It is found in the sediment, the water column and attached to dinoflagellates and. Investigation of the genome sequence identified genes encoding enzymes of the anaerobic metabolism. Correspondingly, anaerobic growth was observed under nitrate respiratory conditions. Furthermore, 7 Crp/Fnr like regulators were annotated, which leads to the question for the gene regulatory network, proteomic and metabolomic networks controlling the transition between aerobic and anaerobic growth.

To answer this question, an aerobic continuously cultivation of *D. shibae* in a chemostate in minimal media supplemented with was established. Time resolved shift experiments from oxic to anoxic growth conditions were performed to characterize the transcriptomic, proteomic and metabolomic adaptation of *D. shibae*. The transcriptome and proteome data revealed a strong expression of operons encoding proteins for the formation of the denitrification machinery. Furthermore, the expression of the genes encoding the Crp/Fnr like regulators *dnrD*, *dnrE* and *dnrF* was also found increased, which leads to the assumption of involvement in the regulatory network for the establishment of nitrate respiratory conditions. Moreover, the synthesis of PHB was observed under these conditions and verified by transmission electronic microscopy and HPLC analyses.

Using a bioinformatics approach the phylogenetic affiliation of DnrE, DnrD and DnrF into the various subfamily of Crp/Fnr like regulators was achieved. Furthermore, comparative transcriptome analyses of wildtype and *dnrF* deletion mutant revealed the mainly repressing influence of DnrF on several genes encoding for enzymes of the energy generation machinery, transcription factors and iron-sulfur cluster proteins under oxic and anoxic conditions. This leads to the consumption of DnrF acts mainly as a oxygen independent repressor.

To identify the essential genes of *D. shibae* for growth under nitrate respiratory conditions a transposon mutagenesis approach was established. Over 4500 mutants were screened for a growth failure under these conditions. Finally, 53 strains showed a growth defect or even no growth. Genes encoding the periplasmic nitrate reductase NapA, the molybdopterin biosynthesis protein MoeB, the cytochrome *c* biogenesis protein DsbC and the pyruvate dehydrogenase PdhB were found to be essential. In comparison with the transcriptomic and proteomic profile of *D. shibae* only 3 genes (*napA*, *phaA* and the Na^+/P_i antiporter gene

Dshi_0543) showed an overlap of induced and essential. Furthermore, highly induced genes (*nirS*) are not essential for the growth under nitrate respiratory conditions.

Overall, this thesis contributed to general understanding of the molecular adaptation strategies of marine bacteria to limited conditions.

6 Zusammenfassung

Dinoroseobacter shibae ist ein Meeresbakterium, das zu den ubiquitär zu findenden Roseobacter Cluster gehört. Es kann im Sediment, freilebend und assoziiert mit Dinoflagellaten gefunden werden. Die Untersuchung des sequenziertem Genoms identifizierte Gene, die für Enzyme des anaeroben Metabolismus codieren. Weiterhin wurden 7 Crp/Fnr ähnliche Transkriptionsregulatoren annotiert, was die Frage nach dem genregulatorischem, proteomischem und metabolomischem Netzwerk aufwirft, das die Anpassung von aeroben zu anaeroben Wachstumsbedingungen kontrolliert.

Daher wurde in dieser Arbeit zunächst eine kontinuierliche Kultivierung von *Dinoroseobacter shibae* im Chemostaten unter aeroben Bedingungen in Minimalmedium etabliert. Zeitaufgelöste Shift Experimente von oxischen zu nitratrespiratorischen Wachstumsbedingungen wurden zur Charakterisierung der Anpassung von *D. shibae* auf transkriptioneller, translationeller und metabolischer Ebene durchgeführt. Die Transkriptom- und Proteomdaten zeigten eine starke Expression der Operons, die für Proteine der Denitrifikation codieren. Weiterhin wurde die Expression von Genen, die für die Proteine der Crp/Fnr Familie *dnrD*, *dnrE* und *dnrF* codieren, auch induziert vorgefunden, was zu der Annahme führt, dass diese in das regulatorische Netzwerk der Adaption an Nitratrespiratorische Bedingungen beteiligt sind. Zusätzlich wurde die Synthese von PHB unter diesen Bedingungen beobachtet und mittels Transmissionselektronenmikroskop und HPLC Analyse nachgewiesen.

Durch eine bioinformatische Stammbaumanalyse konnten DnrD, DnrE und DnrF in die Unterfamilie Dnr klassifiziert werden. Vergleichende DNA Microarray Experimente des Wildtyps und einer *dnrF* Deletionsmutante zeigten einen zumeist reprimierenden Einfluss von DnrF auf die Expression verschiedener Gene, codierend für Energiegewinnung, Transkriptionsfaktoren und Eisen-Schwefel Cluster Proteinen unter aeroben und anaeroben Bedingungen. Diese Ergebnisse weisen darauf hin, dass DnrF meist als Sauerstoff unabhängiger Repressor fungiert.

Zur Identifizierung von essentiellen Genen, die in *D. shibae* für das Wachstum unter Nitratrespiratorischen Bedingungen benötigt werden, wurde eine Transposonmutagenese etabliert. Über 4500 Mutanten wurden nach Wachstumsversuche untersucht. Hier zeigten 53 Mutanten ein geringeres oder kein Wachstum. Essentiell für das Wachstum wurden z. B. die Gene, die für die periplasmatische Nitratreduktase NapA, das Molybdopterin Biosynthese Protein MoeB, das Cytochrome c Biosynthese Protein DsbC und die Pyruvat-dehydrogenase

PdhB identifiziert. Im Vergleich mit dem Transkriptom und Proteom von *D. shibae* wurden nur 3 Gene (*napA*, *phaA* and the Na^+/P_i antiporter gene Dshi_0543) identifiziert, die sowohl essentiell als auch induziert unter diesen Bedingungen sind. Weiterhin konnte gezeigt werden, dass stark induzierte Gene wie z.B. *nirS* nicht essentiell für das Wachstum unter nitratrespiratorischen Bedingungen ist.

7 Outlook

This work investigated the adaptation of *D. shibae* from oxic to anoxic conditions on transcriptomic, proteomic and metabolic level. The results raise new questions of fine tuning gene regulation under anoxic conditions as well in characterizing Crp/Fnr like regulators.

I. Resolution of the anoxic regulatory network in *D. shibae*:

- Construction of Crp/Fnr like regulator mutant strains
- DNA microarray experiments (or RNA-Sequencing) to unravel the transcriptomic response in comparison to the wildtype and other mutant strains

II. Identification of DNA binding sites and target genes:

- Bioinformatics search and identification of possible DNA binding sites in the genome of *D. shibae* with the consensus sequences described of close related transcription factors.
- Identification of DNA binding sites via Electrophoretic Mobility Shift Assay (EMSA) of the Crp/Fnr like regulator with predicted target DNA.
- Reporter gene assay *in vivo* to validate the binding
- Identification of the consensus sequence by using a DNaseI-footprinting assay

III. Characterization of transcriptional regulators:

- Identification of possible cofactors:
- UV/VIS spectroscopy under aerobic and anaerobic conditions and reconstitution of the protein with a predicted cofactor
- A crystallization approach to determine the structure and binding of target DNA and cofactor

References

Allgaier, M., Uphoff, H., Felske, A. & Wagner-Döbler, I. (2003) *Aerobic anoxygenic photosynthesis in Roseobacter clade bacteria from diverse marine habitats. Applied and environmental microbiology*, **69**, 5051–5059.

Allocati, N., Federici, L., Masulli, M. & Di Ilio, C. (2012) *Distribution of glutathione transferases in Gram-positive bacteria and Archaea. Biochimie*, **94**, 588–596.

Ansede, J.H., Friedman, R. & Yoch, D.C. (2001) *Phylogenetic analysis of culturable dimethyl sulfide-producing bacteria from a spartina-dominated salt marsh and estuarine water. Applied and environmental microbiology*, **67**, 1210–1217.

Arai, H. (2011) *Regulation and Function of Versatile Aerobic and Anaerobic Respiratory Metabolism in Pseudomonas aeruginosa. Frontiers in microbiology*, **2**, 103.

Arai, H., Igarashi, Y. & Kodama, T. (1995) *Expression of the nir and nor genes for denitrification of Pseudomonas aeruginosa requires a novel CRP/FNR-related transcriptional regulator, DNR, in addition to ANR. FEBS letters*, **371**, 73–76.

Arai, H., Kodama, T. & Igarashi, Y. (1997) *Cascade regulation of the two CRP/FNR-related transcriptional regulators (ANR and DNR) and the denitrification enzymes in Pseudomonas aeruginosa. Molecular microbiology*, **25**, 1141–1148.

Arai, H., Mizutani, M. & Igarashi, Y. (2003) *Transcriptional regulation of the nos genes for nitrous oxide reductase in Pseudomonas aeruginosa. Microbiology (Reading, England)*, **149**, 29–36.

Arata, H., Shimizu, M. & Takamiya, K. (1992) *Purification and properties of trimethylamine N-oxide reductase from aerobic photosynthetic bacterium Roseobacter denitrificans. Journal of biochemistry*, **112**, 470–475.

Azam, F., Fenchel, T., Field, J., Gray, J., Meyer-Reil, L. & Thingstad, F. (1983) *The ecological role of water-column microbes in the sea. Mar. Ecol. Prog. Ser.*, 257–263.

Barondess, J.J. & Beckwith, J. (1990) *A bacterial virulence determinant encoded by lysogenic coliphage lambda. Nature*, **346**, 871–874.

Barondess, J.J. & Beckwith, J. (1995) *bor gene of phage lambda, involved in serum resistance, encodes a widely conserved outer membrane lipoprotein. Journal of bacteriology*, **177**, 1247–1253.

Beck, B.J. & Downs, D.M. (1998) *The apbE gene encodes a lipoprotein involved in thiamine synthesis in Salmonella typhimurium. Journal of bacteriology*, **180**, 885–891.

Bedzyk, L., Wang, T. & Ye, R.W. (1999) *The periplasmic nitrate reductase in Pseudomonas sp. strain G-179 catalyzes the first step of denitrification. Journal of bacteriology*, **181**, 2802–2806.

Bell, L.C., Richardson, D.J. & Ferguson, S.J. (1990) *Periplasmic and membrane-bound respiratory nitrate reductases in Thiosphaera pantotropha. The periplasmic enzyme catalyzes the first step in aerobic denitrification. FEBS letters*, **265**, 85–87.

Berger, M., Neumann, A., Schulz, S., Simon, M. & Brinkhoff, T. (2011) *Tropodithietic acid production in Phaeobacter gallaeciensis is regulated by N-acyl homoserine lactone-mediated quorum sensing. Journal of bacteriology*, **193**, 6576–6585.

Berkmen, M., Boyd, D. & Beckwith, J. (2005) *The nonconsecutive disulfide bond of Escherichia coli phytase (AppA) renders it dependent on the protein-disulfide isomerase, DsbC. The Journal of biological chemistry*, **280**, 11387–11394.

Bertani, I., Rampioni, G., Leoni, L. & Venturi, V. (2007) *The Pseudomonas putida Lon protease is involved in N-acyl homoserine lactone quorum sensing regulation. BMC microbiology*, **7**, 71.

Bevers, L.E., Hagedoorn, P.-L., Santamaria-Araujo, J.A., Magalon, A., Hagen, W.R. & Schwarz, G. (2008) *Function of MoaB proteins in the biosynthesis of the molybdenum and tungsten cofactors. Biochemistry*, **47**, 949–956.

Bhosale, M., Kumar, A., Das, M., Bhaskarla, C., Agarwal, V. & Nandi, D. (2013) *Catalytic activity of Peptidase N is required for adaptation of Escherichia coli to nutritional downshift and high temperature stress. Microbiological research*, **168**, 56–64.

Biebl, H., Allgaier, M., Tindall, B.J., Koblizek, M., Lünsdorf, H., Pukall, R. & Wagner-Döbler, I. (2005) *Dinoroseobacter shibae gen. nov., sp. nov., a new aerobic phototrophic bacterium isolated from dinoflagellates. International journal of systematic and evolutionary microbiology*, **55**, 1089–1096.

Bird, L.J., Coleman, M.L. & Newman, D.K. (2013) *Iron and copper act synergistically to delay anaerobic growth of bacteria. Applied and environmental microbiology*, **79**, 3619–3627.

Board, P.G. & Menon, D. (2013) *Glutathione transferases, regulators of cellular metabolism and physiology. Biochimica et biophysica acta*, **1830**, 3267–3288.

Börner, J., Buchinger, S. & Schomburg, D. (2007) *A high-throughput method for microbial metabolome analysis using gas chromatography/mass spectrometry. Analytical biochemistry*, **367**, 143–151.

Bradford, M.M. (1976) *A rapid and sensitive method for the quantitation of microgram quantities of protein utilizing the principle of protein-dye binding. Analytical biochemistry*, **72**, 248–254.

Brigé, A., Cole, J.A., Hagen, W.R., Guisez, Y. & van Beeumen, J.J. (2001) *Overproduction, purification and novel redox properties of the dihaem cytochrome c, NapB, from Haemophilus influenzae. The Biochemical journal*, **356**, 851–858.

Brinkhoff, T., Bach, G., Heidorn, T., Liang, L., Schlingloff, A. & Simon, M. (2004) *Antibiotic production by a Roseobacter clade-affiliated species from the German Wadden Sea and its antagonistic effects on indigenous isolates. Applied and environmental microbiology*, **70**, 2560–2565.

Brinkhoff, T., Giebel, H.-A. & Simon, M. (2008) *Diversity, ecology, and genomics of the Roseobacter clade: a short overview. Archives of microbiology*, **189**, 531–539.

Bruhn, J.B., Gram, L. & Belas, R. (2007) *Production of antibacterial compounds and biofilm formation by Roseobacter species are influenced by culture conditions. Applied and environmental microbiology*, **73**, 442–450.

Buchan, A., González, J.M. & Moran, M.A. (2005) *Overview of the marine roseobacter lineage. Applied and environmental microbiology*, **71**, 5665–5677.

Buddruhs, N., Pradella, S., Göker, M., Päuker, O., Pukall, R., Spröer, C., Schumann, P., Petersen, J. & Brinkhoff, T. (2013) *Molecular and phenotypic analyses reveal the non-identity of the Phaeobacter gallaeciensis type strain deposits CIP 105210T and DSM 17395. International journal of systematic and evolutionary microbiology*, **63**, 4340–4349.

Buist, G., Steen, A., Kok, J. & Kuipers, O.P. (2008) *LysM, a widely distributed protein motif for binding to (peptido)glycans. Molecular microbiology*, **68**, 838–847.

Butler, S.M., Festa, R.A., Pearce, M.J. & Darwin, K.H. (2006) *Self-compartmentalized bacterial proteases and pathogenesis. Molecular microbiology*, **60**, 553–562.

Castiglione, N., Rinaldo, S., Giardina, G. & Cutruzzolà, F. (2009) *The transcription factor DNR from Pseudomonas aeruginosa specifically requires nitric oxide and haem for the activation of a target promoter in Escherichia coli. Microbiology (Reading, England)*, **155**, 2838–2844.

Chan, Y.K., McCormick, W.A. & Watson, R.J. (1997) *A new nos gene downstream from nosDFY is essential for dissimilatory reduction of nitrous oxide by Rhizobium (Sinorhizobium) meliloti. Microbiology (Reading, England)*, **143 (Pt 8)**, 2817–2824.

Chandu, D. & Nandi, D. (2003) *PepN is the major aminopeptidase in Escherichia coli: insights on substrate specificity and role during sodium-salicylate-induced stress. Microbiology (Reading, England)*, **149**, 3437–3447.

Chen, Y., Wang, F., Xu, J., Mehmood, M.A. & Xiao, X. (2011) *Physiological and evolutionary studies of NAP systems in Shewanella piezotolerans WP3. The ISME journal*, **5**, 843–855.

Claret, L. & Hughes, C. (2000) *Rapid turnover of FlhD and FlhC, the flagellar regulon transcriptional activator proteins, during Proteus swarming. Journal of bacteriology*, **182**, 833–836.

Comolli, J.C. & Donohue, T.J. (2004) *Differences in two Pseudomonas aeruginosa cbb3 cytochrome oxidases. Molecular microbiology*, **51**, 1193–1203.

Crack, J.C., Gaskell, A.A., Green, J., Cheesman, M.R., Le Brun, N.E. & Thomson, A.J. (2008) *Influence of the environment on the [4Fe-4S]2+ to [2Fe-2S]2+ cluster switch in the transcriptional regulator FNR. Journal of the American Chemical Society*, **130**, 1749–1758.

Crack, J.C., Green, J., Thomson, A.J. & Le Brun, N.E. (2012) *Iron-sulfur cluster sensor-regulators. Current opinion in chemical biology*, **16**, 35–44.

Cumby, N., Edwards, A.M., Davidson, A.R. & Maxwell, K.L. (2012) *The bacteriophage HK97 gp15 moron element encodes a novel superinfection exclusion protein. Journal of bacteriology*, **194**, 5012–5019.

Dahl, J.-U., Urban, A., Bolte, A., Sriyabhaya, P., Donahue, J.L., Nimtz, M., Larson, T.J. & Leimkühler, S. (2011) *The identification of a novel protein involved in molybdenum cofactor biosynthesis in Escherichia coli. The Journal of biological chemistry*, **286**, 35801–35812.

Davies, R.L., Parton, R., Coote, J.G., Gibbs, H.A. & Freer, J.H. (1992) *Outer-membrane protein and lipopolysaccharide variation in Pasteurella haemolytica serotype A1 under different growth conditions. Journal of general microbiology*, **138**, 909–922.

Denoncin, K., Vertommen, D., Paek, E. & Collet, J.-F. (2010) *The protein-disulfide isomerase DsbC cooperates with SurA and DsbA in the assembly of the essential β-barrel protein LptD. The Journal of biological chemistry*, **285**, 29425–29433.

Depuydt, M., Messens, J. & Collet, J.-F. (2011) *How proteins form disulfide bonds. Antioxidants & redox signaling*, **15**, 49–66.

Don, C.D., Hanselmann, K.W., Peduzzi, R. & Bachofen, R. (1994) *Biomass composition and methods for the determination of metabolic reserve polymers in phototrophic sulfur bacteria. Aquat. Sci.*, 1–15.

Douillard, F.P., Ryan, K.A., Hinds, J. & O'Toole, P.W. (2009) *Effect of FliK mutation on the transcriptional activity of the {sigma}54 sigma factor RpoN in Helicobacter pylori. Microbiology (Reading, England)*, **155**, 1901–1911.

Dower, W.J., Miller, J.F. & Ragsdale, C.W. (1988) *High efficiency transformation of E. coli by high voltage electroporation. Nucleic acids research*, **16**, 6127–6145.

Drüppel, K., Hensler, M., Trautwein, K., Koßmehl, S., Wöhlbrand, L., Schmidt-Hohagen, K., Ulbrich, M., Bergen, N., Meier-Kolthoff, J.P., Göker, M., Klenk, H.-P., Schomburg, D. & Rabus, R. (2014) *Pathways and substrate-specific regulation of amino acid degradation in Phaeobacter inhibens DSM 17395 (archetype of the marine Roseobacter clade). Environmental microbiology*, **16**, 218–238.

Durand, S. & Storz, G. (2010) *Reprogramming of anaerobic metabolism by the FnrS small RNA. Molecular microbiology*, **75**, 1215–1231.

Dybvig, K., Sitaraman, R. & French, C.T. (1998) *A family of phase-variable restriction enzymes with differing specificities generated by high-frequency gene rearrangements. Proceedings of the National Academy of Sciences of the United States of America*, **95**, 13923–13928.

Ebert, M. & Laaß, S. (2013) *Transposon mutagenesis identified chromosomal and plasmid genes essential for adaptation of the marine bacterium Dinoroseobacter shibae to anaerobic conditions. Journal of bacteriology*, **195**, 4769–4777.

Edgar, R., Domrachev, M. & Lash, A.E. (2002) *Gene Expression Omnibus: NCBI gene expression and hybridization array data repository. Nucleic acids research*, **30**, 207–210.

Edwards, M.D., Black, S., Rasmussen, T., Rasmussen, A., Stokes, N.R., Stephen, T.-L., Miller, S. & Booth, I.R. (2012) *Characterization of three novel mechanosensitive channel activities in Escherichia coli. Channels (Austin, Tex.)*, **6**, 272–281.

Ekici, S., Pawlik, G., Lohmeyer, E., Koch, H.-G. & Daldal, F. (2012) *Biogenesis of cbb(3)-type cytochrome c oxidase in Rhodobacter capsulatus. Biochimica et biophysica acta*, **1817**, 898–910.

Eser, M., Masip, L., Kadokura, H., Georgiou, G. & Beckwith, J. (2009) *Disulfide bond formation by exported glutaredoxin indicates glutathione's presence in the E. coli periplasm. Proceedings of the National Academy of Sciences of the United States of America*, **106**, 1572–1577.

Ferooz, J., Lemaire, J. & Letesson, J.-J. (2011) *Role of FlbT in flagellin production in Brucella melitensis. Microbiology (Reading, England)*, **157**, 1253–1262.

Fidopiastis, P.M., Rader, B.A., Gerling, D.G., Gutierrez, N.A., Watkins, K.H., Frey, M.W., Nyholm, S.V. & Whistler, C.A. (2012) *Characterization of a Vibrio fischeri aminopeptidase and evidence for its influence on an early stage of squid colonization. Journal of bacteriology*, **194**, 3995–4002.

Figueroa-Bossi, N. & Bossi, L. (1999) *Inducible prophages contribute to Salmonella virulence in mice. Molecular microbiology*, **33**, 167–176.

Fleischhacker, A.S. & Kiley, P.J. (2011) *Iron-containing transcription factors and their roles as sensors. Current opinion in chemical biology*, **15**, 335–341.

Folsom, J.P., Richards, L., Pitts, B., Roe, F., Ehrlich, G.D., Parker, A., Mazurie, A. & Stewart, P.S. (2010) *Physiology of Pseudomonas aeruginosa in biofilms as revealed by transcriptome analysis. BMC microbiology*, **10**, 294.

Forward, J.A., Behrendt, M.C., Wyborn, N.R., Cross, R. & Kelly, D.J. (1997) *TRAP transporters: a new family of periplasmic solute transport systems encoded by the dctPQM genes of Rhodobacter capsulatus and by homologs in diverse gram-negative bacteria. Journal of bacteriology*, **179**, 5482–5493.

Fu, G.K., Smith, M.J. & Markovitz, D.M. (1997) *Bacterial protease Lon is a site-specific DNA-binding protein. The Journal of biological chemistry*, **272**, 534–538.

Fujinaga, K., Taniguchi, Y., Sun, Y., Katayama, S., Minami, J., Matsushita, O. & Okabe, A. (1999) *Analysis of genes involved in nitrate reduction in Clostridium perfringens. Microbiology (Reading, England)*, **145 (Pt 12)**, 3377–3387.

Fürch, T., Preusse, M., Tomasch, J., Zech, H., Wagner-Döbler, I., Rabus, R. & Wittmann, C. (2009) *Metabolic fluxes in the central carbon metabolism of Dinoroseobacter shibae and Phaeobacter gallaeciensis, two members of the marine Roseobacter clade. BMC microbiology*, **9**, 209.

Gade, D., Thiermann, J., Markowsky, D. & Rabus, R. (2003) *Evaluation of two-dimensional difference gel electrophoresis for protein profiling. Soluble proteins of the marine bacterium Pirellula sp. strain 1. Journal of molecular microbiology and biotechnology*, **5**, 240–251.

Gates, A.J., Luque-Almagro, V.M., Goddard, A.D., Ferguson, S.J., Roldán, M.D. & Richardson, D.J. (2011) *A composite biochemical system for bacterial nitrate and nitrite assimilation as exemplified by Paracoccus denitrificans. The Biochemical journal*, **435**, 743–753.

Geng, H. & Belas, R. (2010) *Molecular mechanisms underlying roseobacter-phytoplankton symbioses. Current opinion in biotechnology*, **21**, 332–338.

Giaouris, E., Samoilis, G., Chorianopoulos, N., Ercolini, D. & Nychas, G.-J. (2013) *Differential protein expression patterns between planktonic and biofilm cells of Salmonella enterica serovar Enteritidis PT4 on stainless steel surface. International journal of food microbiology*, **162**, 105–113.

Giardina, G., Castiglione, N., Caruso, M., Cutruzzolà, F. & Rinaldo, S. (2011) *The Pseudomonas aeruginosa DNR transcription factor: light and shade of nitric oxide-sensing mechanisms. Biochemical Society transactions*, **39**, 294–298.

Giardina, G., Rinaldo, S., Castiglione, N., Caruso, M. & Cutruzzolà, F. (2009) *A dramatic conformational rearrangement is necessary for the activation of DNR from Pseudomonas aeruginosa. Crystal structure of wild-type DNR. Proteins*, **77**, 174–180.

Giardina, G., Rinaldo, S., Johnson, K.A., Di Matteo, A., Brunori, M. & Cutruzzolà, F. (2008) *NO sensing in Pseudomonas aeruginosa: structure of the transcriptional regulator DNR. Journal of molecular biology*, **378**, 1002–1015.

Glud, R.N. (2008) *Oxygen dynamics of marine sediments. Marine Biology Research*, **4**, 243–289.

Gonzalez, B., Graaf, A. de, Renaud, M. & Sahm, H. (2000) *Dynamic in vivo (31)P nuclear magnetic resonance study of Saccharomyces cerevisiae in glucose-limited chemostat culture during the aerobic-anaerobic shift. Yeast (Chichester, England)*, **16**, 483–497.

González, J.M., Kiene, R.P. & Moran, M.A. (1999) *Transformation of sulfur compounds by an abundant lineage of marine bacteria in the alpha-subclass of the class Proteobacteria. Applied and environmental microbiology*, **65**, 3810–3819.

González, P.J., Correia, C., Moura, I., Brondino, C.D. & Moura, J.J.G. (2006) *Bacterial nitrate reductases: Molecular and biological aspects of nitrate reduction. Journal of inorganic biochemistry*, **100**, 1015–1023.

Goodman, M.F. (2000) *Coping with replication 'train wrecks' in Escherichia coli using Pol V, Pol II and RecA proteins. Trends in biochemical sciences*, **25**, 189–195.

Görisch, H. (2003) *The ethanol oxidation system and its regulation in Pseudomonas aeruginosa. Biochimica et biophysica acta*, **1647**, 98–102.

Gottesman, S. (2003) *Proteolysis in bacterial regulatory circuits. Annual review of cell and developmental biology*, **19**, 565–587.

Gray, C.T., Wimpenny, J.W., Hughes, D.E. & Mossman, M.R. (1966) *Regulation of metabolism in facultative bacteria. I. Structural and functional changes in Escherichia coli associated with shifts between the aerobic and anaerobic states. Biochimica et biophysica acta*, **117**, 22–32.

Grimaldi, S., Schoepp-Cothenet, B., Ceccaldi, P., Guigliarelli, B. & Magalon, A. (2013) *The prokaryotic Mo/W-bisPGD enzymes family: a catalytic workhorse in bioenergetic. Biochimica et biophysica acta*, **1827**, 1048–1085.

Guo, W., Cui, Y.-P., Li, Y.-R., Che, Y.-Z., Yuan, L., Zou, L.-F., Zou, H.-S. & Chen, G.-Y. (2012) *Identification of seven Xanthomonas oryzae pv. oryzicola genes potentially involved in pathogenesis in rice. Microbiology (Reading, England)*, **158**, 505–518.

Hansen, T., Schlichting, B. & Schönheit, P. (2002) *Glucose-6-phosphate dehydrogenase from the hyperthermophilic bacterium Thermotoga maritima: expression of the g6pd gene and characterization of an extremely thermophilic enzyme. FEMS microbiology letters*, **216**, 249–253.

Herrero, M., Lorenzo, V. de & Timmis, K.N. (1990) *Transposon vectors containing non-antibiotic resistance selection markers for cloning and stable chromosomal insertion of foreign genes in gram-negative bacteria. Journal of bacteriology*, **172**, 6557–6567.

Heuveling, J., Possling, A. & Hengge, R. (2008) *A role for Lon protease in the control of the acid resistance genes of Escherichia coli. Molecular microbiology*, **69**, 534–547.

Hiller, K., Hangebrauk, J., Jäger, C., Spura, J., Schreiber, K. & Schomburg, D. (2009) *MetaboliteDetector: comprehensive analysis tool for targeted and nontargeted GC/MS based metabolome analysis. Analytical chemistry*, **81**, 3429–3439.

Hiniker, A. & Bardwell, J.C.A. (2004) *In vivo substrate specificity of periplasmic disulfide oxidoreductases. The Journal of biological chemistry*, **279**, 12967–12973.

Hino, T., Nagano, S., Sugimoto, H., Tosha, T. & Shiro, Y. (2012) *Molecular structure and function of bacterial nitric oxide reductase. Biochimica et biophysica acta*, **1817**, 680–687.

Hoang, T.T., Karkhoff-Schweizer, R.R., Kutchma, A.J. & Schweizer, H.P. (1998) *A broad-host-range Flp-FRT recombination system for site-specific excision of chromosomally-located DNA sequences: application for isolation of unmarked Pseudomonas aeruginosa mutants. Gene*, **212**, 77–86.

Hopper, A.C., Li, Y. & Cole, J.A. (2013) *A critical role for the cccA gene product, cytochrome c2, in diverting electrons from aerobic respiration to denitrification in Neisseria gonorrhoeae. Journal of bacteriology*, **195**, 2518–2529.

Iobbi-Nivol, C. & Leimkühler, S. (2013) *Molybdenum enzymes, their maturation and molybdenum cofactor biosynthesis in Escherichia coli. Biochimica et biophysica acta*, **1827**, 1086–1101.

Irikura, V.M., Kihara, M., Yamaguchi, S., Sockett, H. & Macnab, R.M. (1993) *Salmonella typhimurium fliG and fliN mutations causing defects in assembly, rotation, and switching of the flagellar motor. Journal of bacteriology*, **175**, 802–810.

Jacobs, M.A., Alwood, A., Thaipisuttikul, I., Spencer, D., Haugen, E., Ernst, S., Will, O., Kaul, R., Raymond, C., Levy, R., Chun-Rong, L., Guenthner, D., Bovee, D., Olson, M.V. & Manoil, C. (2003) *Comprehensive transposon mutant library of Pseudomonas aeruginosa. Proceedings of the National Academy of Sciences of the United States of America*, **100**, 14339–14344.

Jepson, B.J.N., Anderson, L.J., Rubio, L.M., Taylor, C.J., Butler, C.S., Flores, E., Herrero, A., Butt, J.N. & Richardson, D.J. (2004) *Tuning a nitrate reductase for function. The first spectropotentiometric characterization of a bacterial assimilatory nitrate reductase reveals novel redox properties. The Journal of biological chemistry*, **279**, 32212–32218.

Juhala, R.J., Ford, M.E., Duda, R.L., Youlton, A., Hatfull, G.F. & Hendrix, R.W. (2000) *Genomic sequences of bacteriophages HK97 and HK022: pervasive genetic mosaicism in the lambdoid bacteriophages. Journal of molecular biology*, **299**, 27–51.

Kamal, N., Dorrell, N., Jagannathan, A., Turner, S.M., Constantinidou, C., Studholme, D.J., Marsden, G., Hinds, J., Laing, K.G., Wren, B.W. & Penn, C.W. (2007) *Deletion of a previously uncharacterized flagellar-hook-length control gene fliK modulates the sigma54-dependent regulon in Campylobacter jejuni. Microbiology (Reading, England)*, **153**, 3099–3111.

Khoroshilova, N., Popescu, C., Münck, E., Beinert, H. & Kiley, P.J. (1997) *Iron-sulfur cluster disassembly in the FNR protein of Escherichia coli by O2: [4Fe-4S] to [2Fe-2S] conversion with loss of biological activity. Proceedings of the National Academy of Sciences of the United States of America*, **94**, 6087–6092.

Kojima, S. & Blair, D.F. (2004) *The bacterial flagellar motor: structure and function of a complex molecular machine. International review of cytology*, **233**, 93–134.

Körner, H., Sofia, H.J. & Zumft, W.G. (2003) *Phylogeny of the bacterial superfamily of Crp-Fnr transcription regulators: exploiting the metabolic spectrum by controlling alternative gene programs. FEMS microbiology reviews*, **27**, 559–592.

Kouzminova, E.A., Rotman, E., Macomber, L., Zhang, J. & Kuzminov, A. (2004) *RecA-dependent mutants in Escherichia coli reveal strategies to avoid chromosomal fragmentation. Proceedings of the National Academy of Sciences of the United States of America*, **101**, 16262–16267.

Kulasekara, H.D., Ventre, I., Kulasekara, B.R., Lazdunski, A., Filloux, A. & Lory, S. (2005) *A novel two-component system controls the expression of Pseudomonas aeruginosa fimbrial cup genes. Molecular microbiology*, **55**, 368–380.

Kumar, P., Sannigrahi, S., Scoullar, J., Kahler, C.M. & Tzeng, Y.-L. (2011) *Characterization of DsbD in Neisseria meningitidis. Molecular microbiology*, **79**, 1557–1573.

Laass, S., Kleist, S., Bill, N., Drüppel, K., Kossmehl, S., Wöhlbrand, L., Rabus, R., Klein, J., Rohde, M., Bartsch, A., Wittmann, C., Schmidt-Hohagen, K., Tielen, P., Jahn, D. & Schomburg, D. (2014) *Gene regulatory and metabolic adaptation processes of Dinoroseobacter shibae DFL12T during oxygen depletion. The Journal of biological chemistry*, **289**, 13219–13231.

Laemmli, U.K. (1970) *Cleavage of structural proteins during the assembly of the head of bacteriophage T4. Nature*, **227**, 680–685.

Lam, P., Lavik, G., Jensen, M.M., van de Vossenberg, J., Schmid, M., Woebken, D., Gutiérrez, D., Amann, R., Jetten, M.S.M. & Kuypers, M.M.M. (2009) *Revising the nitrogen cycle in the Peruvian oxygen minimum zone. Proceedings of the National Academy of Sciences of the United States of America*, **106**, 4752–4757.

Landini, P. & Zehnder, A.J.B. (2002) *The global regulatory hns gene negatively affects adhesion to solid surfaces by anaerobically grown Escherichia coli by modulating expression of flagellar genes and lipopolysaccharide production. Journal of bacteriology*, **184**, 1522–1529.

Lazazzera, B.A. (2001) *The intracellular function of extracellular signaling peptides. Peptides*, **22**, 1519–1527.

Lebedeva, N.V., Malinina, N.V. & Ivanovskiĭ, R.N. (2002) *A comparative study of the isocitrate dehydrogenases of Chlorobium limicola forma thiosulfatophilum and Rhodopseudomonas palustris. Mikrobiologiia*, **71**, 762–767.

Lebens, M., Lundquist, P., Söderlund, L., Todorovic, M. & Carlin, N.I.A. (2002) *The nptA gene of Vibrio cholerae encodes a functional sodium-dependent phosphate cotransporter homologous to the type II cotransporters of eukaryotes. Journal of bacteriology*, **184**, 4466–4474.

Lessmann, D., Schimz, K.L. & Kurz, G. (1975) *D-glucose-6-phosphate dehydrogenase (Entner-Doudoroff enzyme) from Pseudomonas fluorescens. Purification, properties and regulation. European journal of biochemistry / FEBS*, **59**, 545–559.

Li, Y., Katzmann, E., Borg, S. & Schüler, D. (2012) *The periplasmic nitrate reductase nap is required for anaerobic growth and involved in redox control of magnetite biomineralization in Magnetospirillum gryphiswaldense. Journal of bacteriology*, **194**, 4847–4856.

Linhartová, I., Bumba, L., Mašín, J., Basler, M., Osička, R., Kamanová, J., Procházková, K., Adkins, I., Hejnová-Holubová, J., Sadílková, L., Morová, J. & Sebo, P. (2010) *RTX proteins: a highly diverse family secreted by a common mechanism. FEMS microbiology reviews*, **34**, 1076–1112.

Llewellyn, M., Dutton, R.J., Easter, J., O'donnol, D. & Gober, J.W. (2005) *The conserved flaF gene has a critical role in coupling flagellin translation and assembly in Caulobacter crescentus. Molecular microbiology*, **57**, 1127–1142.

Losada, L.C. & Hutcheson, S.W. (2005) *Type III secretion chaperones of Pseudomonas syringae protect effectors from Lon-associated degradation. Molecular microbiology*, **55**, 941–953.

Lu, M.J. & Henning, U. (1994) *Superinfection exclusion by T-even-type coliphages. Trends in microbiology*, **2**, 137–139.

Lu, M.J., Stierhof, Y.D. & Henning, U. (1993) *Location and unusual membrane topology of the immunity protein of the Escherichia coli phage T4. Journal of virology*, **67**, 4905–4913.

Luo, S., McNeill, M., Myers, T.G., Hohman, R.J. & Levine, R.L. (2008) *Lon protease promotes survival of Escherichia coli during anaerobic glucose starvation. Archives of microbiology*, **189**, 181–185.

Madison, L.L. & Huisman, G.W. (1999) *Metabolic engineering of poly(3-hydroxyalkanoates): from DNA to plastic. Microbiology and molecular biology reviews : MMBR*, **63**, 21–53.

Makovets, S., Doronina, V.A. & Murray, N.E. (1999) *Regulation of endonuclease activity by proteolysis prevents breakage of unmodified bacterial chromosomes by type I restriction enzymes. Proceedings of the National Academy of Sciences of the United States of America*, **96**, 9757–9762.

Malcolm, H.R. & Maurer, J.A. (2012) *The mechanosensitive channel of small conductance (MscS) superfamily: not just mechanosensitive channels anymore. Chembiochem : a European journal of chemical biology*, **13**, 2037–2043.

Malin, G. (2006) *Oceans. New pieces for the marine sulfur cycle jigsaw. Science (New York, N.Y.)*, **314**, 607–608.

Marín, M.M., Yuste, L. & Rojo, F. (2003) *Differential expression of the components of the two alkane hydroxylases from Pseudomonas aeruginosa. Journal of bacteriology*, **185**, 3232–3237.

Matsumoto-Mashimo, C., Guerout, A.-M. & Mazel, D. (2004) *A new family of conditional replicating plasmids and their cognate Escherichia coli host strains. Research in microbiology*, **155**, 455–461.

Metheringham, R., Tyson, K.L., Crooke, H., Missiakas, D., Raina, S. & Cole, J.A. (1996) *Effects of mutations in genes for proteins involved in disulphide bond formation in the periplasm on the activities of anaerobically induced electron transfer chains in Escherichia coli K12. Molecular & general genetics : MGG*, **253**, 95–102.

Miller, J.M. & Alachi, P. (1996) *Evaluation of new computer-enhanced identification program for microorganisms: adaptation of BioBASE for identification of members of the family Enterobacteriaceae. Journal of clinical microbiology*, **34**, 179–181.

Minami, N., Yasuda, T., Ishii, Y., Fujimori, K. & Amano, F. (2011) *Regulatory role of cardiolipin in the activity of an ATP-dependent protease, Lon, from Escherichia coli. Journal of biochemistry*, **149**, 519–527.

Mizusawa, S. & Gottesman, S. (1983) *Protein degradation in Escherichia coli: the lon gene controls the stability of sulA protein. Proceedings of the National Academy of Sciences of the United States of America*, **80**, 358–362.

Moran, M.A., Belas, R., Schell, M.A., González, J.M., Sun, F., Sun, S., Binder, B.J., Edmonds, J., Ye, W., Orcutt, B., Howard, E.C., Meile, C., Palefsky, W., Goesmann, A., Ren, Q., Paulsen, I., Ulrich, L.E., Thompson, L.S., Saunders, E. & Buchan, A. (2007) *Ecological genomics of marine Roseobacters. Applied and environmental microbiology*, **73**, 4559–4569.

Moran, M.A., Buchan, A., González, J.M., Heidelberg, J.F., Whitman, W.B., Kiene, R.P., Henriksen, J.R., King, G.M., Belas, R., Fuqua, C., Brinkac, L., Lewis, M., Johri, S., Weaver, B., Pai, G., Eisen, J.A., Rahe, E., Sheldon, W.M., Ye, W., Miller, T.R., Carlton, J., Rasko, D.A., Paulsen, I.T., Ren, Q., Daugherty, S.C., Deboy, R.T., Dodson, R.J., Durkin, A.S., Madupu, R., Nelson, W.C., Sullivan, S.A., Rosovitz, M.J., Haft, D.H., Selengut, J. & Ward, N. (2004) *Genome sequence of Silicibacter pomeroyi reveals adaptations to the marine environment. Nature*, **432**, 910–913.

Moreno-Vivián, C., Cabello, P., Martínez-Luque, M., Blasco, R. & Castillo, F. (1999) *Prokaryotic nitrate reduction: molecular properties and functional distinction among bacterial nitrate reductases. Journal of bacteriology*, **181**, 6573–6584.

Morgan-Kiss, R.M. & Cronan, J.E. (2004) *The Escherichia coli fadK (ydiD) gene encodes an anerobically regulated short chain acyl-CoA synthetase. The Journal of biological chemistry*, **279**, 37324–37333.

Mulligan, C., Fischer, M. & Thomas, G.H. (2011) *Tripartite ATP-independent periplasmic (TRAP) transporters in bacteria and archaea. FEMS microbiology reviews*, **35**, 68–86.

Mulligan, C., Geertsma, E.R., Severi, E., Kelly, D.J., Poolman, B. & Thomas, G.H. (2009) *The substrate-binding protein imposes directionality on an electrochemical sodium gradient-driven TRAP transporter. Proceedings of the National Academy of Sciences of the United States of America*, **106**, 1778–1783.

Münch, R., Hiller, K., Grote, A., Scheer, M., Klein, J., Schobert, M. & Jahn, D. (2005) *Virtual Footprint and PRODORIC: an integrative framework for regulon prediction in prokaryotes. Bioinformatics (Oxford, England)*, **21**, 4187–4189.

Nam, T.-W., Park, Y.-H., Jeong, H.-J., Ryu, S. & Seok, Y.-J. (2005) *Glucose repression of the Escherichia coli sdhCDAB operon, revisited: regulation by the CRP*cAMP complex. Nucleic acids research*, **33**, 6712–6722.

O'Toole, G.A., Pratt, L.A., Watnick, P.I., Newman, D.K., Weaver, V.B. & Kolter, R. (1999) *Genetic approaches to study of biofilms. Methods in enzymology*, **310**, 91–109.

Ouchane, S., Steunou, A.-S., Picaud, M. & Astier, C. (2004) *Aerobic and anaerobic Mg-protoporphyrin monomethyl ester cyclases in purple bacteria: a strategy adopted to bypass the repressive oxygen control system. The Journal of biological chemistry*, **279**, 6385–6394.

Pallen, M.J. & Matzke, N.J. (2006) *From The Origin of Species to the origin of bacterial flagella. Nature reviews. Microbiology*, **4**, 784–790.

Pardo, M.A., Llama, M.J. & Serra, J.L. (1999) *Purification, properties and enhanced expression under nitrogen starvation of the NADP+-isocitrate dehydrogenase from the cyanobacterium Phormidium laminosum. Biochimica et biophysica acta*, **1431**, 87–96.

Petersen, J., Brinkmann, H., Berger, M., Brinkhoff, T., Päuker, O. & Pradella, S. (2011) *Origin and evolution of a novel DnaA-like plasmid replication type in Rhodobacterales. Molecular biology and evolution*, **28**, 1229–1240.

Petersen, J., Brinkmann, H. & Pradella, S. (2009) *Diversity and evolution of repABC type plasmids in Rhodobacterales. Environmental microbiology*, **11**, 2627–2638.

Petersen, J., Frank, O., Göker, M. & Pradella, S. (2013) *Extrachromosomal, extraordinary and essential--the plasmids of the Roseobacter clade. Applied microbiology and biotechnology*, **97**, 2805–2815.

Piekarski, T., Buchholz, I., Drepper, T., Schobert, M., Wagner-Doebler, I., Tielen, P. & Jahn, D. (2009) *Genetic tools for the investigation of Roseobacter clade bacteria. BMC microbiology*, **9**, 265.

Pradella, S., Allgaier, M., Hoch, C., Päuker, O., Stackebrandt, E. & Wagner-Döbler, I. (2004) *Genome organization and localization of the pufLM genes of the photosynthesis reaction center in phylogenetically diverse marine Alphaproteobacteria. Applied and environmental microbiology*, **70**, 3360–3369.

Priefer, U.B., Kalinowski, J., Rüger, B., Heumann, W. & Pühler, A. (1989) *ISR1, a transposable DNA sequence resident in Rhizobium class IV strains, shows structural characteristics of classical insertion elements. Plasmid*, **21**, 120–128.

Ras, J., van Ophem, P.W., Reijnders, W.N., van Spanning, R.J., Duine, J.A., Stouthamer, A.H. & Harms, N. (1995) *Isolation, sequencing, and mutagenesis of the gene encoding NAD- and glutathione-dependent formaldehyde dehydrogenase (GD-FALDH) from Paracoccus denitrificans, in which GD-FALDH is essential for methylotrophic growth. Journal of bacteriology*, **177**, 247–251.

Reusch, R.N. (2013) *The role of short-chain conjugated poly-(R)-3-hydroxybutyrate (cPHB) in protein folding. International journal of molecular sciences*, **14**, 10727–10748.

Rex, R., Bill, N., Schmidt-Hohagen, K. & Schomburg, D. (2013) *Swimming in light: a large-scale computational analysis of the metabolism of Dinoroseobacter shibae. PLoS computational biology*, **9**, e1003224.

Richard-Fogal, C.L., Frawley, E.R., Bonner, E.R., Zhu, H., San Francisco, B. & Kranz, R.G. (2009) *A conserved haem redox and trafficking pathway for cofactor attachment. The EMBO journal*, **28**, 2349–2359.

Richard-Fogal, C.L., San Francisco, B., Frawley, E.R. & Kranz, R.G. (2012) *Thiol redox requirements and substrate specificities of recombinant cytochrome c assembly systems II and III. Biochimica et biophysica acta*, **1817**, 911–919.

Richardson, D.J., Berks, B.C., Russell, D.A., Spiro, S. & Taylor, C.J. (2001) *Functional, biochemical and genetic diversity of prokaryotic nitrate reductases. Cellular and molecular life sciences : CMLS*, **58**, 165–178.

Righetti, P.G. (1990) *Recent developments in electrophoretic methods. Journal of chromatography*, **516**, 3–22.

Rivas, L., Fegan, N. & Dykes, G.A. (2008) *Expression and putative roles in attachment of outer membrane proteins of Escherichia coli O157 from planktonic and sessile culture. Foodborne pathogens and disease*, **5**, 155–164.

Robertson, I.B., Stevens, J.M. & Ferguson, S.J. (2008) *Dispensable residues in the active site of the cytochrome c biogenesis protein CcmH. FEBS letters*, **582**, 3067–3072.

Roca, A., Rodríguez-Herva, J.-J., Duque, E. & Ramos, J.L. (2008) *Physiological responses of Pseudomonas putida to formaldehyde during detoxification. Microbial biotechnology*, **1**, 158–169.

Rompf, A., Hungerer, C., Hoffmann, T., Lindenmeyer, M., Römling, U., Groß, U., Doss, M.O., Arai, H., Igarashi, Y. & Jahn, D. (1998) *Regulation of Pseudomonas aeruginosa hemF and hemN by the dual action of the redox response regulators Anr and Dnr. Molecular microbiology*, **29**, 985–997.

Saeed, A.I., Sharov, V., White, J., Li, J., Liang, W., Bhagabati, N., Braisted, J., Klapa, M., Currier, T., Thiagarajan, M., Sturn, A., Snuffin, M., Rezantsev, A., Popov, D., Ryltsov, A., Kostukovich, E., Borisovsky, I., Liu, Z., Vinsavich, A., Trush, V. & Quackenbush, J. (2003) *TM4: a free, open-source system for microarray data management and analysis. BioTechniques*, **34**, 374–378.

Sanders, C., Turkarslan, S., Lee, D.-W. & Daldal, F. (2010) *Cytochrome c biogenesis: the Ccm system. Trends in microbiology*, **18**, 266–274.

Santos, C.A., Toledo, M.A.S., Trivella, D.B.B., Beloti, L.L., Schneider, D.R.S., Saraiva, A.M., Crucello, A., Azzoni, A.R., Souza, A.A., Aparicio, R. & Souza, A.P. (2012) *Functional and structural studies of the disulfide isomerase DsbC from the plant pathogen Xylella fastidiosa reveals a redox-dependent oligomeric modulation in vitro. The FEBS journal*, **279**, 3828–3843.

Saunders, N.F., Hornberg, J.J., Reijnders, W.N., Westerhoff, H.V., Vries, S. de & van Spanning, R.J. (2000) *The NosX and NirX proteins of Paracoccus denitrificans are functional homologues: their role in maturation of nitrous oxide reductase. Journal of bacteriology*, **182**, 5211–5217.

Schaeffer, F. & Stanier, R.Y. (1978) *Glucose-6-phosphate dehydrogenase of Anabaena sp. Kinetic and molecular properties. Archives of microbiology*, **116**, 9–19.

Schobert, M. & Görisch, H. (1999) *Cytochrome c550 is an essential component of the quinoprotein ethanol oxidation system in Pseudomonas aeruginosa: cloning and sequencing of the genes encoding cytochrome c550 and an adjacent acetaldehyde dehydrogenase. Microbiology (Reading, England)*, **145 (Pt 2)**, 471–481.

Schobert, M. & Görisch, H. (2001) *A soluble two-component regulatory system controls expression of quinoprotein ethanol dehydrogenase (QEDH) but not expression of*

cytochrome c(550) of the ethanol-oxidation system in Pseudomonas aeruginosa. Microbiology (Reading, England), **147**, 363–372.

Schobert, M. & Tielen, P. (2010) *Contribution of oxygen-limiting conditions to persistent infection of Pseudomonas aeruginosa. Future microbiology*, **5**, 603–621.

Schreiber, K., Krieger, R., Benkert, B., Eschbach, M., Arai, H., Schobert, M. & Jahn, D. (2007) *The anaerobic regulatory network required for Pseudomonas aeruginosa nitrate respiration. Journal of bacteriology*, **189**, 4310–4314.

Schübel, U., Kraut, M., Mörsdorf, G. & Meyer, O. (1995) *Molecular characterization of the gene cluster coxMSL encoding the molybdenum-containing carbon monoxide dehydrogenase of Oligotropha carboxidovorans. Journal of bacteriology*, **177**, 2197–2203.

Senior, P.J. & Dawes, E.A. (1971) *Poly-beta-hydroxybutyrate biosynthesis and the regulation of glucose metabolism in Azotobacter beijerinckii. The Biochemical journal*, **125**, 55–66.

Shiba, T. (1991) *Roseobacter litoralis gen. nov., sp. nov., and Roseobacter denitrificans sp. nov., Aerobic Pink-Pigmented Bacteria which Contain Bacteriochlorophyll a. Systematic and Applied Microbiology*, **14**, 140–145.

Shiba, T., Simidu, U. & Taga, N. (1979) *Distribution of aerobic bacteria which contain bacteriochlorophyll a. Applied and environmental microbiology*, **38**, 43–45.

Shiro, Y., Sugimoto, H., Tosha, T., Nagano, S. & Hino, T. (2012) *Structural basis for nitrous oxide generation by bacterial nitric oxide reductases. Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, **367**, 1195–1203.

Simons, M. & Szczelkun, M.D. (2011) *Recycling of protein subunits during DNA translocation and cleavage by Type I restriction-modification enzymes. Nucleic acids research*, **39**, 7656–7666.

Simpson, P.J.L., Richardson, D.J. & Codd, R. (2010) *The periplasmic nitrate reductase in Shewanella: the resolution, distribution and functional implications of two NAP isoforms, NapEDABC and NapDAGHB. Microbiology (Reading, England)*, **156**, 302–312.

Skovran, E. & Downs, D.M. (2003) *Lack of the ApbC or ApbE protein results in a defect in Fe-S cluster metabolism in Salmonella enterica serovar Typhimurium. Journal of bacteriology*, **185**, 98–106.

Skovran, E., Lauhon, C.T. & Downs, D.M. (2004) *Lack of YggX results in chronic oxidative stress and uncovers subtle defects in Fe-S cluster metabolism in Salmonella enterica. Journal of bacteriology*, **186**, 7626–7634.

Smyth, G.K., Michaud, J. & Scott, H.S. (2005) *Use of within-array replicate spots for assessing differential expression in microarray experiments. Bioinformatics (Oxford, England)*, **21**, 2067–2075.

Spiro, S. (2012) *Nitrous oxide production and consumption: regulation of gene expression by gas-sensitive transcription factors. Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, **367**, 1213–1225.

Spurr, A.R. (1969) *A low-viscosity epoxy resin embedding medium for electron microscopy. Journal of ultrastructure research*, **26**, 31–43.

Stirnimann, C.U., Rozhkova, A., Grauschopf, U., Grütter, M.G., Glockshuber, R. & Capitani, G. (2005) *Structural basis and kinetics of DsbD-dependent cytochrome c maturation. Structure (London, England : 1993)*, **13**, 985–993.

Takaya, A., Tabuchi, F., Tsuchiya, H., Isogai, E. & Yamamoto, T. (2008) *Negative regulation of quorum-sensing systems in Pseudomonas aeruginosa by ATP-dependent Lon protease. Journal of bacteriology*, **190**, 4181–4188.

Taniguchi, Y., Choi, P.J., Li, G.-W., Chen, H., Babu, M., Hearn, J., Emili, A. & Xie, X.S. (2010) *Quantifying E. coli proteome and transcriptome with single-molecule sensitivity in single cells. Science (New York, N.Y.)*, **329**, 533–538.

Thoma, S. & Schobert, M. (2009) *An improved Escherichia coli donor strain for diparental mating. FEMS microbiology letters*, **294**, 127–132.

Thompson, K.M., Rhodius, V.A. & Gottesman, S. (2007) *SigmaE regulates and is regulated by a small RNA in Escherichia coli. Journal of bacteriology*, **189**, 4243–4256.

Thormann, K.M., Saville, R.M., Shukla, S., Pelletier, D.A. & Spormann, A.M. (2004) *Initial Phases of biofilm formation in Shewanella oneidensis MR-1. Journal of bacteriology*, **186**, 8096–8104.

Tielen, P., Rosin, N., Meyer, A.-K., Dohnt, K., Haddad, I., Jänsch, L., Klein, J., Narten, M., Pommerenke, C., Scheer, M., Schobert, M., Schomburg, D., Thielen, B. & Jahn, D. (2013) *Regulatory and metabolic networks for the adaptation of Pseudomonas aeruginosa biofilms to urinary tract-like conditions. PloS one*, **8**, e71845.

Tielen, Schobert, Härtig, & Jahn, ed (2012) *Anaerobic regulatory networks in bacteria. in: Filloux, Alain A. M.Bacterial regulatory networks*. Caister Academic Press, Norfolk.

Tomasch, J., Gohl, R., Bunk, B., Diez, M.S. & Wagner-Döbler, I. (2011) *Transcriptional response of the photoheterotrophic marine bacterium Dinoroseobacter shibae to changing light regimes. The ISME journal*, **5**, 1957–1968.

Tomoyasu, T., Takaya, A., Isogai, E. & Yamamoto, T. (2003) *Turnover of FlhD and FlhC, master regulator proteins for Salmonella flagellum biogenesis, by the ATP-dependent ClpXP protease. Molecular microbiology*, **48**, 443–452.

Trautwein, K., Kühner, S., Wöhlbrand, L., Halder, T., Kuchta, K., Steinbüchel, A. & Rabus, R. (2008) *Solvent stress response of the denitrifying bacterium "Aromatoleum aromaticum" strain EbN1. Applied and environmental microbiology*, **74**, 2267–2274.

Trunk, K., Benkert, B., Quäck, N., Münch, R., Scheer, M., Garbe, J., Jänsch, L., Trost, M., Wehland, J., Buer, J., Jahn, M., Schobert, M. & Jahn, D. (2010) *Anaerobic adaptation in Pseudomonas aeruginosa: definition of the Anr and Dnr regulons. Environmental microbiology*, **12**, 1719–1733.

Uchiyama, I. (2003) *MBGD: microbial genome database for comparative analysis. Nucleic acids research*, **31**, 58–62.

Uc-Mass, A., Loeza, E.J., La Garza, M. de, Guarneros, G., Hernández-Sánchez, J. & Kameyama, L. (2004) *An orthologue of the cor gene is involved in the exclusion of temperate lambdoid phages. Evidence that Cor inactivates FhuA receptor functions. Virology*, **329**, 425–433.

Valentini, M. & Lapouge, K. (2013) *Catabolite repression in Pseudomonas aeruginosa PAO1 regulates the uptake of C4 -dicarboxylates depending on succinate concentration. Environmental microbiology*, **15**, 1707–1716.

van Melderen, L. & Aertsen, A. (2009) *Regulation and quality control by Lon-dependent proteolysis. Research in microbiology*, **160**, 645–651.

Verissimo, A.F., Yang, H., Wu, X., Sanders, C. & Daldal, F. (2011) *CcmI subunit of CcmFHI heme ligation complex functions as an apocytochrome c chaperone during c-type cytochrome maturation. The Journal of biological chemistry*, **286**, 40452–40463.

Vertommen, D., Depuydt, M., Pan, J., Leverrier, P., Knoops, L., Szikora, J.-P., Messens, J., Bardwell, J.C.A. & Collet, J.-F. (2008) *The disulphide isomerase DsbC cooperates with the oxidase DsbA in a DsbD-independent manner. Molecular microbiology*, **67**, 336–349.

Vollack, K.U., Härtig, E., Körner, H. & Zumft, W.G. (1999) *Multiple transcription factors of the FNR family in denitrifying Pseudomonas stutzeri: characterization of four fnr-like genes, regulatory responses and cognate metabolic processes. Molecular microbiology*, **31**, 1681–1694.

Vollmer, W., Rechenberg, M. von & Höltje, J.V. (1999) *Demonstration of molecular interactions between the murein polymerase PBP1B, the lytic transglycosylase MltA, and the scaffolding protein MipA of Escherichia coli. The Journal of biological chemistry*, **274**, 6726–6734.

Vuilleumier, S. (1997) *Bacterial glutathione S-transferases: what are they good for? Journal of bacteriology*, **179**, 1431–1441.

Wagner-Döbler, I., Ballhausen, B., Berger, M., Brinkhoff, T., Buchholz, I., Bunk, B., Cypionka, H., Daniel, R., Drepper, T., Gerdts, G., Hahnke, S., Han, C., Jahn, D., Kalhoefer, D., Kiss, H., Klenk, H.-P., Kyrpides, N., Liebl, W., Liesegang, H., Meincke, L., Pati, A., Petersen, J., Piekarski, T., Pommerenke, C., Pradella, S., Pukall, R., Rabus, R., Stackebrandt, E., Thole, S., Thompson, L., Tielen, P., Tomasch, J., Jan, M. von, Wanphrut, N., Wichels, A., Zech, H. & Simon, M. (2010) *The complete genome sequence of the algal symbiont Dinoroseobacter shibae: a hitchhiker's guide to life in the sea. The ISME journal*, **4**, 61–77.

Wagner-Döbler, I. & Biebl, H. (2006) *Environmental biology of the marine Roseobacter lineage. Annual review of microbiology*, **60**, 255–280.

Wagner-Döbler, I., Thiel, V., Eberl, L., Allgaier, M., Bodor, A., Meyer, S., Ebner, S., Hennig, A., Pukall, R. & Schulz, S. (2005) *Discovery of complex mixtures of novel long-chain quorum sensing signals in free-living and host-associated marine alphaproteobacteria. Chembiochem : a European journal of chemical biology*, **6**, 2195–2206.

Wang, L., Elliott, M. & Elliott, T. (1999) *Conditional stability of the HemA protein (glutamyl-tRNA reductase) regulates heme biosynthesis in Salmonella typhimurium. Journal of bacteriology*, **181**, 1211–1219.

Watanabe, S., Zimmermann, M., Goodwin, M.B., Sauer, U., Barry, C.E. & Boshoff, H.I. (2011) *Fumarate reductase activity maintains an energized membrane in anaerobic Mycobacterium tuberculosis. PLoS pathogens*, **7**, e1002287.

Werner, A. & Kinne, R.K. (2001) *Evolution of the Na-P(i) cotransport systems. American journal of physiology. Regulatory, integrative and comparative physiology*, **280**, R301-12.

Wilcoxen, J., Zhang, B. & Hille, R. (2011) *Reaction of the molybdenum- and copper-containing carbon monoxide dehydrogenase from Oligotropha carboxydovorans with quinones. Biochemistry*, **50**, 1910–1916.

Williams, H.D., Zlosnik, J.E.A. & Ryall, B. (2007) *Oxygen, cyanide and energy generation in the cystic fibrosis pathogen Pseudomonas aeruginosa. Advances in microbial physiology*, **52**, 1–71.

Williams, S.M., Savery, N.J., Busby, S.J. & Wing, H.J. (1997) *Transcription activation at class I FNR-dependent promoters: identification of the activating surface of FNR and the corresponding contact site in the C-terminal domain of the RNA polymerase alpha subunit. Nucleic acids research*, **25**, 4028–4034.

Xiao, N. & Jiao, N. (2011) *Formation of polyhydroxyalkanoate in aerobic anoxygenic phototrophic bacteria and its relationship to carbon source and light availability. Applied and environmental microbiology*, **77**, 7445–7450.

Xiao, N., Jiao, N. & Liu, Y. (2015) *In vivo and in vitro observations of polyhydroxybutyrate granules formed by Dinoroseobacter sp. JL 1447. International journal of biological macromolecules*, **74**, 467–475.

Yamada, M., Sumi, K., Matsushita, K., Adachi, O. & Yamada, Y. (1993) *Topological analysis of quinoprotein glucose dehydrogenase in Escherichia coli and its ubiquinone-binding site. The Journal of biological chemistry*, **268**, 12812–12817.

Yang, J.-N., Wang, C., Guo, C., Peng, X.-X. & Li, H. (2011a) *Outer membrane proteome and its regulation networks in response to glucose concentration changes in Escherichia coli. Molecular bioSystems*, **7**, 3087–3093.

Yang, Y., Zhu, H., Colvin, V.L. & Alvarez, P.J. (2011b) *Cellular and transcriptional response of Pseudomonas stutzeri to quantum dots under aerobic and denitrifying conditions. Environmental science & technology*, **45**, 4988–4994.

Zech, H., Echtermeyer, C., Wöhlbrand, L., Blasius, B. & Rabus, R. (2011) *Biological versus technical variability in 2-D DIGE experiments with environmental bacteria. Proteomics*, **11**, 3380–3389.

Zech, H., Hensler, M., Koßmehl, S., Drüppel, K., Wöhlbrand, L., Trautwein, K., Colby, T., Schmidt, J., Reinhardt, R., Schmidt-Hohagen, K., Schomburg, D. & Rabus, R. (2013a) *Dynamics of amino acid utilization in Phaeobacter inhibens DSM 17395. Proteomics*, **13**, 2869–2885.

Zech, H., Hensler, M., Koßmehl, S., Drüppel, K., Wöhlbrand, L., Trautwein, K., Hulsch, R., Maschmann, U., Colby, T., Schmidt, J., Reinhardt, R., Schmidt-Hohagen, K., Schomburg, D. & Rabus, R. (2013b) *Adaptation of Phaeobacter inhibens DSM 17395 to growth with complex nutrients. Proteomics*, **13**, 2851–2868.

Zech, H., Thole, S., Schreiber, K., Kalhöfer, D., Voget, S., Brinkhoff, T., Simon, M., Schomburg, D. & Rabus, R. (2009) *Growth phase-dependent global protein and metabolite profiles of Phaeobacter gallaeciensis strain DSM 17395, a member of the marine Roseobacter-clade. Proteomics*, **9**, 3677–3697.

Zehr, J.P. & Kudela, R.M. (2011) *Nitrogen cycle of the open ocean: from genes to ecosystems. Annual review of marine science*, **3**, 197–225.

Zhang, W., Urban, A., Mihara, H., Leimkühler, S., Kurihara, T. & Esaki, N. (2010) *IscS functions as a primary sulfur-donating enzyme by interacting specifically with MoeB and MoaD in the biosynthesis of molybdopterin in Escherichia coli. The Journal of biological chemistry*, **285**, 2302–2308.

Zumft, W.G. (1997) *Cell biology and molecular basis of denitrification. Microbiology and molecular biology reviews : MMBR*, **61**, 533–616.

Danksagung

An dieser Stelle möchte allen danken, die mich während meiner Doktorarbeit begleitet und die zum Entstehen der Arbeit beigetragen haben!

Zuerst geht mein Dank an Prof. Dr. Dieter Jahn. Danke, dass du nicht nur ein starker Konkurrent in der Tipspielrunde bist, sondern vor allem, dass ich in deinem Team arbeiten durfte, für die Unterstützung, die du mir in dieser Zeit geboten hast und die Möglichkeit unsere Arbeiten bei vielen verschiedenen Tagungen und Treffen zeigen zu dürfen.

Vielen Dank auch an Prof. Dr. Dietmar Schomburg für die Zusammenarbeit im SFB Roseobacter an unserem Dinoomicsprojekt und für die Übernahme des Zweitgutachtens.

Ein großer Dank geht an Dr. Petra Tielen. Danke für die freundliche Aufnahme in deine Gruppe, die motivierende Betreuung und die vielen Gespräche, die wir auch abseits von Arbeitsthemen hatten. Und ja, du hast die Wette gewonnen. ;-)

Ein großer Dank gilt auch allen meinen Kooperationspartnern ohne die die Arbeit nicht so weit gekommen wäre. Besonders hervorzuheben sind hier Sarah Kleist und Kerstin Schmidt-Hohagen.

Vielen Dank der Arbeitsgruppe Tielen und Schobert es hat Spaß gemacht mit allen zusammen zu arbeiten. Danke Petra, Max, Tanja, Nathalie, Maike, Andrea, Anka, Chema, Jenny und Matze für die lustige Zeit, die vielen kleinen Dinge, die wir so veranstaltet haben.

Ein großer Dank gilt der gesamten Mibi. Sich bei euch nicht wohl zu fühlen kann man gar nicht. Ihr seid ein tolles Team.

Vielen Dank Rebekka für die vielen weiterbringenden Gespräche und das du immer ein offenes Ohr für mich hattest.

Vielen, vielen Dank an die guten Geister des Instituts für Mikrobiologie. Ohne Herrn Hoppe, Christina, Daniela, Dagmar und Barbara würde wohl alles in die Luft fliegen. Und was man mit euch quatschen kann, hehe.

Wichtig für die Zeit und damit vielen Dank verdient haben auch die Freunde, die ich im Institut gewonnen habe und die einen unterstützt haben. Danke Tanja, Mela, Tobi (KT), Jose (Chema), Niesel, Mareike, Jenny (Bambi), Janine, Can, Jens, Tristan, Anka, Matze, Anika, Kristin, Petra, Max, Isam, Jo, Ida, Melli, Dagmar, Christiane, Conny, Sarah, Simon, Ines, Annika, Claudia und alle die ich noch dazu gehören.

Vielen Dank an meine Freunde ohne Biohintergrund. Ob es die Basketballjungs um Micha, Frank Gero und Adrian, die Church ills Jerome und Tobi oder die Salzgitter Jungs und Mädels wie Timo, Rouven und Anett, Thomas, Daniel,…sind, der Zusammenhalt den ich mit euch erfahren durfte haben nicht viele.

Vielen Dank an meine Mutter Ursula und meinen Vater Walter, die es mir überhaupt erst ermöglicht haben zu studieren und mich dabei immer unterstützt haben.

Appendix

Table A1: Transcriptome data of *D. shibae* DFL12T grown under oxygen depletion. Data were compared to the situation before oxygen shutdown. A fold change cut off of 1.7 and a p-value < 0.05 were applied. 0: not defined

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_0001	gltD	1.4.1.13	glutamate synthase (NADPH)	1,29	1,18	-1,24	-1,38	1,51	-1,21	2,71
_0002	gltB	1.4.1.13, 1.4.1.14, 1.4.7.1	glutamate synthase (NADPH),glutamate synthase (NADH),glutamate synthase (ferredoxin)	1,01	1,05	-1,16	-1,48	-2,03	-1,89	1,43
_0004	0		hypothetical protein	-1,05	1,01	1,12	-1,07	1,22	1,21	-1,17
_0005	0		hypothetical protein	-1,03	-1,02	1,02	-1,03	-1,17	-1,14	-1,12
_0006	dapD	2.3.1.117	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyl transferase	1,04	1,05	-1,03	-1,16	-1,44	-2,09	-1,42
_0008	0		hypothetical protein	1,00	-1,03	-1,16	-1,26	-1,81	-2,12	-1,93
_0009	csp2		cold-shock DNA-binding domain-containing protein	-1,03	-1,10	-1,22	-1,27	-1,56	-1,88	-1,12
_0010	0		hypothetical protein	-1,11	-1,04	1,07	1,23	1,15	1,05	1,17
_0011	0		hypothetical protein	-1,01	-1,03	-1,10	-1,31	-1,20	-1,25	1,03
_0012	dapE1	3.5.1.18	Succinyl-diaminopimelate desuccinylase	1,09	1,04	-1,11	-1,18	-1,39	-1,65	-1,29
_0013	elaA		GCN5-related N-acetyltransferase	1,00	1,01	-1,03	1,01	-1,27	-1,36	-1,06
_0014	0		hypothetical protein	-1,15	-1,11	-1,09	-1,03	-1,36	-1,09	-1,16
_0015	rnr	3.1.13.1	exoribonuclease II	1,02	1,04	-1,07	-1,19	-1,29	-1,57	-1,12
_0016	mltB2	3.2.1.-	lytic murein transglycosylase	1,01	1,00	1,07	1,07	1,03	1,12	-1,00
_0017	0		hypothetical protein	-1,06	-1,02	1,02	1,01	-1,05	1,09	1,14
_0018	0		multicopper oxidase type 2	-1,04	-1,07	1,07	1,12	1,06	1,19	1,01
_0019	0		GTP-binding protein TypA	1,23	1,20	-1,10	-1,29	-1,11	-1,73	-1,00
_0020	0		putative transcriptional regulator, CadC	-1,13	-1,04	1,09	1,18	1,24	1,16	-1,01
_0021	0		hypothetical protein	-1,07	-1,05	-1,11	1,10	1,09	1,22	-1,02
_0022	0		hypothetical protein	-1,01	-1,02	-1,01	1,04	1,15	1,26	1,42
_0023	rnhB	3.1.26.4	ribonuclease H	-1,01	1,00	-1,04	-1,07	1,14	1,19	1,06
_0024	dam	2.1.1.72	site-specific DNA-methyl transferase (adenine-specific)	-1,05	-1,06	-1,22	-1,43	-1,55	-1,65	-1,48
_0025	chrR2		anti-ECFsigma factor, ChrR	1,02	-1,03	-1,05	-1,10	-1,05	-1,02	1,10
_0026	0		NAD-dependent epimerase/dehydratase	-1,02	-1,03	-1,06	1,07	-1,08	1,10	1,06
_0027	alkB1	1.14.15.3	alkane 1-monooxygenase	-1,08	-1,09	1,01	1,16	-1,00	1,13	-1,23
_0028	mutY	3.2.2.-	A/G-specific adenine glycosylase	1,02	-1,01	1,02	-1,21	1,08	1,28	-1,03
_0029	0		hypothetical protein	-1,06	-1,06	1,08	1,06	1,03	1,02	-1,01
_0030	dsbA1		thiol-disulfide oxidoreductase D, putative	-1,02	-1,02	1,08	1,06	-1,03	-1,05	-1,04
_0031	lpxK	2.7.1.130	tetraacyl disaccharide 4-kinase	1,00	-1,03	-1,03	1,00	-1,08	-1,09	-1,02
_0032	kdtA		3-deoxy-D-manno-octulosonic-acid transferase domain-containing protein	1,00	1,00	-1,01	-1,18	1,12	1,04	-1,04
_0033	0		hypothetical protein	1,00	-1,03	-1,05	1,06	-1,08	-1,02	-1,06
_0034	0		peptidase S16 lon domain-containing protein	1,03	1,00	-1,12	-1,14	-1,34	-1,19	1,04
_0035	trxA2		thioredoxin domain-containing protein	1,01	1,05	1,00	1,08	-1,15	-1,25	-1,03
_0036	xthA	3.1.11.2	exodeoxyribonuclease III	-1,03	1,02	1,01	1,02	-1,34	-1,47	-1,17
_0037	0		cell wall anchor domain-containing protein	-1,04	-1,06	-1,13	-1,10	-1,49	-1,55	-1,22
_0038	0		two component transcriptional regulator	-1,03	-1,05	-1,11	-1,25	-1,47	-1,15	-1,04
_0039	ribA	3.5.4.25	GTP cyclohydrolase II	-1,06	1,03	1,01	-1,02	-1,12	-1,24	1,09
_0040	0		hypothetical protein	-1,03	-1,03	-1,05	-1,18	-1,37	-1,33	-1,17
_0041	0		hypothetical protein	1,02	-1,02	-1,06	-1,05	-1,10	-1,18	-1,05
_0042	0		alanine racemase domain-containing protein	1,01	1,03	-1,06	-1,02	-1,01	-1,22	-1,02
_0043	0		hypothetical protein	-1,10	-1,03	-1,12	-1,07	-1,07	-1,72	-1,15
_0044	0		hypothetical protein	1,09	1,08	-1,04	-1,09	-1,35	-1,74	-1,27
_0045	0		UspA domain-containing protein	-1,06	-1,04	1,06	1,06	-1,10	1,16	-1,30
_0046	0		hypothetical protein	-1,03	-1,03	-1,00	1,04	1,17	1,29	1,11
_0047	0		hypothetical protein	-1,02	-1,04	-1,03	1,09	1,13	1,27	1,08
_0048	0		putative transposase	-1,11	-1,02	-1,06	1,11	1,08	1,34	1,10
_0049	0		hypothetical protein	1,05	1,09	-1,07	-1,11	1,07	-1,07	1,01
_0050	0		hypothetical protein	-1,02	1,03	1,00	-1,23	-1,02	1,01	-1,00
_0051	0		hypothetical protein	-1,05	-1,03	1,00	-1,00	-1,05	1,01	-1,17
_0052	0		hypothetical protein	-1,13	-1,18	-1,10	-1,01	-1,09	1,17	1,09

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_0053	0		hypothetical protein	1,01	-1,01	-1,06	-1,12	-1,04	-1,16	1,03
_0054	gst2	2.5.1.18	glutathione transferase	-1,01	-1,05	1,01	1,03	-1,30	-1,38	-1,25
_0055	holA	2.7.7.7	DNA-directed DNA polymerase	-1,02	1,00	1,01	-1,21	-1,44	-1,51	-1,26
_0056	0		hypothetical protein	1,01	-1,00	-1,06	-1,21	-1,35	-1,38	-1,19
_0057	leuS	6.1.1.4	Leucine-tRNA ligase	1,06	1,03	-1,08	-1,13	-1,26	-1,57	-1,08
_0058	lolA		outer membrane lipoprotein carrier protein LolA	1,03	-1,05	-1,03	1,16	-1,00	1,11	1,22
_0059	ftsK		cell divisionFtsK/SpoIIIE	-1,02	-1,03	1,03	-1,01	-1,09	-1,11	-1,12
_0060	0		aminotransferase class I and II	-1,06	-1,01	1,08	1,01	1,13	1,10	1,01
_0061	0		amidase	-1,08	-1,01	-1,05	-1,05	-1,14	-1,25	-1,28
_0062	ubiH	1.14.13.-	2-octaprenyl-6-methoxyphenol hydroxylase	1,03	1,12	1,41	1,50	1,73	1,29	1,36
_0063	suhB2	3.1.3.25	inositol-phosphate phosphatase	1,05	1,01	-1,05	-1,08	-1,35	-1,22	-1,13
_0064	pmbA		peptidase U62 modulator of DNA gyrase	1,04	1,04	-1,04	-1,17	-1,18	-1,16	-1,07
_0065	0		hypothetical protein	-1,01	-1,00	-1,04	-1,05	1,02	-1,09	1,04
_0066	0		short-chain dehydrogenase/reductase SDR	-1,07	-1,03	1,07	1,05	-1,25	-1,03	-1,36
_0067	caiD		enoyl-CoA hydratase/isomerase	-1,01	-1,02	-1,00	1,13	1,04	1,08	-1,18
_0068	0		putative lipoprotein	-1,01	-1,02	-1,01	1,16	1,37	1,22	1,05
_0069	0		auxin efflux carrier	1,05	1,06	-1,04	1,04	-1,15	-1,05	-1,06
_0070	yccV		hemimethylated DNA binding protein	-1,01	1,01	1,06	1,05	1,22	1,25	1,27
_0071	ggt1	2.3.2.2	Gamma-glutamyltransferase	1,09	1,04	-1,02	-1,20	-1,11	-1,10	1,02
_0072	rsbW	2.7.11.1	non-specific serine/threonine protein kinase	1,05	-1,04	1,03	-1,04	1,44	1,44	1,50
_0073	0		anti-sigma-factor antagonist	1,01	-1,01	1,05	1,03	1,53	1,39	1,38
_0074	thlA	2.3.1.9	acetyl-CoA C-acetyltransferase	-1,02	-1,02	-1,08	-1,06	-1,22	-1,35	-1,12
_0075	0		hypothetical protein	-1,04	-1,00	-1,03	1,10	-1,04	1,10	1,21
_0076	0		hypothetical protein	-1,03	-1,00	-1,09	1,12	1,02	1,05	1,07
_0077	0		hypothetical protein	-1,14	1,03	1,03	-1,08	-1,04	1,32	1,06
_0078	0		hypothetical protein	1,02	-1,00	1,04	1,20	1,17	1,15	1,18
_0079	0	2.3.1.-	lipid A biosynthesis acyltransferase	-1,04	-1,00	1,01	1,11	-1,01	-1,14	-1,19
_0080	0		hypothetical protein	-1,05	-1,02	-1,06	-1,16	-1,02	-1,12	-1,13
_0081	imdh	1.1.1.85	3-isopropylmalate dehydrogenase	1,13	1,14	-1,20	-1,40	-1,50	-1,97	-1,22
_0082	0		hypothetical protein	1,02	1,01	-1,02	-1,24	1,37	1,50	1,18
_0083	leuD	4.2.1.33	3-isopropylmalate dehydratase	1,02	1,01	-1,15	-1,19	-2,19	-2,24	-1,62
_0084	0		hypothetical protein	1,01	-1,01	-1,08	-1,32	-2,24	-2,07	-1,65
_0085	ipmi1	4.2.1.33	3-isopropylmalate dehydratase	1,10	1,13	-1,10	-1,82	-1,65	-1,83	-1,37
_0086	0		SOUL heme-binding protein	-1,84	-1,58	-1,56	-1,39	1,53	1,40	1,85
_0087	0		iojap-like protein	-1,05	-1,09	-1,07	-1,13	-1,07	1,27	1,37
_0088	0	2.1.1.177	23S rRNA (pseudouridine 1915-N3)-methyltransferase	-1,06	-1,08	-1,07	-1,03	-1,09	1,22	1,45
_0089	ipgm	5.4.2.12	phosphoglycerate mutase	1,08	1,02	-1,07	-1,12	-1,15	-1,06	1,18
_0090	0		peptidase M23B	1,01	-1,02	-1,09	-1,16	-1,21	-1,10	-1,08
_0091	prc	3.4.21.102	C-terminal processing peptidase	-1,06	-1,04	-1,03	-1,22	-1,31	-1,40	-1,30
_0092	0	3.6.1.-	NUDIX hydrolase	1,05	-1,02	-1,01	-1,06	-1,21	-1,11	-1,22
_0093	0		hypothetical protein	1,07	1,02	-1,03	1,13	1,15	1,22	1,28
_0094	0		hypothetical protein	-1,06	-1,01	-1,04	1,00	1,07	1,23	1,01
_0095	0		hypothetical protein	1,06	-1,05	1,01	1,03	1,02	-1,03	1,20
_0096	0		hypothetical protein	1,00	1,01	1,01	1,16	1,14	1,17	1,21
_0097	0		hypothetical protein	-1,05	-1,03	1,10	1,22	-1,19	-1,16	1,02
_0098	0		hypothetical protein	-1,04	-1,00	1,05	1,03	-1,08	-1,04	1,09
_0099	0		hypothetical protein	-1,02	1,01	-1,08	1,19	-1,08	1,01	1,13
_0100	0		transposase, putative	1,02	1,01	-1,03	-1,08	1,10	1,03	1,13
_0101	0		hypothetical protein	1,02	-1,02	1,05	1,13	-1,01	1,07	1,05
_0102	dnaE1	2.7.7.7	DNA-directed DNA polymerase	-1,12	-1,01	1,12	-1,17	-1,08	1,16	1,08
_0103	adhI	1.1.1.284	S-(hydroxymethyl) dehydrogenase	-1,04	-1,03	-1,07	-1,11	-1,18	-1,31	-1,37
_0104	0		GCN5-related N-acetyltransferase	-1,03	-1,01	1,05	1,04	-1,07	-1,17	-1,10
_0105	0		hypothetical protein	1,04	1,04	1,10	1,18	1,28	1,25	1,40
_0106	0		TetR family transcriptional regulator	-1,07	-1,03	1,06	1,03	1,14	1,21	-1,03
_0107	0		rubrerythrin	-1,09	-1,09	-1,11	1,02	-1,04	1,09	1,71
_0108	0		hypothetical protein	-1,03	-1,05	1,04	1,22	1,02	-1,03	-1,18
_0109	0		auxin efflux carrier	-1,08	-1,08	1,01	1,28	1,13	-1,06	-1,17
_0110	0		hypothetical protein	-1,02	-1,05	1,03	1,02	1,11	-1,04	1,03
_0111	0		major facilitator transporter	-1,02	-1,03	1,16	-1,08	1,29	1,10	1,13
_0112	0		AFG1 family ATPase	1,17	1,08	-1,10	-1,04	-1,12	-1,17	1,02
_0113	ahpC	1.11.1.15	peroxiredoxin	1,00	1,00	-1,10	-1,27	-1,87	-2,71	-1,73

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_0114	0		FAD-dependent pyridine nucleotide-disulphide oxidoreductase	1,02	-1,02	1,00	-1,07	1,08	-1,23	-1,00
_0115	0		putative methyltransferase	-1,03	-1,04	1,04	-1,02	-1,11	-1,09	1,01
_0116	0		TRAP dicarboxylate transporter- DctP subunit	1,12	1,10	-1,03	1,07	-1,04	-1,37	1,14
_0117	map	3.4.11.18	methionyl aminopeptidase	-1,03	1,03	-1,05	-1,04	-1,01	1,01	-1,17
_0118	sfsA		sugar fermentation stimulation protein A	1,21	1,04	-1,17	-1,26	-1,04	-1,54	-1,09
_0119	mogA		molybdopterin binding domain-containing protein	1,10	1,05	-1,08	-1,19	-1,21	-1,44	-1,10
_0120	0		GCN5-related N-acetyltransferase	1,09	1,01	-1,10	-1,17	-1,24	-1,29	-1,18
_0121	0		uncharacterized peroxidase-related enzyme	-1,11	-1,05	-1,09	-1,27	-1,26	-1,21	-1,40
_0122	0		OmpA/MotB domain-containing protein	-1,04	-1,00	-1,05	1,01	-1,12	1,07	-1,09
_0123	0		LysR family transcriptional regulator	-1,04	-1,05	-1,12	-1,08	1,01	1,05	1,50
_0124	0		PfpI family intracellular peptidase	-1,09	-1,07	1,02	-1,06	-1,15	-1,22	-1,04
_0125	fadH	1.3.1.34	2,4-dienoyl-CoA reductase (NADPH)	-1,55	-1,38	-1,53	-1,57	-1,97	-1,26	-1,39
_0126	0		hypothetical protein	1,02	-1,01	1,02	1,03	-1,09	1,00	1,20
_0127	0		hypothetical protein	-1,01	-1,00	-1,01	1,08	1,12	1,18	1,03
_0128	0		hypothetical protein	1,00	1,01	-1,03	-1,01	-1,30	-1,54	-1,48
_0129	ilvD1	4.2.1.9	dihydroxy-acid dehydratase	1,05	1,06	-1,06	-1,09	-1,20	-1,71	-1,19
_0130	abi		abortive infection protein	1,05	1,15	1,07	-1,03	-1,17	-1,43	-1,04
_0131	accD	6.4.1.2	acetyl-CoA carboxylase	1,20	1,16	1,00	-1,01	-1,02	-1,35	1,06
_0132	folC	6.3.2.17	tetrahydrofolate synthase	-1,03	1,00	-1,06	-1,18	-1,29	-1,38	-1,02
_0133	0		type I secretion target repeat-containing protein	1,10	1,01	1,16	1,19	1,37	1,8	1,94
_0134	pcd	4.2.1.96	4a-hydroxy tetrahydrobiopterin dehydratase	1,05	-1,03	1,01	1,10	1,07	1,19	1,24
_0135	0		hypothetical protein	1,14	1,00	-1,05	-1,06	-1,01	1,10	1,28
_0136	ugpQ	3.1.4.46	glycerophospho diester phosphodiesterase	1,01	1,01	-1,02	-1,11	-1,18	-1,03	-1,14
_0137	0		endoribonuclease L-PSP	1,04	-1,00	-1,01	-1,02	-1,35	-1,33	-1,25
_0138	hlyD		HlyD family type I secretion membrane fusion protein	1,00	-1,01	-1,02	1,02	-1,03	1,06	-1,09
_0139	0		type I secretion system ATPase	-1,01	-1,01	-1,01	1,12	1,20	1,26	1,31
_0140	0		VacJ family lipoprotein	1,04	1,01	-1,07	-1,23	-1,05	-1,16	1,01
_0141	ttg2D		toluene tolerance family protein	1,05	-1,00	-1,05	1,00	-1,22	-1,24	1,01
_0142	mrcB	2.4.1.129	peptidoglycan glycosyltransferase	1,02	1,00	-1,03	-1,10	-1,03	-1,01	1,13
_0143	glnK		nitrogen regulatory protein P-II	1,02	1,01	-1,05	1,05	1,08	1,18	1,17
_0144	amtB		ammonium transporter	-1,02	-1,03	-1,01	-1,00	1,07	1,04	-1,10
_0145	0	2.6.1.1, 2.6.1.57	aspartate transaminase,aromatic-amino-acid transaminase	-1,04	-1,03	1,06	1,02	-1,03	-1,02	1,02
_0146	sseA		3-mercaptopyruvate sulfurtransferase	-1,02	-1,04	-1,04	-1,37	-1,31	-1,39	-1,30
_0147	smpB		SsrA-binding protein	1,07	1,04	-1,16	-1,38	-1,43	-1,66	-1,29
_0148	0		GCN5-related N-acetyltransferase	1,02	1,05	-1,07	-1,15	-1,17	-1,45	-1,15
_0149	dapA	4.3.3.7	4-hydroxy-tetrahydro dipicolinate synthase	1,06	1,10	-1,01	-1,03	-1,18	-1,78	-1,26
_0150	0	3.2.1.-	putative lytic transglycosylase catalyticsubunit"	1,08	1,04	1,05	-1,07	-1,10	-1,15	1,02
_0151	0		hypothetical protein	-1,04	-1,04	-1,02	-1,02	1,02	1,02	-1,18
_0152	0		hypothetical protein	-1,00	-1,02	-1,00	-1,06	-1,04	1,00	1,03
_0153	dao		FAD dependent oxidoreductase	-1,03	1,02	-1,02	-1,13	-1,13	-1,08	-1,09
_0154	0		NADPH-dependent FMN reductase	1,01	-1,04	-1,07	-1,14	1,00	-1,08	1,05
_0155	lrgA		LrgA family protein	-1,15	-1,06	1,14	-1,02	1,03	1,13	-1,37
_0156	lrgB		LrgB family protein	-1,06	-1,02	1,02	1,07	-1,06	-1,04	-1,18
_0157	cobA2	2.5.1.17	cob(I)yrinic acid a,c-diamide adenosyltransferase	1,01	1,02	-1,03	-1,13	-1,10	-1,29	-1,22
_0158	cobN	6.6.1.2	cobaltochelatase	1,07	1,02	-1,11	-1,09	-1,23	-1,23	-1,03
_0159	0		hypothetical protein	1,03	-1,02	-1,13	-1,06	1,12	1,65	1,99
_0160	cobW		cobalamin biosynthesis protein CobW	1,06	1,07	-1,00	-1,13	1,50	3,35	4,41
_0161	cbtA		cobalt transporter, subunit CbtA	1,04	1,07	1,11	1,23	1,74	4,26	4,88
_0162	cbtB		hypothetical protein	1,01	1,02	1,05	1,07	1,78	3,04	3,78
_0163	smc		chromosome segregation protein SMC	-1,04	-1,02	1,08	-1,00	1,10	1,57	-1,01
_0164	mltB1		lytic murein transglycosylase	-1,11	-1,06	-1,05	-1,51	-1,12	-1,16	-1,30
_0165	cobD	6.3.1.10	Adenosylcobinamide-phosphate synthase	1,00	1,01	-1,09	-1,17	-1,25	-1,43	-1,15
_0166	cobC	4.1.1.81	threonine-phosphate decarboxylase	-1,02	1,05	-1,21	-1,31	-1,65	-1,56	-1,45
_0167	0		hypothetical protein	1,09	1,09	-1,05	-1,10	-1,40	-1,87	-1,38
_0168	0		response regulator receiver protein	-1,02	-1,00	-1,02	1,09	1,15	1,19	1,06
_0169	0		putative glutathione S-transferase	-1,03	1,00	1,15	-1,22	1,11	1,13	1,08
_0170	0		hypothetical protein	1,12	1,15	1,10	-1,03	-1,08	-1,60	1,00
_0171	cbiX2	4.99.1.3	sirohydrochlorin cobaltochelatase	1,15	1,16	1,09	-1,05	-1,08	-1,79	1,06
_0172	cobH	5.4.1.2	Precorrin-8X methylmutase	1,06	1,05	1,07	-1,11	-1,48	-2,05	-1,07
_0173	cobL	2.1.1.132	precorrin-6B C5,15-methyltransferase	-1,02	1,03	1,03	1,07	-1,36	-1,73	-1,23

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
			(decarboxylating)							
_0174	cobI	2.1.1.15, 2.1.1.130	fatty-acid O-methyltransferase,Precorrin-2 C20-methyl transferase	1,02	-1,00	-1,06	1,02	-1,43	-1,78	-1,17
_0175	cbiG	2.1.1.131, 1.14.13.83	Precorrin-3B C17-methyl transferase,precorrin-3B synthase	-1,04	-1,03	1,01	1,03	-1,29	-1,65	-1,15
_0176	cobM	2.1.1.133	Precorrin-4 C11-methyl transferase	-1,02	1,01	1,05	1,28	-1,27	-1,64	-1,12
_0177	0		hypothetical protein	-1,00	-1,00	1,11	-1,03	1,01	-1,06	1,03
_0178	0	4.4.1.8	cystathionine beta-lyase	-1,09	-1,02	-1,01	-1,01	-1,08	-1,15	-1,35
_0179	def1	3.5.1.88	peptide deformylase	1,10	1,07	-1,10	-1,38	-1,19	-1,44	-1,07
_0180	def2	3.5.1.88	peptide deformylase	1,06	1,00	-1,12	-1,45	-1,49	-1,39	-1,11
_0181	fmt	2.1.2.9	methionyl-tRNA formyltransferase	-1,03	-1,04	-1,08	-1,42	-1,42	-1,30	-1,36
_0182	rnhA	3.1.26.4	ribonuclease H	1,03	1,01	-1,04	-1,20	-1,22	-1,31	-1,09
_0183	0		methyltransferase type 11	-1,01	1,00	-1,10	-1,20	-1,28	-1,28	-1,25
_0184	0		hypothetical protein	1,00	1,01	-1,07	1,08	-1,21	-1,33	-1,15
_0185	cdsA2	2.7.7.41	phosphatidate cytidylyltransferase	-1,02	-1,05	-1,04	-1,03	1,05	1,08	1,02
_0186	plsC		phospholipid/glycerol acyltransferase	-1,09	-1,05	-1,06	-1,01	1,09	1,17	-1,11
_0187	0		lysine exporter protein LysE/YggA	-1,09	-1,04	-1,03	1,02	-1,01	1,17	-1,20
_0188	ispH	1.17.1.2	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	-1,04	-1,01	-1,00	-1,03	-1,01	-1,06	-1,02
_0189	0		cytochrome c class I	-1,02	-1,02	1,01	-1,04	1,02	1,10	1,16
_0190	0		membrane protein-like protein	-1,02	-1,01	-1,05	-1,04	-1,01	1,05	1,20
_0191	0		hypothetical protein	-1,01	1,00	-1,14	-1,15	-1,29	-1,11	-1,10
_0192	hppk	2.7.6.3	2-amino-4-hydroxy-6-hydroxymethyl dihydropteridine diphosphokinase	1,05	1,07	1,09	1,14	1,03	-1,10	1,01
_0193	rpoZ	2.7.7.6	DNA-directed RNA polymerase	1,08	1,11	-1,07	-1,19	-1,13	-1,53	-1,40
_0194	relA	2.7.6.5	GTP diphosphokinase	1,09	1,01	-1,10	-1,16	-1,14	-1,21	-1,13
_0195	0		hypothetical protein	1,05	1,08	1,06	1,22	1,49	1,64	1,9
_0196	pdxJ	2.6.99.2	pyridoxine 5-phosphate synthase	1,03	1,05	1,09	1,03	1,27	1,24	1,58
_0197	0		hypothetical protein	1,11	1,01	1,13	1,10	1,11	1,33	1,66
_0198	acpS	2.7.8.7	holo-[acyl-carrier-protein] synthase	1,03	-1,00	-1,07	-1,07	-1,21	-1,33	-1,11
_0199	lepB	3.4.21.89	Signal peptidase I	1,27	1,16	-1,09	-1,63	-1,40	-2,17	-1,27
_0200	rnc	3.1.26.3	ribonuclease III	1,06	1,05	-1,04	-1,29	-1,43	-1,66	-1,22
_0201	era		GTP-binding protein Era	1,03	1,02	-1,03	-1,41	-1,35	-1,53	-1,18
_0202	0		hypothetical protein	1,00	-1,01	1,03	-1,00	-1,15	-1,24	-1,07
_0203	recO		DNA repair protein RecO	-1,02	-1,03	1,06	1,02	1,04	1,18	-1,01
_0204	mmgC		acyl-CoA dehydrogenase domain-containing protein	-1,27	-1,18	-1,12	-1,23	-1,10	-1,25	-1,17
_0205	0		hypothetical protein	1,01	1,02	-1,05	1,08	-1,18	-1,48	-1,18
_0206	0		hypothetical protein	1,04	1,03	1,01	1,05	-1,10	-1,20	-1,05
_0207	ptsH		phosphotransferase system, phosphocarrier protein HPr	-1,00	-1,03	-1,06	-1,02	-1,14	-1,26	-1,22
_0208	ptsL	2.7.1.69	Protein-Npi-phosphohistidine-sugar phosphotransferase	-1,02	-1,07	-1,12	-1,09	-1,02	-1,14	-1,15
_0209	0		hypothetical protein	1,05	1,00	1,13	1,17	1,04	1,15	1,27
_0210	hprK		HPr kinase	-1,02	-1,01	1,12	1,03	1,07	1,58	1,33
_0211	0	2.7.13.3	histidine kinase	1,06	1,01	1,02	-1,01	1,28	1,49	1,56
_0212	0		two component transcriptional regulator	1,05	1,01	-1,04	-1,01	1,40	1,39	1,67
_0213	pckA	4.1.1.49	phosphoenolpyruvate carboxykinase (ATP)	1,33	1,30	1,09	1,02	1,77	1,21	2,32
_0214	hbdA	1.1.1.157	3-hydroxybutyryl-CoA dehydrogenase	-1,02	-1,02	1,02	-1,15	-1,05	-1,12	-1,17
_0215	0		hypothetical protein	1,07	1,02	1,04	1,21	1,48	1,46	1,91
_0216	eftA		electron transfer flavoprotein alpha subunit	-1,10	-1,07	-1,11	-1,28	-2,03	-2,55	-1,45
_0217	eftB		electron transfer flavoprotein alpha/beta-subunit	-1,07	1,02	-1,10	-1,27	-2,01	-2,38	-1,47
_0218	0		ATP--cobalamin adenosyltransferase	-1,00	1,06	-1,08	-1,19	-1,65	-2,11	-1,31
_0219	0		hypothetical protein	1,06	1,08	-1,09	-1,19	-1,11	-1,46	-1,03
_0220	0		short-chain dehydrogenase/reductase SDR	-1,05	-1,02	-1,09	1,05	-1,09	-1,35	-1,14
_0221	parC	5.99.1.3	DNA topoisomerase (ATP-hydrolysing)	-1,01	-1,01	-1,03	-1,04	-1,14	-1,20	-1,14
_0222	0		hypothetical protein	1,03	-1,01	1,03	1,09	-1,25	-1,24	-1,14
_0223	tufA2		elongation factor Tu	1,03	1,11	-1,13	-1,36	-3,66	-4,99	-1,98
_0224	0		hypothetical protein	-1,02	1,04	-1,06	1,04	-1,16	-1,57	-1,29
_0225	0		hypothetical protein	-1,00	-1,06	-1,08	-1,16	3,64	10,3	9,25
_0226	0		hypothetical protein	-1,02	-1,00	1,04	-1,15	-1,05	-1,30	-1,12
_0227	0		N-formylglutamate amidohydrolase	1,05	-1,01	-1,10	-1,21	-1,07	-1,12	-1,02
_0228	pykA	2.7.1.40	pyruvate kinase	-1,49	-1,18	1,01	-1,02	-3,7	-2,44	-3,23
_0229	0		hypothetical protein	-1,19	-1,22	1,06	1,22	-1,56	-1,42	-1,50
_0230	rpmI		50S ribosomal protein L35	1,16	1,14	-1,14	-1,15	-1,45	-2,93	-1,59

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_0231	rplT		50S ribosomal protein L20	1,12	1,12	-1,17	-1,44	-1,59	-2,86	-1,68
_0232	0		hypothetical protein	1,02	1,01	-1,06	-1,21	-1,11	-1,26	-1,27
_0233	0		citrate transporter	1,00	-1,07	-1,02	1,08	-1,12	-1,11	-1,29
_0234	0		hypothetical protein	-1,01	1,01	-1,00	1,26	1,35	1,49	1,46
_0235	pheS	6.1.1.20	Phenylalanine-tRNA ligase	1,07	1,07	-1,02	-1,20	-1,32	-1,63	-1,16
_0236	0		hypothetical protein	1,04	-1,05	1,01	1,18	-1,12	1,02	-1,04
_0237	pheT	6.1.1.20	Phenylalanine-tRNA ligase	1,12	1,13	-1,05	-1,18	-1,42	-1,92	-1,20
_0238	0		hypothetical protein	-1,03	-1,02	-1,07	-1,25	-1,15	-1,19	-1,18
_0239	nadX	1.4.1.21	aspartate dehydrogenase	-1,08	-1,05	-1,04	-1,06	-1,06	-1,01	1,05
_0240	gst3	2.5.1.18	glutathione transferase	-1,07	1,01	1,08	-1,27	-1,05	-1,05	1,05
_0241	mscL		large conductance mechanosensitive channel protein	-1,03	-1,02	-1,00	1,14	1,14	1,18	1,03
_0242	0		fatty acid hydroxylase	1,03	-1,03	-1,01	1,15	1,36	1,67	1,64
_0243	0		acyltransferase 3	1,03	-1,02	1,10	1,23	1,39	1,79	1,9
_0244	adh	1.4.1.1	alanine dehydrogenase	-1,09	-1,02	1,18	1,08	1,21	1,06	2,04
_0245	asnC		AsnC family transcriptional regulator	1,01	-1,01	1,05	1,15	1,50	1,56	1,07
_0246	rpsU		30S ribosomal protein S21	1,05	1,06	-1,05	-1,15	-2,03	-2,61	-1,38
_0247	0		rpsU-divergently transcribed protein	-1,07	-1,03	-1,00	-1,04	-1,03	1,19	-1,10
_0248	0		quinone oxidoreductase putative PIG3	-1,00	1,01	-1,03	-1,21	-1,16	-1,14	-1,06
_0249	0		acriflavin resistance protein	-1,01	1,01	1,08	1,07	1,17	1,43	1,43
_0250	0		acriflavin resistance protein	-1,00	1,02	1,03	1,20	1,02	1,20	1,22
_0251	0		RND family efflux transporter MFP subunit	1,05	-1,01	1,00	-1,22	1,14	1,16	1,06
_0252	0		TetR family transcriptional regulator	-1,01	1,01	1,07	1,15	1,08	1,09	1,24
_0253	0	6.2.1.12	4-Coumarate-CoA ligase	-1,04	-1,10	-1,08	-1,03	-1,25	-1,15	-1,42
_0254	0	3.1.27.1	ribonuclease T2	-1,02	1,01	1,02	1,04	1,15	1,18	1,01
_0255	0		hypothetical protein	1,13	1,12	-1,20	-1,69	-1,53	-2,34	-1,41
_0256	0		hypothetical protein	-1,08	-1,01	1,06	1,06	-1,13	1,21	-1,45
_0257	0		peptidase S8 and S53 subtilisin kexin sedolisin	1,04	-1,02	-1,11	-1,20	-1,01	1,11	-1,04
_0258	secE		preprotein translocase, SecE subunit	1,11	1,15	1,01	-1,05	-1,16	-1,25	-1,09
_0259	nusG		NusG antitermination factor	1,23	1,19	-1,12	-1,19	-1,11	-2,26	-1,24
_0260	rplK		50S ribosomal protein L11	1,05	1,07	-1,17	-1,54	-2,23	-4,51	-1,95
_0261	rplA		50S ribosomal protein L1	1,00	1,04	-1,14	-1,37	-2,37	-4,54	-2,11
_0262	0		hypothetical protein	-1,04	-1,09	-1,27	-1,54	-1,59	-1,32	-1,05
_0263	fkbM		FkbM family methyltransferase	-1,03	-1,06	-1,11	-1,05	-1,12	-1,05	1,04
_0264	0		hypothetical protein	1,07	-1,02	-1,03	-1,05	1,24	1,39	1,62
_0265	rplJ		50S ribosomal protein L10	1,04	1,04	-1,12	-1,39	-3,21	-7,83	-2,68
_0266	rplL		50S ribosomal protein L7/L12	-1,01	1,04	-1,14	-1,29	-3,22	-7,95	-2,97
_0267	0		hypothetical protein	-1,09	-1,10	-1,10	-1,51	-1,02	1,16	-1,16
_0268	rpoB	2.7.7.6	DNA-directed RNA polymerase	1,08	1,09	-1,14	-1,29	-1,55	-2,37	-1,37
_0269	rpoC	2.7.7.6	DNA-directed RNA polymerase	-1,03	1,01	-1,09	-1,19	-2,06	-3,01	-1,84
_0270	0		hypothetical protein	-1,00	-1,02	-1,10	1,04	-1,14	-1,21	-1,06
_0271	rpsL		30S ribosomal protein S12	1,21	1,17	-1,33	-1,81	-2,08	-4,15	-1,36
_0272	rpsG		30S ribosomal protein S7	1,10	1,13	-1,37	-2,05	-2,26	-3,89	-1,58
_0273	fusA		elongation factor G	1,01	1,04	-1,35	-1,94	-3,58	-5,16	-2,05
_0274	tufA1		elongation factor Tu	1,04	1,07	-1,13	-1,26	-3,69	-4,97	-1,99
_0275	rpsJ		30S ribosomal protein S10	-1,03	-1,01	-1,15	-1,17	-4,36	-6,47	-2,64
_0276	rplC		ribosomal protein L3	-1,01	1,01	-1,07	-1,10	-3,95	-5,76	-2,38
_0277	rplD		50S ribosomal protein L4	-1,05	-1,01	-1,06	-1,06	-3,7	-5,28	-2,38
_0278	rplW		50S ribosomal protein L23	-1,03	1,01	-1,01	-1,12	-3,74	-6,68	-2,51
_0279	0		hypothetical protein	-1,12	-1,06	1,14	1,08	1,00	1,07	-1,29
_0280	0		hypothetical protein	-1,03	-1,02	1,01	-1,01	1,14	1,23	1,00
_0281	0		YHS domain-containing protein	-1,03	-1,04	1,02	1,05	-1,31	-1,44	-1,52
_0282	0		hypothetical protein	-1,05	-1,03	1,13	1,41	1,52	1,06	1,11
_0283	0		hypothetical protein	-1,01	-1,04	1,05	1,09	1,44	1,14	1,08
_0284	0		hypothetical protein	1,01	-1,00	-1,05	1,09	1,40	-1,23	1,04
_0285	rplB		50S ribosomal protein L2	1,12	1,11	-1,22	-2,03	-2,29	-4,68	-1,8
_0286	rpsS		30S ribosomal protein S19	1,02	1,06	-1,31	-1,65	-2,8	-4,38	-2,49
_0287	rplV		50S ribosomal protein L22	1,00	1,04	-1,31	-1,55	-3,92	-5,80	-2,69
_0289	rplP		50S ribosomal protein L16	-1,01	1,03	-1,19	-1,40	-3,17	-4,28	-2,5
_0290	0		hypothetical protein	1,06	1,00	-1,20	-1,10	-1,40	-1,58	-1,50
_0291	0		hypothetical protein	-1,07	-1,03	-1,10	1,07	-1,05	1,01	1,24
_0292	0		hypothetical protein	1,06	1,03	-1,05	-1,03	-1,20	-1,31	1,02
_0293	rpmC		50S ribosomal protein L29	1,31	1,28	-1,12	-1,56	-1,38	-2,71	-1,26

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_0294	rpsQ		ribosomal protein S17	1,22	1,29	-1,22	-1,71	-1,69	-3,12	-1,50
_0295	rplN		50S ribosomal protein L14	1,12	1,15	-1,31	-2,02	-2,69	-4,9	-2,01
_0296	rplX		50S ribosomal protein L24	1,08	1,11	-1,28	-2,19	-2,81	-4,27	-1,87
_0297	rplE		50S ribosomal protein L5	1,01	1,05	-1,32	-1,83	-4,25	-5,62	-2,58
_0298	rpsN		30S ribosomal protein S14	1,01	1,04	-1,29	-1,79	-3,89	-4,89	-2,01
_0299	rpsH		30S ribosomal protein S8	-1,00	1,03	-1,27	-1,41	-3,74	-4,9	-2,21
_0300	rplF		50S ribosomal protein L6	1,01	1,01	-1,20	-1,51	-3,89	-4,92	-2,27
_0301	rplR		50S ribosomal protein L18	-1,02	1,01	-1,16	-1,32	-3,38	-3,72	-1,92
_0302	rpsE		30S ribosomal protein S5	1,02	1,04	-1,18	-1,12	-2,72	-4,09	-2,18
_0303	rpmD		50S ribosomal protein L30	-1,01	1,03	-1,12	-1,26	-3,25	-4,89	-2,2
_0304	rplO		50S ribosomal protein L15	1,03	1,03	-1,18	-1,17	-3,03	-4,15	-2,15
_0305	secY		preprotein translocase subunit SecY	1,00	1,02	1,02	1,07	-1,50	-1,67	-1,17
_0306	adk	2.7.4.3	adenylate kinase	-1,00	1,02	-1,05	-1,26	-1,83	-2,19	-1,66
_0307	rpsM		ribosomal protein S13	1,18	1,15	1,01	-1,11	-1,50	-2,97	-1,46
_0308	rpsK		30S ribosomal protein S11	1,13	1,09	-1,04	-1,20	-1,58	-2,81	-1,51
_0309	rpoA	2.7.7.6	DNA-directed RNA polymerase	1,07	1,07	-1,08	-1,36	-2,02	-2,96	-1,72
_0310	rplQ		50S ribosomal protein L17	1,02	1,06	-1,26	-1,83	-2,07	-4,06	-1,94
_0311	luxR1		LuxR family transcriptional regulator	-1,05	-1,04	-1,09	-1,28	-1,47	-1,41	-1,53
_0312	luxI		N-acyl-L-homoserine lactone synthetase-like protein	-1,01	-1,01	-1,07	-1,20	-1,30	-1,13	-1,34
_0313	0		recombination factor protein RarA	1,02	1,01	-1,02	-1,03	-1,08	-1,13	-1,09
_0314	0		camphor resistance CrcB protein	1,05	1,01	-1,04	-1,05	-1,12	-1,33	1,02
_0315	rluC		RluA family pseudouridine synthase	1,09	1,04	-1,06	-1,23	-1,16	-1,27	1,09
_0316	gph	3.1.3.18	phosphoglycolate phosphatase	-1,02	1,01	1,01	-1,21	-1,36	-1,38	-1,07
_0317	0		ATP12 ATPase	1,02	1,03	1,03	1,01	-1,15	-1,20	-1,12
_0318	bztA		glutamate/glutamine/aspartate/asparagine ABC transporter	-1,11	-1,07	-1,13	-1,16	-2,51	-2,41	-2,76
_0319	bztB		polar amino acid ABC transporter, inner membrane subunit	-1,07	-1,08	-1,07	-1,20	-1,83	-1,55	-2,14
_0320	bztC		polar amino acid ABC transporter, inner membrane subunit	-1,03	-1,04	1,05	-1,02	-1,47	-1,48	-1,62
_0321	bztD		glutamate/glutamine/aspartate/asparagine ABC transport ATP-binding	-1,02	-1,03	1,00	1,11	-1,43	-1,26	-1,82
_0322	0		putative phosphohistidine phosphatase, SixA	-1,02	-1,02	-1,04	-1,13	-1,14	-1,11	-1,13
_0323	0		hypothetical protein	1,02	1,05	-1,00	-1,33	-1,29	-1,12	-1,06
_0324	argB		acetylglutamate kinase	1,06	1,08	-1,14	-1,34	-1,34	-1,84	-1,25
_0325	fabG3	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase	-1,03	-1,04	1,15	1,34	1,55	1,75	1,39
_0326	engB		ribosome biogenesis GTP-binding protein YsxC	-1,02	-1,01	-1,08	-1,27	-1,78	-1,89	-1,30
_0327	mosc		MOSC domain-containing protein	1,01	-1,04	-1,05	-1,04	-1,95	-2	-1,30
_0328	yidC		putative inner membrane protein translocase component YidC	1,15	1,11	-1,08	-1,20	-1,19	-1,55	1,02
_0329	ydaM		diguanylate cyclase/phosphodiesterase	1,09	1,00	1,01	-1,03	1,23	1,84	1,85
_0330	ydaO		PP-loop domain-containing protein	1,06	1,05	-1,01	1,01	1,03	-1,15	1,15
_0331	0		hypothetical protein	1,04	-1,02	-1,05	-1,06	-1,25	-1,18	1,03
_0332	rnpA	3.1.26.5	ribonuclease P	1,13	1,06	-1,12	-1,18	-1,19	-1,38	-1,05
_0333	rpmH		50S ribosomal protein L34	1,25	1,21	-1,07	-1,22	-1,00	-1,89	-1,11
_0334	0	2.7.13.3	histidine kinase	-1,00	1,00	-1,05	-1,11	-1,03	-1,14	-1,01
_0335	merA	1.16.1.1	mercury(II) reductase	1,00	-1,05	-1,06	-1,02	-1,19	-1,21	1,00
_0336	0		SNARE associated Golgi protein	1,01	-1,07	-1,10	1,02	-1,31	-1,32	1,04
_0337	parA2		ATPase MipZ	1,07	1,05	-1,03	-1,03	1,23	1,04	1,24
_0338	0		beta-lactamase domain-containing protein	-1,16	-1,07	-1,03	-1,04	-1,44	-1,39	-1,84
_0339	0		hypothetical protein	-1,02	-1,02	1,03	1,05	1,05	-1,04	1,07
_0340	rpmE		50S ribosomal protein L31	1,09	1,09	-1,15	-1,38	-1,44	-2,01	-1,26
_0341	rplS		50S ribosomal protein L19	1,16	1,15	-1,18	-1,52	-1,74	-3,15	-1,44
_0342	trmD	2.1.1.228	tRNA (guanine37-N1)-methyltransferase	1,04	1,06	-1,01	1,03	-1,19	-1,48	-1,08
_0343	aph		aminoglycoside phosphotransferase	1,05	-1,04	-1,02	1,05	1,32	1,57	1,46
_0344	rimM		16S rRNA-processing protein RimM	-1,02	-1,04	-1,10	-1,05	-2,14	-2,53	-2,18
_0345	0		hypothetical protein	-1,01	-1,00	-1,04	-1,06	-1,76	-2,07	-1,75
_0346	0		hypothetical protein	-1,01	-1,00	-1,13	-1,14	-1,84	-2,02	-1,68
_0347	bluB	1.16.8.1	cob(II)yrinic acid a,c-diamide reductase	1,01	1,01	-1,05	-1,19	-2,26	-3,14	-2,23
_0348	rpsP		30S ribosomal protein S16	-1,04	-1,02	-1,11	-1,27	-4,37	-5,20	-2,89
_0349	pheA1	5.4.99.5	Chorismate mutase	-1,02	-1,01	-1,22	-1,69	-2,31	-2,33	-1,89
_0350	0		hypothetical protein	1,05	-1,01	-1,29	-1,39	-1,97	-2,23	-1,55
_0351	0		GCN5-related N-acetyltransferase	-1,02	1,00	-1,19	-1,33	-2,06	-2,65	-1,46

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_0352	0		acetyltransferase	1,05	1,01	-1,21	-1,20	-1,45	-1,9	-1,25
_0353	ffh		signal recognition particle protein	1,20	1,18	-1,06	-1,67	-1,18	-1,58	-1,13
_0354	azoR1		0	-1,04	-1,00	-1,05	-1,18	1,09	1,13	1,02
_0355	lysR		LysR family transcriptional regulator	-1,04	-1,03	-1,12	-1,15	1,01	1,07	-1,04
_0356	0		hypothetical protein	-1,07	-1,04	-1,03	1,15	1,01	1,12	1,15
_0357	arsR		ArsR family transcriptional regulator	-1,01	1,03	1,10	1,25	-1,03	-1,17	-1,13
_0358	purH	2.1.2.3	phosphoribosyl aminoimidazole carboxamide formyltransferase	1,18	1,10	-1,10	-1,29	-1,59	-2,06	-1,16
_0359	lspA	3.4.23.36	Signal peptidase II	1,02	-1,02	-1,04	-1,54	-1,69	-2,38	-1,38
_0360	0		hypothetical protein	1,02	1,00	-1,07	-1,07	-1,37	-1,49	-1,20
_0361	pqqL2		peptidase M16 domain-containing protein	1,03	-1,01	1,05	-1,08	1,08	1,28	1,24
_0362	pqqL1		peptidase M16 domain-containing protein	-1,03	-1,03	-1,02	1,06	-1,03	1,17	1,22
_0363	mutL		DNA mismatch repair protein	-1,00	-1,03	-1,02	-1,01	1,27	1,49	1,36
_0364	rmuC		hypothetical protein	-1,03	-1,04	1,02	-1,02	-1,00	1,39	1,09
_0365	chrR1		anti-ECFsigma factor, ChrR	-1,42	-1,32	-1,43	-1,42	-1,00	-1,24	1,08
_0366	rpoE2		RNA polymerase sigma factor RpoE	-1,30	-1,29	-1,38	-1,33	-1,00	1,03	1,04
_0367	0		amine oxidase	-1,98	-1,81	-1,9	-2,17	1,03	-1,51	-1,29
_0368	0		hypothetical protein	-1,16	-1,38	-1,16	-1,29	-1,08	-1,55	-1,10
_0369	0		sodium:galactoside symporter family protein, putative	1,02	-1,15	-1,01	1,01	-1,01	-1,11	-1,00
_0370	0		hypothetical protein	1,00	-1,05	1,07	1,08	-1,03	-1,11	-1,05
_0371	0		short-chain dehydrogenase/reductase SDR	-1,02	-1,00	1,03	1,19	1,15	-1,01	1,14
_0372	0		hypothetical protein	-1,13	1,02	1,25	1,08	1,12	1,12	-1,31
_0373	fadD3	6.2.1.3	Long-chain-fatty-acid-CoA ligase	-1,13	-1,14	-1,26	-1,54	-2,09	-1,83	-2,45
_0374	0		hypothetical protein	-1,04	-1,03	-1,15	-1,24	-1,59	-1,43	-1,46
_0375	livG		ABC transporter related	-1,01	-1,05	-1,14	-1,20	-1,70	-1,48	-1,65
_0376	livH		inner-membrane translocator	-1,06	-1,06	-1,09	1,08	-1,82	-1,84	-2,05
_0377	0		hypothetical protein	1,04	-1,01	-1,01	1,17	1,66	1,82	2,79
_0378	0		hypothetical protein	-1,05	-1,13	-1,25	-1,40	-2,5	-2,02	-2,56
_0379	livM		inner-membrane translocator	-1,01	-1,01	-1,02	-1,01	-1,62	-1,49	-1,83
_0380	livK		hypothetical protein	-1,05	-1,09	-1,08	-1,01	-1,95	-1,89	-2,56
_0381	livF1		ABC transporter related	1,00	-1,04	-1,05	-1,12	-1,65	-1,85	-2,03
_0382	paaK	6.2.1.30	phenylacetate-CoA ligase	1,01	1,02	1,04	-1,11	-1,20	-1,30	-1,34
_0383	0		hypothetical protein	-1,04	1,04	1,06	-1,06	1,12	1,19	1,24
_0384	0		hypothetical protein	-1,05	-1,02	1,12	1,13	-1,02	-1,01	1,08
_0385	dinB	2.7.7.7	DNA-directed DNA polymerase	-1,01	-1,01	1,03	-1,07	1,06	1,07	-1,07
_0386	hutG	3.5.1.68, 3.5.3.8	N-formylglutamate deformylase,formimidoylglutamase	-1,05	-1,02	1,06	1,08	1,00	1,05	-1,09
_0387	rpmJ		50S ribosomal protein L36	1,20	1,16	-1,16	-1,19	-1,24	-2,36	-1,23
_0388	rbsA5	3.6.3.17	Monosaccharide-transporting ATPase	-1,00	1,00	-1,09	-1,11	-1,59	-1,47	-1,65
_0389	rbsC2	3.6.3.17	Monosaccharide-transporting ATPase	-1,03	-1,07	-1,13	-1,28	-1,98	-1,77	-2,15
_0390	rbsB3	3.6.3.17	Monosaccharide-transporting ATPase	-1,08	-1,15	-1,38	-1,86	-3,06	-2,65	-3,3
_0391	0		hypothetical protein	-1,06	-1,04	-1,10	1,06	-1,15	-1,22	-1,20
_0392	0		hypothetical protein	-1,03	1,01	-1,02	1,07	1,12	1,21	1,21
_0393	0		hypothetical protein	-1,05	-1,04	1,03	1,14	1,10	1,17	-1,04
_0394	0		hypothetical protein	-1,06	-1,04	1,03	1,13	1,17	1,35	1,09
_0395	0		integrase family protein	-1,02	-1,01	1,04	-1,07	-1,12	-1,05	1,03
_0396	0		recombinase	1,02	-1,01	-1,00	-1,09	1,03	-1,03	1,09
_0397	xerDC2		integrase family protein	-1,03	-1,02	1,05	1,09	1,09	1,15	1,13
_0398	xerDC1		integrase family protein	1,01	-1,02	1,02	1,11	1,10	1,24	1,12
_0399	0		DNA binding domain-containing protein	-1,01	-1,01	-1,06	-1,02	1,14	1,24	1,34
_0400	0		CRISPR-associated endonuclease Csn1 family protein	-1,04	-1,01	1,00	1,06	1,15	1,38	-1,08
_0401	0		CRISPR-associated Cas1 family protein	-1,02	-1,01	1,03	1,04	1,00	1,09	1,10
_0402	0		CRISPR-associated Cas2 family protein	-1,03	-1,04	-1,05	-1,00	-1,12	1,21	-1,09
_0403	0		transposase IS3/IS911 family protein	-1,01	-1,01	-1,10	-1,12	-1,04	1,15	1,08
_0404	0		integrase catalytic region	-1,07	-1,02	-1,04	1,16	1,02	1,14	1,06
_0405	0		hypothetical protein	-1,04	1,03	1,09	1,01	-1,04	-1,08	-1,01
_0406	0		hypothetical protein	-1,03	-1,03	-1,07	-1,19	-1,18	-1,06	-1,15
_0407	0		XRE family transcriptional regulator	1,08	1,07	-1,19	-1,61	-1,47	-1,64	-1,09
_0408	0		hypothetical protein	1,03	1,08	-1,14	-1,45	-1,60	-1,56	-1,24
_0409	0		hypothetical protein	-1,06	-1,03	-1,07	1,05	1,17	1,16	1,16
_0410	0		hypothetical protein	-1,07	1,03	1,12	1,27	1,76	1,98	1,29
_0411	0		hypothetical protein	-1,00	1,03	1,20	1,48	1,87	1,92	1,44

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_0412	fas		beta-Ig-H3/fasciclin	-1,02	-1,00	-1,00	-1,02	-1,24	-1,07	-1,15
_0413	0		hypothetical protein	-1,02	1,02	1,02	1,11	1,14	1,20	1,20
_0414	0		GreA/GreB family elongation factor	-1,03	1,02	1,02	-1,00	-1,04	1,08	1,31
_0415	0		hypothetical protein	-1,01	-1,03	1,11	-1,05	1,18	1,15	1,29
_0416	0		hypothetical protein	-1,02	1,00	1,08	1,16	1,25	1,47	1,55
_0417	0		hypothetical protein	1,03	1,01	1,02	1,15	1,19	1,34	1,55
_0418	uspA2		UspA domain-containing protein	1,08	1,05	1,01	1,14	1,14	1,32	1,34
_0419	0		major facilitator transporter	-1,02	-1,03	1,07	1,16	1,02	1,09	-1,03
_0420	0		endonuclease/exonuclease/phosphatase	1,06	1,02	1,08	1,30	1,08	1,08	1,18
_0421	0		phospholipase D/transphosphatidylase	1,02	1,00	1,04	1,10	1,19	1,16	1,23
_0422	0		peptidase	-1,04	-1,05	1,15	1,33	1,13	1,20	1,32
_0423	pap		phosphoesterase PA-phosphatase related	-1,01	-1,03	1,04	1,13	-1,03	-1,15	-1,28
_0424	0		peptidase M41	-1,03	1,26	2,2	4,06	5,7	3,12	2,15
_0426	0		hypothetical protein	1,01	1,07	1,25	1,27	2,05	1,85	1,26
_0427	0		hypothetical protein	-1,07	-1,02	1,13	1,21	1,61	1,54	1,17
_0428	phaC	2.3.1.-	poly(3-hydroxyalkanoate) polymerase	-1,02	-1,01	1,01	1,18	1,58	1,39	1,21
_0429	0		hypothetical protein	-1,00	1,03	1,39	2,07	5,06	4	3,41
_0430	0		hypothetical protein	-1,00	1,07	1,86	3,32	8,81	6,21	4,62
_0431	dcuC		C4-dicarboxylate anaerobic carrier	1,00	1,03	1,04	1,30	1,77	1,60	2,05
_0432	arcA	3.5.3.6	arginine deiminase	-1,07	-1,03	1,08	1,22	2,49	1,86	2,17
_0433	arcB	2.1.3.3	ornithine carbamoyltransferase	-1,06	1,02	1,16	-1,10	1,82	1,61	2,02
_0434	arcC	2.7.2.2	carbamate kinase	1,06	-1,02	-1,01	1,10	1,55	1,43	1,50
_0435	atpD1	3.6.3.14	H+-transporting two-sector ATPase	-1,01	-1,01	-1,02	1,03	1,24	1,25	1,31
_0436	atpC2	3.6.3.14	H+-transporting two-sector ATPase	1,02	-1,02	1,04	1,17	1,15	1,17	1,41
_0437	0		F0F1-ATPase subunit, putative	-1,03	1,00	1,01	1,10	1,10	1,23	1,25
_0438	0		hypothetical protein	-1,02	-1,04	-1,02	1,06	1,15	1,36	1,27
_0439	atpB2	3.6.3.14	H+-transporting two-sector ATPase	-1,03	-1,01	1,04	1,17	1,20	1,33	1,13
_0440	atpE1	3.6.3.14	H+-transporting two-sector ATPase	-1,06	-1,02	1,00	-1,06	1,13	1,33	1,31
_0441	atpF1	3.6.3.14	H+-transporting two-sector ATPase	-1,03	-1,02	1,05	1,14	1,04	1,27	1,21
_0442	atpA2	3.6.3.14	H+-transporting two-sector ATPase	1,02	1,02	-1,03	1,08	1,11	1,41	1,24
_0443	atpG1	3.6.3.14	H+-transporting two-sector ATPase	1,03	1,02	-1,01	-1,05	1,06	1,22	1,18
_0444	0		hypothetical protein	-1,02	1,03	-1,06	-1,00	1,05	1,04	-1,08
_0445	0		hypothetical protein	-1,08	1,01	-1,09	1,19	1,07	-1,06	1,02
_0446	0		signal transduction protein	1,02	1,03	1,12	1,56	1,79	1,60	1,28
_0447	0		Crp/FNR family transcriptional regulator	-1,00	-1,03	-1,13	-1,36	1,12	1,14	1,08
_0448	0		integral membrane sensor signal transduction histidine kinase	1,01	-1,01	-1,06	1,03	-1,15	-1,43	-1,09
_0449	0		two component transcriptional regulator	-1,09	-1,07	1,09	1,22	-1,08	1,00	-1,33
_0450	pqqA		coenzyme PQQ biosynthesis protein A	-1,15	-1,11	-1,46	-2,11	-5,78	-3,14	-4,29
_0451	pqqB		pyrroloquinoline quinone biosynthesis protein PqqB	-1,08	-1,11	-1,16	-1,53	-1,58	-1,17	-1,64
_0452	pqqC	1.3.3.11	Pyrroloquinoline-quinone synthase	-1,06	-1,16	-1,10	-1,24	-1,65	-1,17	-1,74
_0453	pqqD		coenzyme PQQ synthesis D	-1,02	-1,06	-1,09	-1,48	-1,49	-1,10	-1,46
_0454	pqqE		pyrroloquinoline quinone biosynthesis protein PqqE	1,03	-1,01	-1,05	-1,34	-1,42	-1,05	-1,42
_0455	0		hypothetical protein	-1,04	-1,08	-1,04	-1,04	-1,13	1,02	-1,17
_0456	moxR		ATPase	-1,06	-1,04	-1,02	-1,26	-1,04	1,15	-1,22
_0457	0		hypothetical protein	-1,02	-1,06	1,05	1,02	-1,21	-1,04	-1,21
_0458	0		hypothetical protein	1,04	1,00	1,06	-1,14	1,00	1,06	-1,09
_0459	0		von Willebrand factor type A	1,03	-1,03	-1,04	1,05	-1,03	1,26	1,08
_0460	0		hypothetical protein	-1,06	-1,06	-1,04	1,15	1,04	1,17	-1,03
_0461	0		hypothetical protein	1,00	-1,06	1,05	1,22	1,03	1,13	1,10
_0462	0		hypothetical protein	-1,07	-1,04	1,03	1,12	-1,01	1,08	-1,32
_0465	luxR2		two component LuxR family transcriptional regulator	-1,01	-1,02	-1,01	-1,16	-1,18	-1,30	-1,47
_0466	0		hypothetical protein	1,04	1,03	-1,06	-1,25	-1,31	-1,37	-1,38
_0467	0	2.7.13.3	histidine kinase	-1,02	1,01	1,05	-1,05	-1,20	-1,08	-1,36
_0468	0		hypothetical protein	-1,05	-1,03	-1,01	-1,03	-1,29	-1,15	-1,34
_0469	0		hypothetical protein	-1,07	-1,05	-1,01	1,02	-1,11	-1,15	-1,31
_0470	soxZ		sulphur oxidation protein SoxZ	-1,03	1,01	-1,03	-1,16	-1,17	-1,17	-1,08
_0471	0		beta-lactamase domain-containing protein	-1,05	-1,05	-1,00	-1,16	1,07	1,23	-1,15
_0472	0		hypothetical protein	-1,06	-1,04	-1,04	-1,11	-1,18	-1,06	-1,50
_0473	0	1.1.1.284	S-(hydroxymethyl) dehydrogenase	-1,13	-1,12	-1,16	-1,25	-1,50	-1,13	-1,65
_0474	0	3.1.2.12	S-formylglutathione hydrolase	-1,06	-1,10	-1,07	-1,00	-1,29	-1,15	-1,49
_0475	cytC		cytochrome c class I	1,02	-1,03	1,00	-1,04	-1,10	1,29	1,13

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_0476	gcd	1.1.5.2, 1.1.99.8	quinoprotein glucose dehydrogenase,alcohol dehydrogenase (acceptor)	-1,03	-1,09	-1,16	-1,17	-2,11	-1,40	-2,06
_0477	cccA		hypothetical protein	-1,01	-1,07	-1,03	-1,18	-1,22	-1,25	-1,44
_0478	0		extracellular solute-binding protein	-1,03	-1,09	-1,10	1,03	-1,33	-1,05	-1,29
_0479	0		hypothetical protein	-1,02	-1,08	1,08	-1,02	-1,04	1,00	-1,02
_0480	0		hypothetical protein	-1,04	-1,04	-1,01	-1,40	-1,27	-1,14	-1,44
_0481	0		hypothetical protein	1,03	-1,04	-1,07	-1,01	-1,16	-1,17	-1,51
_0482	0		hypothetical protein	1,02	-1,03	1,05	1,00	1,21	1,37	1,16
_0483	0		hypothetical protein	-1,10	-1,10	-1,13	-1,15	-1,54	-1,23	-1,83
_0484	0		YVTN beta-propeller repeat-containing protein	-1,02	-1,05	-1,11	-1,19	-1,96	-1,32	-2,33
_0485	0		hypothetical protein	-1,05	-1,06	-1,09	-1,02	-1,92	-1,35	-2,25
_0486	0		hypothetical protein	-1,05	-1,03	-1,06	-1,04	-2,27	-1,78	-2,87
_0487	0		hypothetical protein	-1,01	-1,02	-1,06	-1,12	-1,32	1,01	-1,39
_0488	0		hypothetical protein	-1,01	-1,05	-1,04	-1,01	-1,19	-1,09	-1,16
_0489	0		hypothetical protein	-1,02	-1,07	-1,09	-1,12	1,04	1,20	-1,10
_0490	0		hypothetical protein	-1,05	-1,03	-1,06	1,16	1,27	1,39	1,26
_0491	ssuA1		putative sulfonate/nitrate transport system substrate-binding protein	-1,09	-1,01	-1,21	1,03	1,08	1,15	1,32
_0492	ssuC1		binding-protein-dependent transport systems inner membrane component	-1,02	-1,03	-1,08	1,07	1,10	1,27	1,27
_0493	ssuB1		ABC transporter related	-1,11	-1,02	1,01	-1,02	1,26	1,45	1,08
_0494	nnrS		NnrS family protein	-1,04	1,02	-1,01	-1,04	1,04	1,36	1,15
_0495	0		hypothetical protein	1,00	-1,02	1,10	1,22	1,40	1,48	1,39
_0496	0		4Fe-4S ferredoxin iron-sulfur binding domain-containing protein	-1,02	-1,03	-1,11	-1,06	-1,13	-1,22	-1,19
_0497	0		hypothetical protein	1,00	-1,04	1,05	1,01	1,07	1,14	-1,10
_0498	0		hypothetical protein	-1,03	-1,02	-1,03	-1,03	1,07	1,06	-1,07
_0499	0		hypothetical protein	1,02	1,01	-1,05	-1,38	-1,08	1,05	-1,03
_0500	0		molybdopterin-guanine dinucleotide biosynthesis protein A	-1,02	-1,07	-1,04	-1,04	-1,17	1,06	-1,09
_0501	0		hypothetical protein	-1,01	-1,04	-1,03	1,01	-1,13	1,15	-1,15
_0502	torD		cytoplasmic chaperone TorD family protein	-1,11	-1,11	-1,07	-1,08	-1,44	-1,14	-1,54
_0503	0		twin-arginine translocation pathway signal	-1,07	-1,10	-1,11	-1,37	-2,1	-1,66	-2,1
_0504	fdnG	1.2.1.2	formate dehydrogenase	-1,05	-1,06	-1,12	-1,23	-1,94	-1,51	-2,06
_0505	fdnH	1.2.1.2	formate dehydrogenase	-1,02	-1,07	-1,12	-1,02	-2,26	-1,81	-2,45
_0506	fdnI	1.2.1.2	formate dehydrogenase	-1,04	-1,07	-1,06	-1,13	-2,15	-1,8	-2,42
_0507	0		MRP-like protein (ATP/GTP-binding protein)	-1,00	-1,05	1,00	-1,08	-1,58	-1,28	-1,82
_0508	0		cytochrome c class I	1,00	-1,02	1,07	1,14	-1,19	1,07	-1,15
_0509	0		hypothetical protein	-1,03	1,00	-1,06	1,08	1,04	1,17	1,09
_0510	0		putative beta-lactamase	1,00	-1,02	-1,08	1,05	1,18	1,24	1,01
_0511	0		hypothetical protein	-1,01	-1,05	1,07	1,22	1,13	1,08	1,13
_0512	0		beta-lactamase domain-containing protein	-1,03	1,01	1,02	1,17	1,21	1,31	1,01
_0513	0		LuxR family transcriptional regulator	1,04	1,03	1,15	1,14	1,14	1,14	1,24
_0514	0		response regulator receiver protein	1,04	1,02	1,18	1,15	1,08	1,15	1,16
_0515	0		histidine kinase	1,00	1,03	-1,03	1,31	1,08	1,14	1,20
_0516	0		putative two-component sensor kinase	1,01	-1,05	1,14	1,08	1,06	1,12	1,18
_0517	araF2	3.6.3.17	Monosaccharide-transporting ATPase	-1,05	-1,04	-1,02	1,11	-1,51	-1,48	-1,56
_0518	araH1	3.6.3.17	Monosaccharide-transporting ATPase	-1,07	-1,01	-1,12	1,01	-1,40	-1,36	-1,21
_0519	araG1	3.6.3.17	Monosaccharide-transporting ATPase	-1,09	-1,05	-1,20	-1,24	-1,40	-1,12	-1,32
_0520	mtnK	2.7.1.100	S-methyl-5-thioribose kinase	-1,02	-1,02	-1,02	-1,42	-1,19	-1,17	-1,10
_0521	mtnA	5.3.1.23	S-methyl-5-thioribose-1-phosphate isomerase	-1,01	1,01	-1,05	-1,34	-1,06	-1,04	-1,14
_0522	deoR3		DeoR family transcriptional regulator	1,01	-1,04	-1,04	1,09	-1,13	-1,01	-1,19
_0523	fucA	4.1.2.17	L-Fuculose-phosphate aldolase	1,02	1,01	-1,08	1,01	-1,08	-1,01	-1,06
_0524	0		aldo/keto reductase	-1,00	1,00	-1,05	-1,01	1,01	1,05	-1,01
_0525	0		hypothetical protein	1,00	1,02	-1,04	-1,10	-1,03	1,09	-1,05
_0526	dahL		Dak phosphatase	-1,05	-1,07	-1,01	1,02	-1,54	-1,92	-1,72
_0527	dahK	2.7.1.29	glycerone kinase	-1,06	-1,04	-1,09	-1,18	-1,51	-1,43	-1,47
_0528	araH2	3.6.3.17	Monosaccharide-transporting ATPase	-1,01	-1,00	-1,06	-1,40	-1,41	-1,41	-1,44
_0529	araH3	3.6.3.17	Monosaccharide-transporting ATPase	-1,03	-1,03	-1,11	-1,12	-1,68	-1,71	-1,98
_0530	araG2	3.6.3.17	Monosaccharide-transporting ATPase	-1,02	-1,08	-1,17	-1,15	-1,63	-1,51	-1,78
_0531	araF1	3.6.3.17	Monosaccharide-transporting ATPase	-1,12	-1,12	-1,29	-1,46	-2,38	-2,12	-2,84
_0532	deoR2		DeoR family transcriptional regulator	1,02	-1,01	-1,11	-1,02	-1,07	-1,17	-1,08
_0533	0		xylose isomerase domain-containing protein	1,00	1,04	-1,03	-1,16	-1,21	-1,27	-1,10

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_0534	pdhA2	1.2.4.1	pyruvate dehydrogenase (acetyl-transferring)	1,01	-1,01	-1,09	-1,10	-1,25	-1,42	-1,24
_0535	pdhB1	1.2.4.1	pyruvate dehydrogenase (acetyl-transferring)	-1,00	-1,03	-1,07	1,01	-1,50	-1,52	-1,69
_0536	pdhC2	2.3.1.12	Dihydrolipoyllysine-residue acetyltransferase	-1,01	1,01	-1,06	-1,08	-1,25	-1,15	-1,36
_0537	0		carbohydrate kinase FGGY	-1,09	-1,03	1,00	-1,20	-1,48	-1,40	-1,57
_0538	0		hypothetical protein	1,01	1,00	1,08	-1,02	-1,24	-1,46	-1,22
_0539	0		aldo/keto reductase	-1,06	1,02	1,07	1,14	1,12	1,10	-1,18
_0540	0		NnrU family protein	1,04	1,14	1,38	1,66	1,77	2,05	1,8
_0541	hemN1	1.3.99.22	coproporphyrinogen dehydrogenase	1,84	3,37	6,43	8,53	16,4	10,8	8,11
_0542	0		phosphate transporter	1,07	1,64	3,72	7,51	8,34	3,66	2,81
_0543	0		Na+/H+ antiporter	1,14	1,28	1,88	2,81	3,53	3,36	1,81
_0544	0		hypothetical protein	-1,05	1,12	1,38	1,70	2,03	2,34	1,44
_0545	0		HAD family hydrolase	1,06	-1,04	-1,19	-1,05	-1,41	-1,50	-1,18
_0546	ugpC2	3.6.3.20	glycerol-3-phosphate-transporting ATPase	-1,10	-1,10	-1,26	-1,22	-1,48	-1,45	-1,39
_0547	ugpB4		extracellular solute-binding protein	-1,14	-1,16	-1,34	-1,91	-4,19	-2,82	-4,16
_0548	ugpA1		binding-protein-dependent transport systems inner membrane component	-1,05	-1,08	-1,34	-1,47	-2,41	-2,08	-2,04
_0549	ugpE4		binding-protein-dependent transport systems inner membrane component	-1,01	-1,04	-1,12	1,00	-1,48	-1,46	-1,38
_0550	deoR1		DeoR family transcriptional regulator	-1,07	-1,03	-1,07	1,05	-1,42	-1,50	-1,35
_0551	xylD	1.1.1.9	D-xylulose reductase	1,01	-1,02	-1,13	-1,21	-1,25	-1,27	-1,27
_0552	0		sugar isomerase (SIS)	-1,02	-1,02	-1,05	-1,01	-1,26	-1,25	-1,25
_0553	0		short-chain dehydrogenase/reductase SDR	1,00	1,02	-1,04	-1,00	-1,24	-1,23	-1,12
_0554	rbtD	1.1.1.56	ribitol 2-dehydrogenase	-1,05	-1,00	-1,03	1,13	-1,17	-1,06	-1,20
_0555	araB	2.7.1.16	ribulokinase	-1,03	-1,01	-1,02	1,09	-1,03	-1,07	1,02
_0556	0		GreA/GreB family elongation factor	-1,11	1,01	1,07	-1,10	-1,09	1,01	-1,15
_0557	greA2		GreA/GreB family elongation factor	-1,04	-1,02	-1,06	-1,20	-1,09	-1,14	-1,01
_0558	dadA	1.4.99.1	D-amino-acid dehydrogenase	-1,03	1,01	-1,08	-1,27	-1,19	-1,08	-1,07
_0559	0		hypothetical protein	1,00	-1,01	1,03	-1,04	1,29	2,63	2,46
_0560	fhuC	3.6.3.34	Iron-chelate-transporting ATPase	1,03	1,02	-1,14	-1,16	1,11	3,35	2,83
_0561	fhuD		periplasmic binding protein	-1,02	-1,01	-1,03	-1,33	-1,03	3,03	2,94
_0562	fhuB		transport system permease protein	-1,01	-1,03	-1,04	1,11	1,00	2,9	2,79
_0563	irpA		putative lipoprotein	-1,08	-1,04	-1,04	1,01	2,14	4,62	4,05
_0564	0		hypothetical protein	-1,05	1,00	1,01	-1,08	1,27	2,52	2,41
_0565	0		hypothetical protein	-1,06	1,02	-1,03	-1,15	1,24	3,58	3,42
_0566	0		hypothetical protein	-1,05	-1,01	-1,06	1,16	1,15	2,69	2,43
_0567	0		TonB family protein	-1,17	1,02	-1,01	1,20	1,09	1,18	1,32
_0568	exbD		biopolymer transport protein ExbD/TolR	-1,03	-1,05	1,00	1,15	1,07	1,12	1,62
_0569	exbB		MotA/TolQ/ExbB proton channel	-1,03	-1,06	-1,06	1,05	1,09	1,39	1,99
_0570	fhuA		TonB-dependent receptor	1,06	-1,06	1,07	1,04	1,13	1,31	1,49
_0571	hmuV	3.6.3.-	hemin importer ATP-binding subunit	-1,02	1,01	1,07	1,02	1,13	1,31	1,59
_0572	hmuU		transport system permease protein	1,01	-1,03	-1,12	1,08	1,06	1,56	2,06
_0573	hmuT		periplasmic binding protein	-1,07	-1,04	1,03	-1,07	1,16	1,58	2,78
_0574	hmuS		hemin-degrading family protein	-1,08	-1,00	-1,09	-1,02	1,10	1,53	2,62
_0575	0		hypothetical protein	1,02	1,00	1,05	-1,00	1,04	1,85	2,77
_0576	0		LysR family transcriptional regulator	-1,03	-1,02	1,02	1,09	1,04	1,15	1,03
_0577	aldH2	1.2.1.3	aldehyde dehydrogenase (NAD+)	-1,10	-1,03	1,05	1,02	1,07	1,06	1,20
_0578	rDP		peptidase M19 renal dipeptidase	-1,04	1,00	1,07	-1,09	-1,08	1,03	1,19
_0579	betT		BCCT transporter	-1,04	1,03	1,01	1,03	1,01	1,26	1,13
_0580	0		hypothetical protein	-1,03	-1,00	1,05	1,30	1,09	1,01	1,12
_0581	0		hypothetical protein	1,03	-1,03	1,06	-1,29	-1,02	1,09	1,04
_0582	0		endoribonuclease L-PSP	1,03	-1,03	-1,02	1,03	-1,16	-1,00	1,09
_0583	kdsA	2.5.1.55	3-deoxy-8-phosphooctulonate synthase	1,07	1,06	1,01	-1,04	-1,05	-1,02	1,17
_0584	kpsE		lipopolysaccharide biosynthesis protein	1,03	-1,00	-1,03	1,02	1,13	1,29	1,39
_0585	kpsT	3.6.3.38	Capsular-polysaccharide-transporting ATPase	1,05	1,00	-1,09	-1,05	1,47	1,47	1,59
_0586	kpsM		permease	-1,02	-1,06	-1,00	1,08	1,14	1,51	1,69
_0587	0		ArsR family transcriptional regulator	-1,06	-1,02	-1,01	-1,27	1,13	1,63	1,35
_0588	0		uracil-DNA glycosylase superfamily protein	-1,03	-1,00	-1,03	1,04	1,05	1,00	-1,04
_0589	0		hypothetical protein	1,03	1,03	-1,06	-1,32	-1,13	-1,34	-1,10
_0590	0		D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding	-1,01	1,00	-1,07	-1,08	-1,17	-1,20	-1,04
_0591	mreD1		rod shape-determining protein RodA	1,04	1,01	-1,04	-1,09	1,00	1,03	1,05
_0592	ftsI1	2.4.1.129	peptidoglycan glycosyltransferase	-1,02	-1,03	-1,02	-1,13	-1,07	-1,05	-1,07

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_0593	mreD2		putative rod shape-determining protein MreD	1,01	1,03	1,01	-1,07	1,05	1,07	1,09
_0594	mreC		rod shape-determining protein MreC	1,02	1,01	1,01	1,12	-1,00	-1,10	1,02
_0595	mreB		rod shape-determining protein MreB	1,04	1,04	-1,07	-1,16	-1,36	-1,78	-1,32
_0596	leuA		2-isopropylmalate synthase	1,01	1,01	-1,09	-1,01	-1,23	-1,36	-1,13
_0597	0		hypothetical protein	1,06	1,04	1,14	1,45	2,06	2,41	2,32
_0598	0		short-chain dehydrogenase/reductase SDR	-1,07	1,02	1,00	1,18	1,12	1,15	1,32
_0599	0		deoxyribodipyrimidine photolyase-related protein	-1,03	-1,04	1,14	1,11	1,08	1,12	1,19
_0600	0		MORN repeat-containing protein	-1,08	-1,06	1,02	-1,06	1,03	-1,06	-1,24
_0601	nadE	6.3.5.1	NAD+ synthase (glutamine-hydrolysing)	-1,03	1,01	1,06	-1,06	1,02	-1,20	-1,02
_0602	0		hypothetical protein	-1,02	1,03	1,08	1,11	-1,04	-1,01	1,04
_0603	0		thioesterase superfamily protein	1,00	1,01	1,07	1,03	1,27	1,48	1,29
_0604	0		amidohydrolase 2	-1,02	1,01	1,07	1,26	1,30	1,43	1,24
_0605	dctM5		TRAP dicarboxylate transporter, DctM subunit	-1,04	-1,04	-1,07	1,10	-1,01	-1,07	-1,14
_0606	0		hypothetical protein	-1,07	-1,03	-1,05	1,11	1,10	1,14	-1,04
_0607	dctP5		TRAP dicarboxylate transporter- DctP subunit	-1,01	-1,03	1,07	1,15	1,06	1,04	-1,10
_0608	0		hypothetical protein	-1,01	1,02	1,03	-1,03	1,15	1,26	1,21
_0609	0		transcriptional regulator	-1,07	-1,02	-1,04	1,05	-1,12	-1,15	-1,06
_0610	0		hypothetical protein	-1,02	1,03	-1,04	1,05	-1,02	1,00	-1,03
_0611	0		NIPSNAP family protein	1,04	-1,03	1,01	1,08	1,00	1,04	-1,04
_0612	0		beta-lactamase domain-containing protein	1,07	-1,08	-1,02	1,04	1,02	1,12	1,26
_0613	0		band 7 protein	1,05	1,01	1,02	1,03	1,23	1,20	1,24
_0614	0		hypothetical protein	1,02	-1,00	-1,01	1,03	1,10	1,24	1,27
_0615	pyrF	4.1.1.23	Orotidine-5-phosphate decarboxylase	1,08	1,07	-1,18	-1,16	-1,41	-1,70	-1,26
_0616	0		hypothetical protein	-1,04	-1,03	-1,09	1,06	1,08	1,14	1,23
_0617	clpB		ATPase	-1,00	1,00	1,08	1,32	1,34	2,22	1,74
_0618	0		hypothetical protein	-1,06	-1,00	-1,04	-1,20	-1,49	-1,55	-1,56
_0619	0		hypothetical protein	1,05	-1,02	-1,01	-1,03	1,36	1,73	1,41
_0620	fabG2	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase	-1,05	-1,04	-1,05	-1,30	-1,14	-1,26	-1,14
_0621	0		beta-Ig-H3/fasciclin	1,29	-1,09	-1,05	-1,06	-1,06	1,07	1,56
_0622	0		beta-Ig-H3/fasciclin	1,28	-1,17	1,03	1,01	-1,11	1,06	1,9
_0623	yedY		putative sulfite oxidase subunit YedY	1,05	1,05	-1,05	-1,02	-1,21	-1,27	1,06
_0624	yedZ		ferric reductase domain-containing protein	1,03	-1,01	-1,02	1,04	-1,05	1,07	1,06
_0625	0		hypothetical protein	1,05	-1,02	-1,12	1,09	-1,23	-1,51	-1,30
_0626	0		binding-protein-dependent transport systems inner membrane component	-1,05	-1,08	-1,14	-1,17	-1,36	-1,24	-1,53
_0627	0		ABC transporter related	-1,03	-1,08	-1,14	-1,12	-1,29	-1,29	-1,49
_0628	0		extracellular solute-binding protein	-1,04	-1,02	-1,04	-1,03	-1,75	-1,60	-1,93
_0629	0		DNA binding domain-containing protein	-1,04	-1,02	1,08	1,23	1,08	1,06	-1,04
_0630	glpD	1.1.5.3	glycerol-3-phosphate dehydrogenase	-1,04	-1,03	-1,05	-1,00	-1,08	-1,06	1,16
_0631	glpR		DeoR family transcriptional regulator	-1,02	-1,03	1,04	1,06	-1,00	-1,02	-1,07
_0632	ackA	2.7.2.1	acetate kinase	-1,01	1,07	1,44	1,24	1,40	1,30	1,25
_0633	pta2	2.3.1.8	phosphate acetyltransferase	-1,07	1,14	1,38	1,27	1,62	1,62	1,13
_0634	0		glycosyltransferase, putative	1,13	1,06	-1,05	-1,19	-1,15	-1,13	-1,03
_0635	0		cyclic nucleotide-binding	-1,04	-1,03	-1,06	-1,15	-1,06	1,04	1,06
_0636	0		phospholipase/carboxylesterase	-1,05	1,01	1,08	-1,04	1,11	1,10	1,07
_0637	0		glyoxalase/bleomycin resistance protein/dioxygenase	-1,02	1,01	-1,02	-1,15	-1,06	1,08	1,24
_0638	0		ABC transporter related	-1,01	1,01	1,01	1,06	-1,03	-1,06	-1,10
_0639	0		ABC-2 type transporter	-1,01	-1,02	-1,00	1,15	1,07	-1,05	-1,34
_0640	0		peptidase S49	1,12	1,05	-1,05	1,01	1,31	1,14	1,30
_0641	0		hypothetical protein	1,08	1,06	-1,09	1,08	1,19	1,05	1,09
_0642	0		CaCA family Na(+)/Ca(+) antiporter	-1,03	-1,02	-1,09	-1,11	-1,06	-1,04	-1,05
_0643	0		short chain dehydrogenase	1,01	1,00	-1,06	-1,24	-1,19	-1,10	1,11
_0644	uvrC		excinuclease ABC subunit C	-1,01	-1,00	-1,10	-1,09	-1,08	-1,04	1,01
_0645	0		TRAP transporter solute receptor TAXI family protein	-1,09	-1,11	-1,21	-1,25	-2,63	-2,3	-2,8
_0646	0		TRAP transporter, 4TM/12TM fusion protein	-1,04	-1,04	-1,10	-1,12	-1,65	-1,75	-1,71
_0647	0		hypothetical protein	1,09	-1,02	-1,06	-1,00	-1,02	-1,00	1,16
_0648	recR		recombination protein RecR	-1,03	-1,05	-1,02	1,15	-1,21	-1,09	-1,14
_0649	0		conserved hypothetical protein DUF149	-1,06	-1,02	1,03	1,00	-1,32	-1,16	-1,29
_0650	dnaX	2.7.7.7	DNA-directed DNA polymerase	-1,05	-1,05	-1,02	-1,07	1,11	1,03	-1,04
_0651	0	3.6.1.22	NAD+ diphosphatase	1,02	1,03	-1,05	-1,29	-1,61	-1,88	-1,68
_0652	0		hypothetical protein	1,00	1,00	-1,10	-1,25	-1,56	-1,70	-1,49
_0653	pheA2	4.2.1.51	prephenate dehydratase	1,05	1,10	-1,11	-1,09	-1,25	-1,43	-1,24

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_0654	cycM		cytochrome c class I	1,23	1,35	1,44	1,72	2,01	1,20	2,43
_0655	oppA		extracellular solute-binding protein	-1,01	-1,02	-1,01	-1,22	-1,07	-1,03	-1,04
_0656	oppBC1		binding-protein-dependent transport systems inner membrane component	-1,02	-1,02	1,04	-1,06	-1,06	-1,02	-1,14
_0657	oppBC2		binding-protein-dependent transport systems inner membrane component	-1,01	-1,02	-1,05	-1,08	-1,16	1,02	-1,11
_0658	oppDF		ABC transporter related	-1,02	1,01	1,10	1,17	-1,23	1,12	-1,23
_0659	hemN2	1.3.99.22	coproporphyrinogen dehydrogenase	2	3,52	5,88	9,21	11,6	8,56	5,03
_0660	fixK		Crp/FNR family transcriptional regulator	-1,10	-1,18	-1,57	-1,92	-2,4	-1,56	-1,04
_0661	fixN	1.9.3.1	cytochrome-c oxidase	1,92	4,3	5,48	6,22	8,74	5,7	4,26
_0662	fixO	1.9.3.1	cytochrome-c oxidase	1,69	3,81	5,26	4,6	7,84	5,95	4,53
_0663	fixQ	1.9.3.1	cytochrome-c oxidase	1,43	2,69	3,38	3,79	4,29	3,89	3,39
_0664	fixP	1.9.3.1	cytochrome-c oxidase	1,44	3,28	4,35	4,86	5,75	5,03	4,51
_0665	fixG		cytochrome c oxidase cbb3 type accessory protein FixG	1,67	3,36	5,28	6,39	10,8	7,21	5,38
_0666	fixH		FixH family protein	1,41	2,75	3,94	4,92	6,92	4,94	4,65
_0667	fixI	3.6.3.4	Cu2+-exporting ATPase	1,19	2,03	2,8	3,92	4,27	4,12	3,56
_0668	fixS		cytochrome oxidase maturation protein, cbb3-type	1,07	1,23	1,54	1,94	2,06	2,42	1,91
_0669	dacC2	3.4.16.4	serine-type D-Ala-D-Ala carboxypeptidase	-1,04	-1,03	1,01	1,16	1,15	1,13	1,17
_0670	0		hydrolase	-1,01	1,05	1,08	1,10	1,05	-1,10	1,04
_0671	rsmC		methyltransferase small	1,07	-1,02	-1,00	1,04	1,03	1,09	1,18
_0672	0		short-chain dehydrogenase/reductase SDR	1,03	1,02	-1,02	-1,35	-1,33	-1,30	-1,19
_0673	0		hypothetical protein	1,09	1,01	1,05	1,06	1,38	1,79	1,43
_0674	hemF	1.3.3.3	coproporphyrinogen oxidase	-1,00	-1,02	-1,10	-1,18	-1,19	-1,34	-1,15
_0675	ggt2	2.3.2.2	Gamma-glutamyltransferase	-1,04	-1,05	-1,06	-1,03	-1,16	-1,12	-1,24
_0676	0		beta-lactamase	1,04	-1,01	-1,06	1,03	1,15	1,19	1,28
_0677	0		hypothetical protein	1,00	-1,01	1,01	1,02	1,15	1,14	1,04
_0678	0		glycosyl transferase family protein	-1,00	-1,02	-1,03	-1,10	1,19	1,22	1,10
_0679	0		histidine triad (HIT) protein	-1,04	1,01	-1,04	-1,03	-1,03	1,19	1,09
_0680	purK	4.1.1.21	phosphoribosyl aminoimidazole carboxylase	-1,01	-1,01	-1,02	-1,08	-1,35	-1,47	-1,27
_0681	purE	4.1.1.21	phosphoribosyl aminoimidazole carboxylase	1,02	1,03	-1,04	-1,07	-1,41	-1,94	-1,46
_0682	0		hypothetical protein	1,00	1,03	1,06	1,05	1,17	1,09	1,08
_0683	ibpAB		heat shock protein Hsp20	-1,03	-1,03	-1,00	-1,11	-1,00	1,49	1,25
_0684	0		hypothetical protein	-1,03	1,01	-1,05	1,01	1,15	1,76	1,39
_0685	apbE2		ApbE family lipoprotein	1,06	1,02	-1,01	-1,01	1,03	1,21	1,12
_0686	nosR1		regulatory protein, putative	-1,04	-1,01	-1,01	-1,03	-1,11	1,00	-1,00
_0687	0		binding-protein-dependent transport systems inner membrane component	-1,06	-1,08	1,03	1,01	1,01	1,13	-1,04
_0688	0	1.3.99.1	succinate dehydrogenase	-1,01	1,00	1,03	-1,06	-1,31	1,16	-1,05
_0689	prpB	4.1.3.30	Methylisocitrate lyase	1,01	1,03	-1,01	1,17	-1,00	-1,03	1,06
_0690	entB	3.3.2.1	isochorismatase	1,04	-1,04	-1,09	-1,01	-1,03	1,05	1,20
_0691	hyuA	3.5.2.9	5-oxoprolinase (ATP-hydrolysing)	-1,04	-1,01	-1,01	-1,19	-1,11	-1,03	1,09
_0692	hyuB	3.5.2.9	5-oxoprolinase (ATP-hydrolysing)	1,01	-1,02	-1,07	1,05	1,02	-1,02	1,02
_0693	pptA		4-oxalocrotonate tautomerase	-1,06	-1,01	-1,09	1,00	-1,05	1,09	1,08
_0694	0		GntR family transcriptional regulator	-1,03	-1,04	-1,02	-1,08	1,03	1,07	1,05
_0695	leuC	4.2.1.33	3-isopropylmalate dehydratase	-1,01	1,02	-1,06	-1,20	1,04	-1,08	-1,09
_0696	leuD	4.2.1.33	3-isopropylmalate dehydratase	-1,02	-1,06	1,04	1,04	1,09	1,17	1,08
_0697	dctP1		TRAP dicarboxylate transporter- DctP subunit	-1,01	-1,05	-1,03	-1,05	-1,26	-1,02	-1,26
_0698	dctQ3		tripartite ATP-independent periplasmic transporter DctQ	-1,04	-1,02	-1,05	1,11	-1,25	-1,13	-1,23
_0699	dctM1		TRAP C4-dicarboxylate transport system permease DctM subunit	-1,03	-1,08	-1,05	1,03	-1,11	1,04	-1,35
_0700	0		AMP-dependent synthetase and ligase	-1,04	1,00	1,00	-1,20	1,03	1,16	1,06
_0701	0		methyltransferase domain protein	-1,02	-1,01	-1,03	-1,34	1,05	1,11	1,18
_0702	0		WbqC-like family protein	-1,09	-1,09	-1,09	-1,29	-1,02	1,32	1,18
_0703	0		hypothetical protein	1,04	-1,01	-1,04	1,18	1,26	1,24	1,26
_0704	0		DegT/DnrJ/EryC1/StrS aminotransferase	-1,03	-1,05	1,02	-1,09	1,27	1,26	1,10
_0705	0		hypothetical protein	-1,04	-1,07	-1,03	-1,08	1,05	1,41	1,12
_0707	0		hypothetical protein	1,05	-1,02	1,03	-1,08	1,01	1,13	1,05
_0708	0		hypothetical protein	1,06	-1,03	1,09	1,11	-1,07	1,12	1,03
_0709	atoDA	2.8.3.8	acetate CoA-transferase	-1,05	-1,02	1,07	1,09	1,05	1,01	1,09
_0710	0		hypothetical protein	-1,01	-1,04	-1,01	1,19	1,06	1,21	1,09
_0711	0		chromosome replication initiation inhibitor protein	-1,05	-1,01	1,02	1,02	1,04	1,28	1,19

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_0712	lysE		lysine exporter protein LysE/YggA	-1,04	-1,01	-1,09	1,02	-1,09	-1,05	-1,12
_0713	0		Poly(3-hydroxybutyrate) depolymerase-like protein	1,09	1,04	1,10	1,10	-1,05	-1,04	1,24
_0714	0		hypothetical protein	1,04	1,03	1,03	1,07	-1,09	-1,29	-1,10
_0715	0		hypothetical protein	2,1	3,9	6,9	13,2	20,3	12,3	8,22
_0716	0		XRE family transcriptional regulator	-1,03	-1,07	-1,06	-1,12	1,05	-1,05	1,12
_0717	0		Bcr/CflA subfamily drug resistance transporter	1,06	1,01	-1,00	1,14	1,04	-1,13	1,07
_0718	pccB	6.4.1.3	propionyl-CoA carboxylase	-1,20	1,07	1,11	-1,04	1,12	-1,38	-1,13
_0719	0		hypothetical protein	-1,03	-1,01	1,00	1,06	1,03	-1,05	1,13
_0720	0		endoribonuclease L-PSP	1,02	1,03	1,15	1,26	1,29	-1,17	1,21
_0721	0		hypothetical protein	-1,04	-1,02	1,02	1,16	1,03	-1,08	1,11
_0722	0		hypothetical protein	1,00	1,03	1,05	1,15	1,06	-1,06	1,14
_0723	pccA	6.4.1.3	propionyl-CoA carboxylase	1,00	1,04	1,23	1,19	1,24	-1,12	1,09
_0724	0		hypothetical protein	-1,03	-1,01	1,09	1,12	1,16	1,46	1,28
_0725	0		hypothetical protein	1,01	1,02	1,15	1,12	1,16	1,27	1,33
_0726	bhbA	5.4.99.2	Methylmalonyl-CoA mutase	-1,00	1,00	1,06	-1,03	1,29	1,28	1,31
_0727	0		LysR family transcriptional regulator	-1,05	-1,02	-1,11	-1,09	-1,32	-1,11	-1,04
_0728	mnhA	1.6.99.5	NADH dehydrogenase (quinone)	1,13	-1,02	-1,05	-1,01	-1,13	-1,15	1,08
_0729	mnhB		Na+/H+ antiporter MnhB subunit-related protein	1,02	-1,08	-1,07	-1,12	-1,08	-1,13	1,13
_0730	mnhC		putative monovalent cation/H+ antiporter subunit C	1,08	-1,00	-1,07	1,14	-1,09	-1,21	1,20
_0731	mnhD	1.6.99.5	NADH dehydrogenase (quinone)	1,04	-1,03	-1,01	1,11	-1,11	-1,15	1,10
_0732	mnhE		cation antiporter	1,05	-1,03	-1,03	1,02	-1,06	-1,02	1,13
_0733	mnhF		multiple resistance and pH regulation protein F	-1,03	-1,02	-1,04	1,13	-1,16	-1,13	-1,13
_0734	mnhG		monovalent cation/proton antiporter, MnhG/PhaG subunit	1,03	-1,02	1,08	1,15	-1,04	-1,08	1,09
_0735	0		hypothetical protein	1,03	-1,03	-1,01	-1,06	1,07	1,03	1,23
_0736	0		GCN5-related N-acetyltransferase	-1,01	-1,00	-1,01	1,12	1,06	-1,04	1,16
_0737	0		heat shock protein DnaJ domain-containing protein	-1,04	1,11	1,29	1,39	1,70	1,87	1,40
_0738	0		hypothetical protein	-1,02	1,00	1,14	1,07	1,32	1,42	1,22
_0739	ppx	3.6.1.40, 3.6.1.11	guanosine-5-triphosphate,3-diphosphate phosphatase,exopolyphosphatase	-1,06	-1,02	-1,02	-1,06	-1,33	1,06	-1,28
_0740	ppk1	2.7.4.1	polyphosphate kinase	-1,04	-1,02	1,10	-1,21	-1,44	-1,22	-1,30
_0741	0		chromosomal replication initiator, DnaA	1,01	1,01	1,04	-1,02	-1,01	-1,01	-1,15
_0742	0		hypothetical protein	1,03	1,00	-1,08	-1,00	-1,20	-1,51	-1,24
_0743	mcsS		MscS mechanosensitive ion channel	-1,03	1,03	1,08	1,04	1,15	1,26	1,16
_0744	proS	6.1.1.15	Proline-tRNA ligase	1,04	1,05	1,01	-1,00	-1,11	-1,72	-1,13
_0745	0		redoxin domain-containing protein	1,01	1,02	1,07	1,04	-1,16	-1,38	-1,32
_0746	aqpZ		MIP family channel protein	-1,07	-1,12	-1,13	-1,12	-1,35	-1,13	-1,52
_0747	lolC		LolC/E family lipoprotein releasing system, transmembrane protein	-1,01	1,06	-1,04	-1,30	-1,22	-1,71	-1,34
_0748	lolD	3.6.3.-	ABC transporter-like protein	1,04	1,03	-1,01	1,03	-1,39	-1,67	-1,17
_0749	0	5.99.1.3	DNA topoisomerase (ATP-hydrolysing)	-1,05	-1,01	-1,00	-1,08	1,12	1,02	1,04
_0750	0		hypothetical protein	-1,07	-1,09	-1,05	-1,12	-1,42	-1,34	-1,13
_0751	ppk2		hypothetical protein	1,48	2,56	4,77	6,93	10,4	7,08	4,79
_0752	0		hypothetical protein	-1,02	-1,02	-1,03	-1,01	1,18	1,14	1,10
_0753	nicO		high-affinity nickel-transporter	-1,03	1,00	-1,02	-1,15	-1,03	1,01	1,03
_0754	0		methyltransferase type 11	1,02	-1,02	-1,01	-1,03	-1,23	-1,09	1,02
_0755	0		MATE efflux family protein	-1,02	1,04	-1,07	1,14	-1,36	-1,63	-1,01
_0756	0		hypothetical protein	-1,01	1,00	1,03	1,08	1,11	1,17	1,11
_0757	0		selenium-binding protein	-1,03	-1,02	-1,03	1,16	1,16	1,10	1,08
_0758	0		MarR family transcriptional regulator	-1,02	-1,03	1,03	-1,12	1,01	1,05	-1,01
_0759	0		hypothetical protein	-1,02	-1,03	-1,08	-1,00	-1,06	1,01	1,02
_0760	0		hypothetical protein	1,08	-1,02	-1,07	-1,03	-1,13	-1,06	1,18
_0761	0		hypothetical protein	1,04	1,02	1,00	-1,02	-1,20	-1,27	1,08
_0762	aspC	2.6.1.1	aspartate transaminase	1,01	1,05	1,02	-1,01	-1,26	-1,67	-1,22
_0763	0		XRE family transcriptional regulator	-1,01	1,06	1,14	1,33	1,32	1,11	1,23
_0764	0		hypothetical protein	1,03	1,06	1,08	1,20	1,44	1,23	1,37
_0765	0		MarR family transcriptional regulator	1,01	-1,01	-1,01	1,03	1,24	1,26	1,43
_0766	0		hypothetical protein	1,04	-1,06	1,02	1,13	1,08	1,00	1,24
_0767	0	4.4.1.5	lactoylglutathione lyase	1,05	-1,05	1,01	1,22	1,13	1,03	1,30
_0768	thyX	2.1.1.148	thymidylate synthase (FAD)	-1,06	-1,03	1,09	1,06	1,15	-1,00	-1,37
_0769	csp1		cold-shock DNA-binding domain-containing protein	1,15	-1,06	1,00	1,01	1,01	1,17	1,15
_0770	0		arsenate reductase and related	-1,06	-1,01	-1,01	-1,13	-1,12	-1,11	-1,58

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_0771	0		DoxX family protein	-1,00	-1,05	-1,11	-1,09	-1,23	-1,23	-1,18
_0772	0		hypothetical protein	1,05	-1,03	-1,07	1,01	-1,16	-1,13	-1,10
_0773	0		hypothetical protein	-1,01	-1,02	-1,03	-1,04	-1,22	-1,17	-1,08
_0774	0		hypothetical protein	-1,00	-1,04	-1,10	-1,11	-1,74	-1,56	-1,78
_0775	ttuC	1.1.1.93, 1.1.1.83, 4.1.1.73	tartrate dehydrogenase,D-malate dehydrogenase (decarboxylating),tartrate decarboxylase	-1,05	-1,06	1,01	-1,07	1,20	1,17	-1,05
_0776	0		cobalamin B12-binding domain-containing protein	1,07	-1,03	1,15	-1,02	1,03	1,07	1,34
_0777	thrS	6.1.1.3	Threonine-tRNA ligase	1,17	1,15	1,00	1,01	-1,06	-1,70	1,09
_0778	0		hypothetical protein	1,01	-1,05	-1,17	-1,13	-1,25	-1,59	-1,13
_0779	0		MarR family transcriptional regulator	-1,02	1,00	-1,01	-1,07	-1,14	-1,21	-1,34
_0780	0	3.1.1.5	lysophospholipase	-1,08	-1,07	-1,04	-1,25	-1,37	-1,39	-1,51
_0781	0		sterol-binding domain-containing protein	-1,06	-1,04	-1,06	-1,14	-1,33	-1,28	-1,51
_0782	0		TPR repeat-containing protein	-1,03	-1,05	1,01	1,10	1,13	1,36	1,05
_0783	0		helicase domain-containing protein	1,01	1,01	-1,04	1,02	-1,01	1,01	-1,06
_0784	0		RNA-binding S4	1,01	-1,01	-1,04	1,05	1,07	1,01	1,11
_0785	fdxA		4Fe-4S ferredoxin iron-sulfur binding domain-containing protein	1,05	1,06	-1,11	-1,05	1,06	-1,19	1,17
_0786	0		CarD family transcriptional regulator	1,04	-1,03	-1,28	-1,47	-1,52	-1,44	1,16
_0787	cobS1	2.7.8.26	adenosyl cobinamide-GDP ribazoletransferase	1,07	1,00	-1,03	-1,08	-1,01	-1,19	1,11
_0788	cobT	2.4.2.21	Nicotinate-nucleotide-dimethyl benzimidazole phosphoribosyl transferase	-1,02	1,04	1,18	1,20	1,03	1,03	1,09
_0789	kefC		potassium efflux system protein	-1,05	1,08	1,28	1,27	1,57	1,60	1,33
_0790	0		hypothetical protein	1,02	-1,02	1,05	1,04	-1,04	-1,06	-1,14
_0791	0		hypothetical protein	-1,03	1,03	1,07	1,22	1,04	1,08	-1,02
_0792	0		hypothetical protein	-1,09	-1,04	1,05	1,00	-1,19	-1,06	-1,54
_0793	metB2	2.5.1.49	O-acetylhomoserine aminocarboxypropyl transferase	-1,03	1,02	-1,08	-1,18	-1,75	-2,13	-1,75
_0794	hisB	4.2.1.19	Imidazoleglycerol-phosphate dehydratase	1,07	1,06	-1,04	-1,13	-1,34	-1,82	-1,15
_0795	hisH	2.4.2.-	imidazole glycerol phosphate synthase subunitHisH"	1,12	1,09	-1,12	-1,48	-1,43	-1,81	-1,13
_0796	argF	2.1.3.3	ornithine carbamoyltransferase	1,00	-1,02	-1,14	-1,26	-1,51	-1,81	-1,66
_0797	0		GCN5-related N-acetyltransferase	-1,00	-1,03	-1,07	-1,18	-1,24	-1,46	-1,42
_0798	argD	2.6.1.11	acetylornithine transaminase	1,03	1,01	-1,05	-1,08	1,00	-1,26	-1,32
_0799	0		putative DNA-binding protein	-1,07	-1,01	1,02	-1,03	1,01	1,11	1,16
_0800	0		IclR family transcriptional regulator	-1,00	-1,01	-1,03	-1,23	-1,44	-1,21	-1,38
_0801	0		TRAP C4-dicarboxylate transport system permease DctM subunit	-1,01	-1,06	-1,17	-1,20	-1,66	-1,57	-1,53
_0802	0		tripartite ATP-independent periplasmic transporter DctQ	-1,06	-1,08	-1,24	-1,41	-2,2	-1,52	-2,01
_0803	0		TRAP dicarboxylate transporter- DctP subunit	-1,17	-1,17	-1,29	-1,99	-3,27	-1,99	-3,14
_0804	0	1.1.99.1	choline dehydrogenase	-1,06	-1,06	-1,20	-1,29	-1,45	-1,36	-1,30
_0805	0	2.3.3.15	sulfoacetaldehyde acetyltransferase	-1,00	-1,01	1,01	-1,03	-1,31	-1,05	-1,10
_0806	tauZ		hypothetical protein	1,08	-1,00	-1,09	-1,01	-1,25	1,03	1,12
_0807	0		hypothetical protein	-1,06	-1,04	1,06	-1,02	-1,04	-1,01	-1,02
_0808	mipA		MltA-interacting MipA family protein	-1,04	-1,05	-1,08	1,01	1,05	1,05	-1,09
_0809	lepA	3.6.5.n1	GTP-binding protein LepA	1,11	1,08	-1,16	-1,17	-1,23	-1,49	-1,18
_0810	0		hypothetical protein	-1,04	-1,05	-1,00	1,10	1,17	1,38	1,13
_0811	0		hypothetical protein	1,06	-1,03	-1,03	1,08	1,19	1,36	1,26
_0812	0		TraR/DksA family transcriptional regulator	1,53	2,1	4,27	8,39	10,2	5,83	3,18
_0813	0		hypothetical protein	1,24	1,45	2,46	3,74	4,36	3,15	1,89
_0814	0		hypothetical protein	2,1	4,54	7,65	10,5	17,6	13,9	10,7
_0815	0	4.4.1.5	lactoylglutathione lyase	1,02	1,06	1,38	1,62	1,66	1,48	1,24
_0816	0		hypothetical protein	1,26	1,81	3,47	5,92	6,79	4,4	2,81
_0817	0		hypothetical protein	1,17	1,35	1,72	2,41	4,05	2,96	2,91
_0818	0		hypothetical protein	1,24	1,96	3,5	5,61	7,8	5,33	5,84
_0819	0		hypothetical protein	-1,00	-1,01	1,21	1,75	1,82	2,11	1,43
_0820	0		alpha/beta hydrolase fold	1,06	1,12	1,18	1,16	1,02	-1,24	1,03
_0821	glyA	2.1.2.1	glycine hydroxymethyl transferase	1,13	1,09	1,03	-1,18	-1,12	-1,75	-1,24
_0822	ppnK	2.7.1.23	NAD+ kinase	-1,10	1,00	-1,00	-1,09	-1,15	-1,00	-1,34
_0823	0		two component, sigma54 specific, Fis family transcriptional regulator	1,01	-1,03	-1,04	-1,27	-1,25	1,07	-1,08
_0824	0	2.7.13.3	histidine kinase	-1,01	-1,03	-1,06	-1,21	1,14	1,23	-1,03
_0825	0	6.2.1.17, 6.2.1.1	Propionate-CoA ligase,acetate-CoA ligase	1,13	1,22	1,43	1,60	3,92	3,01	2,39

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_0826	0	1.1.1.39	malate dehydrogenase (decarboxylating)	1,12	1,14	1,01	-1,08	1,02	-1,23	-1,16
_0827	cdd	3.5.4.5	cytidine deaminase	-1,04	-1,04	1,02	-1,10	-1,01	1,01	-1,22
_0828	deoA	2.4.2.4	thymidine phosphorylase	-1,01	-1,07	-1,01	-1,13	-1,06	-1,04	-1,21
_0829	deoB	5.4.2.7	phosphopentomutase	-1,02	-1,05	-1,01	-1,04	-1,20	-1,10	-1,13
_0830	add	3.5.4.4	adenosine deaminase	-1,04	-1,03	1,02	-1,10	-1,13	-1,12	-1,20
_0831	upp	2.4.2.9	uracil phosphoribosyl transferase	-1,00	-1,00	1,01	-1,00	-1,15	-1,18	-1,19
_0832	0		hypothetical protein	-1,03	-1,01	1,02	1,07	1,11	1,13	1,01
_0833	0		AMP-dependent synthetase and ligase	-1,15	-1,11	-1,15	-1,14	-1,22	-1,07	-1,40
_0834	0		hypothetical protein	-1,04	1,03	-1,04	-1,07	-1,40	-1,82	-1,46
_0835	fadJ	4.2.1.17, 1.1.1.35, 5.1.2.3	enoyl-CoA hydratase,3-hydroxyacyl-CoA dehydrogenase,3-Hydroxybutyryl-CoA epimerase	1,10	-1,03	1,04	1,20	1,19	1,19	1,13
_0836	fadA	2.3.1.16	acetyl-CoA C-acyltransferase	1,14	-1,04	1,06	1,28	1,25	1,14	1,19
_0837	0		glutathione S-transferase domain-containing protein	1,03	-1,05	1,06	1,23	1,12	1,06	1,14
_0838	0		acyl-CoA dehydrogenase domain-containing protein	1,07	-1,01	1,12	1,21	1,07	1,01	1,16
_0839	0	1.3.99.3	acyl-CoA dehydrogenase	-1,9	-2,1	-1,73	-1,62	-1,99	-1,13	-1,34
_0840	0		MerR family transcriptional regulator	-1,65	-1,55	-1,43	-1,92	-3,83	-1,52	-1,54
_0841	0		hypothetical protein	-1,08	-1,09	-1,07	-1,23	-1,31	-1,33	-1,08
_0842	0		MerR family transcriptional regulator	-1,08	-1,04	-1,04	-1,08	-1,09	-1,20	-1,37
_0843	0		thioesterase superfamily protein	-1,14	-1,06	-1,02	1,20	-1,06	-1,05	-1,23
_0844	0		thioesterase superfamily protein	-1,04	-1,08	-1,02	-1,08	-1,00	-1,08	-1,18
_0845	0		MATE efflux family protein	-1,04	-1,05	-1,03	-1,31	-1,15	-1,05	-1,30
_0846	arsC	1.20.4.1	arsenate reductase (glutaredoxin)	1,05	1,02	-1,04	-1,31	-1,15	-1,10	-1,12
_0847	pyrD2	1.3.5.2	dihydroorotate dehydrogenase (quinone)	1,00	-1,01	-1,08	-1,10	-1,21	-1,36	-1,38
_0848	0		hypothetical protein	1,05	1,01	-1,04	-1,17	-1,20	-1,33	-1,14
_0849	0	3.1.3.5	5-nucleotidase	-1,11	-1,07	-1,10	-1,61	-2,44	-2,28	-3
_0850	deaD		DEAD/DEAH box helicase domain-containing protein	1,10	1,10	-1,14	-1,08	1,01	-1,49	-1,05
_0851	0		hypothetical protein	1,00	-1,03	1,01	1,02	1,12	1,22	1,15
_0852	msbA		lipid ABC transporter ATPase/inner membrane protein	1,04	1,10	1,15	1,26	1,47	1,16	1,46
_0853	fadD2	6.2.1.3	Long-chain-fatty-acid-CoA ligase	-1,32	-1,27	-1,30	-1,47	-1,47	-1,30	-1,52
_0854	0		hypothetical protein	-1,03	-1,06	1,00	-1,04	-1,04	1,53	1,07
_0855	0		transglutaminase domain-containing protein	1,02	-1,02	-1,01	-1,02	1,00	1,10	1,08
_0856	0		hypothetical protein	-1,04	-1,01	-1,00	-1,04	1,05	1,12	-1,05
_0857	0		transglutaminase domain-containing protein	-1,03	1,01	1,01	1,02	-1,03	-1,39	-1,07
_0858	0		ABC transporter related	-1,00	-1,02	-1,06	-1,14	-1,29	-1,42	-1,32
_0859	0		ABC transporter related	-1,01	-1,02	-1,09	-1,22	-1,72	-1,87	-1,78
_0860	0		inner-membrane translocator	-1,05	-1,04	-1,00	1,00	-1,15	-1,07	-1,02
_0861	0		inner-membrane translocator	1,05	-1,01	-1,05	-1,28	-1,76	-2,14	-2,02
_0862	0		extracellular ligand-binding receptor	-1,05	-1,05	-1,05	-1,08	-1,67	-1,82	-1,9
_0863	0		AsnC family transcriptional regulator	-1,08	-1,01	-1,02	-1,28	-1,23	-1,31	-1,38
_0864	0		2Fe-2S iron-sulfur cluster binding domain-containing protein	-1,03	-1,04	-1,09	-1,03	-1,27	-1,22	-1,31
_0865	0		aldehyde oxidase and xanthine dehydrogenase molybdopterin binding	-1,04	-1,04	-1,06	-1,12	-1,30	-1,30	-1,29
_0866	0		alpha/beta hydrolase fold	-1,05	-1,01	-1,02	-1,11	1,08	1,29	-1,09
_0867	0		amidohydrolase 2	-1,07	-1,05	-1,05	-1,03	-1,01	1,11	1,02
_0868	0		putative peptidase	-1,05	-1,09	1,11	-1,11	-1,07	1,14	1,05
_0869	0		hypothetical protein	-1,03	-1,01	-1,04	1,16	1,11	1,29	1,04
_0870	0		SARP family transcriptional regulator	1,03	1,04	1,01	1,04	1,15	1,21	1,03
_0871	0		hypothetical protein	1,03	-1,02	-1,00	1,00	1,06	1,07	1,13
_0872	0		extracellular solute-binding protein	-1,10	-1,10	-1,10	-1,32	-2,82	-2,5	-2,95
_0873	0		hypothetical protein	-1,06	-1,06	-1,06	-1,25	1,10	1,28	1,24
_0874	0		extracellular solute-binding protein	-1,01	-1,02	1,00	-1,11	-1,06	-1,05	1,14
_0877	0		4-phytase	1,04	-1,02	1,05	1,08	1,03	1,08	1,18
_0878	0		hypothetical protein	-1,03	-1,06	-1,20	-1,71	-1,55	-1,33	-1,9
_0879	0		membrane protein-like protein	-1,03	-1,04	1,04	1,05	1,09	1,39	-1,32
_0880	0		hydratase/decarboxylase	-1,09	-1,08	1,11	-1,02	-1,09	1,07	-1,35
_0881	0		binding-protein-dependent transport systems inner membrane component	-1,05	-1,04	-1,05	-1,04	-1,11	-1,02	-1,45
_0882	0		binding-protein-dependent transport systems inner membrane component	-1,03	-1,04	-1,05	1,05	-1,13	-1,27	-1,33
_0883	0		hypothetical protein	-1,05	-1,04	1,04	1,20	1,10	1,09	1,32
_0884	0		oligopeptide/dipeptide ABC transporter, ATPase	-1,00	-1,00	1,02	1,05	-1,03	-1,12	-1,16

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
			subunit							
_0885	0		oligopeptide/dipeptide ABC transporter, ATPase subunit	1,02	-1,03	1,07	-1,04	-1,30	-1,32	-1,53
_0886	0		IclR family transcriptional regulator	-1,00	1,02	1,11	1,04	1,30	1,21	1,25
_0887	sgaA2	2.6.1.45	serine-glyoxylate transaminase	-1,02	1,03	-1,11	-1,05	1,40	-1,13	1,42
_0888	0	4.3.1.19	threonine ammonia-lyase	1,05	-1,05	-1,06	-1,02	-1,06	1,11	1,10
_0889	0		alanine racemase domain-containing protein	-1,02	-1,01	-1,02	-1,03	-1,17	-1,09	-1,01
_0890	0	4.3.1.12	ornithine cyclodeaminase	1,01	-1,01	-1,06	1,07	-1,20	-1,09	-1,05
_0891	cysK	2.5.1.47	cysteine synthase	-1,02	-1,02	1,12	-1,15	-1,03	1,05	-1,01
_0892	0		transposase IS4 family protein	-1,13	-1,02	-1,01	1,03	-1,12	-1,11	-1,39
_0893	0		peptidoglycan binding domain-containing protein	1,03	1,00	-1,04	-1,05	1,19	1,23	1,16
_0894	0		peptidoglycan binding domain-containing protein	-1,10	-1,07	-1,01	-1,06	-1,10	1,03	-1,17
_0895	0		peptidase S1 and S6 chymotrypsin/Hap	-1,03	-1,03	-1,01	-1,04	-1,20	1,08	-1,20
_0896	0		hypothetical protein	1,01	-1,02	-1,00	-1,18	-1,25	-1,04	-1,25
_0897	0		virulence protein SrfB	-1,04	-1,02	1,05	-1,01	-1,21	-1,19	-1,46
_0898	0		hypothetical protein	1,00	-1,00	1,10	1,13	-1,11	1,01	-1,20
_0899	0		hypothetical protein	1,04	1,02	1,14	-1,13	1,08	1,04	-1,06
_0900	0		hypothetical protein	-1,01	-1,03	1,02	-1,29	1,05	1,12	-1,19
_0901	0		ABC transporter related	-1,01	-1,03	1,04	1,11	1,09	1,34	-1,06
_0902	0		hypothetical protein	-1,02	-1,02	1,07	-1,00	1,01	1,37	-1,16
_0903	0		hypothetical protein	-1,01	-1,05	1,04	1,20	1,14	1,41	-1,23
_0904	0		hypothetical protein	-1,05	-1,04	-1,06	1,05	-1,11	1,19	-1,24
_0905	0		hypothetical protein	1,01	-1,02	1,04	1,05	1,09	1,10	1,10
_0906	0		binding-protein-dependent transport systems inner membrane component	-1,01	-1,00	-1,02	-1,11	-1,43	-1,27	-1,09
_0907	0		ABC transporter related	1,01	-1,01	-1,05	-1,04	-1,69	-1,60	-1,29
_0908	0		TenA family transcription regulator	-1,00	-1,01	-1,09	1,01	-1,94	-2,02	-1,44
_0909	0		NMT1/THI5-like domain-containing protein	-1,05	-1,01	-1,02	-1,07	-2,02	-2,2	-1,48
_0910	thiF		UBA/THIF-type NAD/FAD binding protein	-1,01	-1,02	1,03	1,17	-1,64	-1,78	-1,33
_0911	thiE	2.5.1.3	thiamine-phosphate diphosphorylase	-1,00	-1,02	-1,10	-1,07	-1,92	-1,92	-1,31
_0912	thiG	2.8.1.10	thiazole synthase	-1,00	-1,00	-1,04	-1,27	-2,02	-2,03	-1,37
_0913	0		thiamine biosynthesis protein ThiS	-1,00	1,01	-1,17	-1,46	-1,58	-1,56	-1,24
_0914	thiO	1.4.3.19	glycine oxidase	1,02	1,02	-1,17	-1,34	-1,42	-1,54	-1,16
_0915	thiD	2.7.4.7	phosphomethyl pyrimidine kinase	1,06	1,05	-1,11	-1,34	-1,13	-1,64	-1,10
_0916	0		RND family efflux transporter MFP subunit	1,03	1,00	-1,10	-1,07	-1,09	-1,04	-1,11
_0917	0		acriflavin resistance protein	1,01	-1,05	1,09	-1,11	-1,06	-1,17	1,02
_0918	0		auxin efflux carrier	1,05	-1,01	-1,06	-1,19	-1,30	-1,19	-1,03
_0919	0		beta-lactamase domain-containing protein	1,07	1,03	-1,06	-1,14	-1,18	-1,35	1,09
_0920	0	3.1.21.-	hydrolase	1,00	1,02	-1,05	1,11	-1,09	-1,16	-1,04
_0921	0	2.7.7.7	DNA-directed DNA polymerase	-1,03	-1,03	-1,00	1,00	-1,02	-1,02	1,01
_0922	tmk	2.7.4.9	dTMP kinase	-1,03	-1,03	1,02	-1,07	-1,02	-1,03	-1,06
_0923	dacC1	3.4.16.4	serine-type D-Ala-D-Ala carboxypeptidase	-1,03	1,01	1,05	-1,03	1,05	-1,08	-1,04
_0924	0		sporulation domain-containing protein	-1,02	1,00	-1,04	1,01	-1,07	-1,06	-1,16
_0925	0		hypothetical protein	-1,03	1,02	1,07	1,09	-1,00	1,10	1,09
_0926	0		integrase catalytic region	-1,00	-1,01	-1,08	1,01	1,04	1,21	1,13
_0927	0		transposase IS3/IS911 family protein	-1,02	-1,00	-1,05	-1,07	1,01	1,17	1,01
_0928	0		hypothetical protein	1,02	-1,03	-1,06	1,00	-1,12	-1,03	-1,04
_0929	0		UspA domain-containing protein	-1,06	1,00	1,08	1,08	1,07	1,45	1,14
_0930	0		sodium/hydrogen exchanger	-1,06	-1,07	-1,04	-1,11	1,08	1,50	1,19
_0931	adhA	1.1.1.1	alcohol dehydrogenase	-1,05	-1,05	1,02	1,28	1,12	1,68	1,06
_0932	0		ATPase, P-type (transporting), HAD superfamily, subfamily IC	1,00	1,01	-1,01	1,13	1,26	1,59	1,27
_0933	0		DNA binding domain-containing protein	-1,13	-1,05	-1,00	1,15	1,24	1,29	-1,02
_0934	0		transposase IS3/IS911 family protein	1,04	-1,02	1,01	1,07	1,20	1,26	1,26
_0935	0		hypothetical protein	1,01	1,03	1,01	1,33	1,14	1,21	1,23
_0936	0	3.1.6.1	arylsulfatase	1,05	1,20	1,32	1,45	1,40	1,18	-1,07
_0937	0		hypothetical protein	1,14	1,21	1,45	1,61	1,70	1,30	1,01
_0938	0		AraC family transcriptional regulator	-1,13	-1,18	-1,20	-1,48	-1,20	-1,24	-1,17
_0939	0		IS5 family transposase OrfA	-1,06	-1,00	1,05	-1,16	1,14	1,23	1,19
_0940	0		hypothetical protein	1,02	1,00	1,01	1,11	1,22	1,21	1,21
_0941	0		hypothetical protein	1,16	1,30	2,13	2,7	5,34	4,4	2,08
_0942	0		peptidase M23B	1,03	1,15	2,01	2,76	4,88	3,1	1,93

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_0943	0		abortive infection protein	1,09	1,10	1,97	3,96	5,5	3,76	2,21
_0944	0		hypothetical protein	1,02	-1,05	-1,05	-1,01	-1,03	1,14	1,07
_0945	0		peptidoglycan binding domain-containing protein	-1,08	-1,03	-1,05	1,00	1,02	1,07	1,05
_0946	0		hypothetical protein	-1,10	-1,07	1,06	1,12	-1,08	-1,05	-1,23
_0947	pthA	3.1.1.29	aminoacyl-tRNA hydrolase	1,03	1,04	-1,04	1,01	-1,14	-1,31	-1,11
_0948	lldD2	1.1.2.3	L-lactate dehydrogenase (cytochrome)	1,11	1,11	1,06	1,12	1,19	1,10	1,27
_0949	0		hypothetical protein	-1,04	-1,04	1,10	1,20	1,06	1,23	1,15
_0950	rplY		50S ribosomal protein L25/general stress protein Ctc	1,05	1,08	-1,16	-1,58	-2,46	-3,7	-2,19
_0951	0		hypothetical protein	-1,01	-1,02	-1,16	1,01	-1,27	-1,32	-1,20
_0952	trpA	4.2.1.20	tryptophan synthase	1,16	1,09	-1,12	-1,27	-1,44	-2,17	-1,18
_0953	0		MATE efflux family protein	1,01	-1,01	1,01	-1,10	1,04	1,18	1,13
_0954	engD		GTP-dependent nucleic acid-binding protein EngD	1,15	1,11	-1,14	-1,25	-1,52	-2,25	-1,29
_0955	0		hydantoin racemase	-1,00	1,01	-1,07	1,01	1,09	1,27	1,06
_0956	0		TRAP dicarboxylate transporter, DctM subunit	-1,08	-1,03	1,04	1,07	1,01	-1,04	1,06
_0957	0		tripartite ATP-independent periplasmic transporter DctQ	-1,01	1,03	1,02	-1,06	-1,04	1,07	1,18
_0958	0		TRAP dicarboxylate transporter, DctP subunit	-1,06	-1,03	-1,04	1,14	1,11	1,07	-1,05
_0959	0		RpiR family transcriptional regulator	-1,11	-1,03	1,17	1,32	1,29	1,35	-1,05
_0960	0		GntR family transcriptional regulator	-1,04	1,00	1,01	1,17	1,19	1,23	-1,07
_0961	0		catechol dioxygenase domain-containing protein	1,01	-1,01	-1,02	-1,06	1,16	1,13	1,18
_0964	0		hypothetical protein	-1,01	1,04	1,13	-1,01	1,06	1,21	1,17
_0965	0		hypothetical protein	1,01	-1,00	1,03	1,07	1,19	1,26	1,16
_0967	0		fumarylacetoacetate (FAA) hydrolase	-1,04	-1,03	-1,10	-1,03	1,10	1,23	1,05
_0968	0		YCII-related	-1,05	1,01	1,01	1,08	-1,02	1,09	1,06
_0969	mtlK	1.1.1.67	mannitol 2-dehydrogenase	1,02	-1,01	-1,05	-1,06	-1,11	-1,03	1,05
_0970	0		short-chain dehydrogenase/reductase SDR	-1,05	-1,01	-1,02	1,11	-1,09	1,05	-1,03
_0971	0		ABC transporter related	-1,03	-1,03	-1,01	-1,20	-1,16	-1,12	-1,02
_0972	0		binding-protein-dependent transport systems inner membrane component	1,01	-1,04	-1,04	-1,07	-1,18	-1,05	-1,03
_0973	0		binding-protein-dependent transport systems inner membrane component	1,00	-1,05	-1,15	-1,07	-1,30	-1,16	-1,13
_0974	0		extracellular solute-binding protein	-1,06	-1,07	-1,21	-1,27	-2,38	-1,82	-2,22
_0975	0		LacI family transcription regulator	-1,09	-1,06	-1,16	-1,53	-1,35	1,02	-1,02
_0976	0		resolvase-like protein	1,00	1,03	-1,01	1,01	1,18	1,14	1,27
_0977	murA	2.5.1.7	UDP-N-acetylglucosamine 1-carboxyvinyl transferase	1,11	1,07	-1,08	-1,23	-1,05	-1,42	-1,03
_0978	0		hypothetical protein	1,03	1,03	-1,04	-1,22	-1,53	-1,97	-1,19
_0979	hisD	1.1.1.23	histidinol dehydrogenase	1,09	1,02	-1,01	-1,10	-1,22	-1,54	-1,06
_0980	0		hypothetical protein	1,03	1,04	1,02	1,09	-1,49	-1,95	-1,14
_0981	0		protein tyrosine phosphatase	-1,01	1,02	-1,09	-1,01	-1,42	-1,58	-1,16
_0982	infA		translation initiation factor IF-1	1,18	1,12	-1,13	-1,14	-1,31	-1,69	-1,14
_0983	0		maf protein	1,20	1,08	-1,13	-1,25	-1,40	-1,67	1,03
_0984	0		ribonuclease	1,00	-1,01	-1,14	-1,24	-1,55	-1,46	-1,12
_0985	0		hypothetical protein	-1,02	-1,01	1,00	1,02	1,08	1,16	1,26
_0986	0		helix-turn-helix domain-containing protein	-1,02	-1,03	1,01	1,12	1,16	1,27	1,05
_0987	0		hypothetical protein	-1,01	-1,03	1,06	1,12	1,23	1,25	1,13
_0988	0		integrase family protein	-1,00	-1,02	1,03	1,11	1,11	1,48	1,07
_0989	0		hypothetical protein	-1,08	-1,01	1,08	1,07	1,06	1,14	1,12
_0990	0		putative DNA helicase related protein	1,04	-1,00	-1,03	1,15	2,1	2,32	1,89
_0991	0		hypothetical protein	1,05	1,13	1,03	1,24	1,11	1,18	1,20
_0992	0		type III restriction protein res subunit	1,06	1,02	1,03	1,07	1,18	1,36	1,13
_0993	0		TRAP transporter solute receptor TAXI family protein	-1,05	-1,01	-1,14	-1,33	-1,44	-1,33	-1,63
_0994	0		TRAP transporter, 4TM/12TM fusion protein	-1,17	-1,05	-1,14	-1,17	-1,49	-1,39	-1,8
_0995	0		LysR family transcriptional regulator	-1,00	-1,04	-1,10	-1,08	-1,02	1,13	1,06
_0996	0	1.6.99.5	NADH dehydrogenase (quinone)	1,02	1,02	-1,05	-1,25	1,08	1,10	1,26
_0997	0		hypothetical protein	-1,05	-1,07	-1,06	-1,03	-1,05	-1,02	1,09
_0998	ade	3.5.4.2	adenine deaminase	-1,06	-1,06	-1,03	-1,07	-1,20	-1,18	-1,39
_0999	0		bile acid:sodium symporter	-1,06	-1,05	-1,15	-1,40	-1,67	-1,44	-1,91
_1000	fadD4	6.2.1.3	Long-chain-fatty-acid-CoA ligase	-1,03	-1,05	-1,22	-1,29	-1,39	-1,26	-1,34
_1001	serA2	1.1.1.95	phosphoglycerate dehydrogenase	-1,01	-1,09	-1,26	-1,32	-1,29	-1,19	-1,35
_1002	metB1	2.5.1.48	cystathionine gamma-synthase	1,02	1,01	-1,02	-1,12	-1,27	-1,22	-1,21
_1003	0		aminoglycoside phosphotransferase	1,02	1,01	1,02	-1,04	-1,07	1,11	-1,21
_1004	0		acyl-CoA dehydrogenase domain-containing protein	-1,05	-1,03	-1,03	1,02	-1,05	-1,04	-1,55

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_1005	0		putative ribonuclease BN	-1,09	-1,03	1,12	-1,03	1,06	1,11	-1,07
_1006	0		major facilitator transporter	-1,02	-1,05	1,02	1,31	1,99	1,92	1,51
_1007	catD		3-oxoadipate enol-lactonase	1,00	-1,01	-1,07	-1,21	-1,40	-1,53	-1,22
_1008	fabI1	1.3.1.9	enoyl-[acyl-carrier-protein] reductase (NADH)	-1,01	1,02	-1,11	-1,42	-1,82	-2,04	-1,43
_1009	fabB	2.3.1.41	beta-ketoacyl-[acyl-carrier-protein] synthase I	1,07	1,10	-1,11	-1,22	-1,59	-2,11	-1,25
_1010	fabA	4.2.1.60	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase	1,14	1,10	-1,14	-1,23	-1,34	-1,84	-1,22
_1011	0		ferric uptake regulator family protein	1,02	1,03	1,08	1,23	1,38	1,24	1,31
_1012	metK	2.5.1.6	methionine adenosyltransferase	1,09	1,09	-1,13	-1,19	-1,18	-1,69	-1,01
_1013	0		apolipoprotein N-acyltransferase	1,02	1,00	1,02	-1,14	1,11	1,35	1,48
_1014	0		CBS domain-containing protein	-1,02	-1,05	-1,10	-1,16	1,09	1,25	1,19
_1015	0		0	-1,04	-1,05	1,04	-1,10	1,12	1,43	1,05
_1016	0		PhoH family protein	-1,12	-1,08	1,09	1,07	-1,04	1,16	-1,18
_1017	hemB2		TonB-dependent heme/hemoglobin receptor family protein	-1,02	-1,01	1,03	-1,05	1,04	1,08	1,22
_1018	0		hypothetical protein	-1,04	-1,02	1,04	1,14	1,06	1,15	1,14
_1019	0			1,16	1,22	-1,09	-1,05	-1,16	-1,76	1,03
_1020	0		hypothetical protein	1,01	-1,03	-1,02	1,17	1,12	1,31	1,27
_1021	trmB	2.1.1.33	tRNA (guanine46-N7)-methyltransferase	1,14	1,08	-1,10	-1,12	-1,23	-1,46	-1,02
_1022	aroA	2.5.1.19	3-phosphoshikimate 1-carboxyvinyl transferase	1,10	1,07	-1,09	-1,24	-1,34	-1,65	-1,12
_1023	cmk	2.7.4.25	(d)CMP kinase	1,01	1,00	-1,12	-1,08	-1,43	-1,65	-1,20
_1024	0		histone family protein nucleoid-structuring protein H-NS	1,01	1,01	-1,06	-1,26	-1,96	-2,75	-1,74
_1025	rpsA		30S ribosomal protein S1	1,04	1,01	-1,31	-1,88	-3,16	-3,72	-1,81
_1026	0		intracellular septation protein A	-1,08	1,00	-1,03	-1,07	1,08	1,42	1,24
_1027	ihfB		integration host factor subunit beta	-1,04	-1,04	-1,10	-1,24	-1,33	-1,12	-1,18
_1028	0		hypothetical protein	-1,04	-1,04	-1,11	-1,23	-1,16	-1,07	-1,09
_1029	trpF	5.3.1.24	phosphoribosyl anthranilate isomerase	1,02	-1,03	-1,07	-1,19	-1,14	-1,07	-1,01
_1030	0		hypothetical protein	-1,01	-1,06	-1,06	1,01	1,28	1,48	1,21
_1031	trpB	4.2.1.20	tryptophan synthase	1,12	1,08	-1,11	-1,15	-1,12	-1,53	-1,05
_1032	0		hypothetical protein	1,02	1,00	1,04	1,07	-1,09	-1,14	-1,07
_1033	0		hypothetical protein	-1,06	1,01	-1,04	-1,04	-1,23	-1,28	-1,54
_1034	0		LuxR family transcriptional regulator	-1,01	1,02	-1,00	-1,19	-1,16	-1,28	-1,20
_1035	0		TRAP dicarboxylate transporter- DctP subunit	-1,09	-1,06	-1,15	-1,39	-1,92	-1,85	-2,37
_1036	0		tripartite ATP-independent periplasmic transporter DctQ	-1,05	-1,05	1,01	-1,16	-1,63	-1,38	-1,98
_1037	0		TRAP dicarboxylate transporter, DctM subunit	-1,10	-1,03	1,03	1,08	-1,39	-1,29	-1,69
_1038	0		Asp/Glu racemase	1,04	-1,01	1,05	1,01	1,02	1,23	1,03
_1039	0		monooxygenase FAD-binding	-1,09	-1,03	1,03	-1,02	-1,13	1,12	-1,17
_1040	0		aldehyde oxidase and xanthine dehydrogenase molybdopterin binding	1,02	1,03	-1,04	1,00	1,04	1,25	1,09
_1041	0		TRAP dicarboxylate transporter, DctM subunit	-1,04	-1,07	1,04	1,06	1,13	1,23	1,03
_1042	0		tripartite ATP-independent periplasmic transporter DctQ	-1,03	-1,05	-1,04	1,08	1,13	-1,04	-1,11
_1043	0		TRAP dicarboxylate transporter- DctP subunit	-1,02	-1,06	-1,11	-1,17	1,29	1,09	-1,09
_1044	0		GntR family transcriptional regulator	-1,02	1,03	1,20	1,40	1,94	1,76	1,44
_1045	0		HpcH/HpaI aldolase	1,00	1,00	1,24	1,08	1,54	1,77	1,70
_1046	0	6.3.5.6, 6.3.5.7	asparaginyl-tRNA synthase (glutamine-hydrolysing),glutaminyl-tRNA synthase (glutamine-hydrolysing)	1,04	-1,02	1,06	1,23	1,36	1,55	1,56
_1047	0		hypothetical protein	-1,02	-1,01	-1,01	1,13	1,42	1,34	1,27
_1048	0		enoyl-CoA hydratase/isomerase	1,08	1,01	-1,01	1,06	1,48	1,47	1,65
_1049	0		short chain dehydrogenase	1,07	1,03	-1,01	-1,15	1,56	1,51	1,52
_1050	0		hypothetical protein	-1,06	-1,02	1,21	1,10	1,37	1,42	1,38
_1051	0	4.2.1.79	2-Methylcitrate dehydratase	1,02	-1,01	1,06	1,35	1,64	1,38	1,65
_1052	0		spermidine/putrescine-binding periplasmic protein-like protein	-1,07	-1,07	-1,02	-1,00	1,08	-1,12	-1,20
_1053	0		binding-protein-dependent transport systems inner membrane component	-1,02	-1,03	-1,09	1,07	1,12	-1,19	-1,41
_1054	0		binding-protein-dependent transport systems inner membrane component	-1,05	-1,03	-1,07	-1,03	-1,00	-1,16	-1,05
_1055	0		ABC transporter related	-1,01	-1,03	-1,08	-1,15	1,08	1,01	-1,00
_1056	0		polysaccharide deacetylase	-1,02	-1,01	-1,07	-1,04	1,02	-1,03	-1,11
_1057	0		L-carnitine dehydratase/bile acid-inducible protein F	-1,02	-1,04	-1,02	-1,25	1,03	-1,09	-1,09
_1058	0		acyl-CoA dehydrogenase domain-containing protein	-1,03	1,01	-1,07	1,12	1,02	-1,09	-1,09

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_1059	0		hypothetical protein	-1,05	-1,03	-1,02	1,20	1,07	1,07	-1,09
_1060	0		hypothetical protein	-1,07	-1,02	1,13	1,25	1,15	1,01	-1,13
_1061	0		hypothetical protein	1,01	1,07	1,01	-1,04	-1,15	-1,40	-1,28
_1062	0		isoprenylcysteine carboxyl methyltransferase	1,00	1,01	-1,02	-1,09	-1,03	-1,02	1,02
_1063	0		hypothetical protein	1,01	1,02	-1,00	1,03	-1,15	-1,30	-1,26
_1064	rufX		Holliday junction resolvase YqgF	1,11	1,07	-1,01	-1,07	-1,17	-1,58	-1,17
_1065	0		hypothetical protein	-1,03	-1,03	1,03	1,03	1,03	1,07	-1,12
_1066	0		hypothetical protein	-1,03	-1,04	-1,00	1,09	1,15	1,10	-1,23
_1067	sod	1.15.1.1	superoxide dismutase	-1,03	-1,00	-1,09	-1,16	-1,66	-1,95	-1,52
_1068	0		hypothetical protein	1,07	1,06	-1,02	1,10	-1,05	-1,39	-1,08
_1069	0		Fe-S metabolism associated SufE	1,08	1,03	-1,11	-1,15	-1,18	-1,39	-1,04
_1070	0		hypothetical protein	-1,07	-1,12	-1,05	1,12	1,04	1,36	1,14
_1071	0		hypothetical protein	-1,02	-1,09	-1,13	1,02	-1,04	1,11	1,37
_1072	0		hypothetical protein	-1,06	-1,17	-1,22	-1,16	-1,22	-1,08	1,21
_1073	0	2.1.1.13	methionine synthase	-1,19	-1,39	-1,85	-1,89	-2,51	-2,46	-1,72
_1074	0		methionine synthase I	-1,52	-1,62	-1,87	-2,13	-2,3	-1,89	-1,47
_1075	0		protein of unknown function DUF1476	-1,01	1,09	1,11	1,20	1,54	1,16	1,48
_1076	purC	6.3.2.6	phosphoribosyl aminoimidazole succinocarboxamide synthase	1,15	1,11	-1,12	-1,20	-1,33	-2,25	-1,10
_1077	purS		phosphoribosylformylglycinamidine synthase, purS	1,15	1,08	-1,08	-1,21	-1,31	-1,82	-1,09
_1078	0	1.1.1.1	alcohol dehydrogenase	1,13	1,13	-1,08	-1,59	-1,36	-1,67	-1,13
_1079	purQ	6.3.5.3	phosphoribosylformyl glycinamidine synthase	1,05	1,06	-1,14	-1,43	-1,87	-2,23	-1,30
_1080	0	2.7.13.3	histidine kinase	1,01	-1,03	-1,01	1,04	1,02	1,09	1,02
_1081	0		two component, sigma54 specific, Fis family transcriptional regulator	-1,03	1,01	1,03	-1,05	-1,10	-1,22	-1,30
_1082	ate	2.3.2.8	arginyltransferase	-1,07	-1,05	-1,01	-1,10	-1,03	-1,04	-1,18
_1083	0		RDD domain-containing protein	1,01	-1,03	-1,05	1,05	1,09	1,18	1,40
_1084	0		hypothetical protein	-1,02	-1,00	-1,11	-1,03	-1,05	-1,01	1,25
_1085	0		YbaK/prolyl-tRNA synthetase associated region	1,03	1,01	-1,08	-1,04	1,01	-1,11	1,05
_1086	0		hypothetical protein	1,04	1,02	1,14	1,19	1,67	1,93	1,67
_1087	0		TRAP transporter solute receptor TAXI family protein	-1,04	-1,07	-1,12	-1,16	-1,78	-1,73	-1,89
_1088	0		TRAP transporter, 4TM/12TM fusion protein	-1,04	-1,06	-1,16	-1,27	-1,88	-2	-2,26
_1089	0		TRAP dicarboxylate transporter- DctP subunit	-1,09	-1,12	-1,34	-1,53	-3,07	-2,57	-3,33
_1090	0		tripartite ATP-independent periplasmic transporter DctQ	-1,01	-1,12	-1,39	-1,34	-3,14	-3,12	-3,52
_1091	0		TRAP dicarboxylate transporter, DctM subunit	-1,03	-1,10	-1,23	-1,49	-2,78	-2,95	-2,92
_1092	0		carboxyvinyl-carboxyphosphonate phosphorylmutase	-1,03	-1,04	-1,16	-1,30	-1,68	-1,56	-1,77
_1093	0		hypothetical protein	1,03	-1,00	-1,09	1,00	-1,09	-1,03	1,08
_1094	0		Fis family transcriptional regulator	-1,05	-1,04	-1,06	-1,01	-1,15	1,05	1,64
_1095	0	1.2.1.3	aldehyde dehydrogenase (NAD+)	-1,03	-1,02	-1,10	-1,10	-1,22	-1,31	-1,16
_1096	0		lipolytic enzyme, G-D-S-L	1,05	1,07	1,38	1,64	2,37	2,17	2,05
_1097	0		protein of unknown function DUF395 YeeE/YedE	1,20	1,63	3,16	4,34	7,19	4,65	2,86
_1098	0		major facilitator transporter	1,09	1,05	-1,04	1,02	-1,16	-1,47	-1,15
_1099	msrA2	1.8.4.11	peptide-methionine (S)-S-oxide reductase	1,03	-1,03	-1,01	1,13	1,11	1,35	1,21
_1100	prmA	2.1.1.-	ribosomal L11 methyltransferase	1,10	1,03	1,03	1,12	1,08	1,01	1,15
_1101	0		hypothetical protein	1,01	-1,00	-1,05	-1,08	-1,05	1,04	-1,04
_1102	0		hypothetical protein	1,19	1,05	1,22	2,35	2,36	1,56	2,65
_1103	ruvC	3.1.22.4	crossover junction endodeoxy ribonuclease	1,03	-1,01	-1,01	-1,02	1,29	1,29	1,46
_1104	ruvA	3.6.4.12	DNA helicase	1,01	-1,01	1,00	1,07	1,18	1,13	1,39
_1105	ruvB	3.6.4.12, 1.3.1.76, 2.1.1.107, 4.99.1.4	DNA helicase,precorrin-2 dehydrogenase,uroporphyrinogen-III C-methyltransferase,sirohydrochlorin ferrochelatase	-1,00	-1,02	1,01	1,02	1,01	1,19	1,37
_1106	0		hypothetical protein	-1,01	-1,01	-1,05	-1,03	-1,14	1,02	1,11
_1107	0	3.1.2.-	Pol-Pal system-associated acyl-CoA thioesterase	-1,03	1,02	1,01	-1,03	-1,14	-1,07	1,08
_1108	tolQ		Tol-Pal system TolQ	-1,02	-1,02	-1,05	-1,01	-1,03	1,04	1,13
_1109	tolR		biopolymer transport TolR	1,02	-1,00	-1,07	-1,08	-1,08	-1,06	1,05
_1110	tolA		hypothetical protein	-1,00	-1,04	1,01	1,03	-1,06	-1,02	1,06
_1111	tolB		translocation protein TolB	1,00	-1,00	1,03	1,03	-1,14	-1,01	-1,02
_1112	pal		peptidoglycan-associated lipoprotein	-1,02	-1,01	-1,03	1,04	-1,13	-1,08	1,00
_1113	0		Tol-Pal system YbgF	-1,02	-1,02	-1,03	-1,09	-1,16	-1,12	-1,03
_1114	tilS	6.3.4.19	tRNAIle-lysidine synthase	1,02	-1,01	-1,07	-1,30	-1,11	-1,04	1,15
_1115	ftsH	3.4.24.-	ATP-dependent metalloprotease FtsH	-1,03	-1,05	-1,05	1,07	1,09	1,10	-1,03

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_1116	0		hypothetical protein	1,03	-1,00	-1,11	1,03	-1,05	-1,41	-1,27
_1117	0		thioesterase superfamily protein	-1,05	1,03	1,03	1,17	-1,04	-1,11	-1,27
_1118	0		hypothetical protein	1,06	1,02	-1,13	1,03	-1,18	-1,39	1,06
_1119	0		DEAD/DEAH box helicase domain-containing protein	-1,01	1,01	1,10	1,05	1,05	-1,07	-1,00
_1120	0		hypothetical protein	1,02	1,01	-1,02	1,18	1,36	1,34	1,35
_1121	0		peptidase A24A prepilin type IV	1,04	-1,03	1,01	1,09	1,46	1,17	1,73
_1122	0		tetratricopeptide region	-1,02	-1,02	1,08	1,39	1,34	-1,00	1,08
_1123	0		TPR repeat-containing protein	1,01	-1,05	1,03	1,38	1,26	1,13	1,26
_1124	0		type II secretion system protein	1,06	-1,00	1,02	-1,01	1,07	1,48	1,69
_1125	0		type II secretion system protein	1,05	1,01	1,05	1,12	1,05	1,58	1,75
_1126	0		type II secretion system protein E	1,07	1,01	1,02	1,10	1,25	1,60	1,87
_1127	0		response regulator receiver protein	1,06	1,06	1,01	1,08	1,44	1,59	1,73
_1128	0		OmpA/MotB domain-containing protein	-1,04	-1,02	-1,05	1,08	1,17	1,03	-1,01
_1129	0		type II and III secretion system protein	-1,02	-1,06	-1,06	-1,01	1,14	-1,06	-1,03
_1130	0		SAF domain-containing protein	1,01	-1,02	-1,07	-1,07	1,04	-1,05	1,84
_1131	0		hypothetical protein	1,01	1,00	-1,01	-1,05	-1,03	1,17	1,81
_1132	0		hypothetical protein	-1,01	1,01	-1,02	1,03	-1,07	1,07	1,70
_1133	0		lytic transglycosylase catalytic	1,00	-1,03	-1,03	1,00	1,05	1,26	1,02
_1134	0	2.8.3.5	3-oxoacid CoA-transferase	-1,01	-1,01	-1,04	-1,34	-1,72	-2,04	-1,42
_1135	0		putative signal transduction histidine kinase	1,01	1,03	-1,09	-1,32	-1,33	-1,79	-1,32
_1136	0	2.8.3.5	3-oxoacid CoA-transferase	1,06	1,07	-1,08	-1,18	-1,26	-1,77	-1,21
_1137	topA	5.99.1.2	DNA topoisomerase	1,05	1,03	-1,05	-1,32	-1,23	-1,36	1,07
_1138	0		DNA protecting protein DprA	1,05	-1,03	-1,06	1,12	1,39	1,32	1,35
_1139	tldD		peptidase U62 modulator of DNA gyrase	-1,05	-1,06	-1,14	-1,08	-1,32	-1,11	-1,08
_1140	ctaC	1.9.3.1	cytochrome-c oxidase	-1,15	-1,41	-2,03	-2,26	-4,23	-3,75	-2,28
_1141	ctaB	2.5.1.-	protoheme IX farnesyltransferase	-1,10	-1,37	-1,8	-1,77	-2,34	-2,53	-1,68
_1142	0		hypothetical protein	-1,06	-1,32	-1,69	-2,09	-2,67	-2,62	-1,73
_1143	ctaG		cytochrome C oxidase assembly protein	-1,10	-1,25	-1,64	-1,96	-2,98	-3,21	-1,99
_1144	ctaE	1.9.3.1	cytochrome-c oxidase	-1,06	-1,23	-1,44	-1,58	-2,88	-2,67	-1,71
_1145	0		hypothetical protein	1,01	-1,01	-1,10	-1,15	-1,23	-1,18	-1,01
_1146	thrC	4.2.3.1	threonine synthase	1,05	1,04	-1,09	-1,20	-1,19	-1,50	1,04
_1147	0	3.4.24.64	mitochondrial processing peptidase	1,01	1,02	-1,12	-1,57	-1,40	-1,72	-1,06
_1148	0		GCN5-related N-acetyltransferase	1,01	1,01	-1,00	-1,07	-1,48	-1,61	-1,10
_1149	infC		translation initiation factor IF-3	-1,03	-1,01	-1,09	-1,32	-1,66	-1,34	-1,24
_1150	0	1.18.1.2	ferredoxin-NADP+ reductase	-1,04	-1,00	-1,04	-1,02	-1,34	1,02	1,34
_1151	0		hypothetical protein	-1,10	-1,06	-1,02	-1,13	-2,31	-1,08	1,20
_1152	cysH	1.8.4.8	Phosphoadenylyl-sulfate reductase (thioredoxin)	-1,05	-1,05	-1,08	-1,04	-1,98	-1,02	1,23
_1153	cysI	1.8.7.1	sulfite reductase (ferredoxin)	-1,09	-1,01	-1,10	-1,28	-1,85	1,12	1,23
_1154	0		hypothetical protein	-1,12	-1,07	-1,31	-1,54	-1,67	1,11	1,15
_1155	0		uroporphyrin-III C-methyltransferase	-1,11	1,00	-1,21	-1,51	-1,75	1,22	1,05
_1156	0		AsnC family transcriptional regulator	-1,05	-1,02	-1,07	-1,12	-1,13	1,18	1,13
_1157	0		hypothetical protein	-1,03	-1,03	-1,00	1,17	1,06	1,22	1,17
_1158	rih	3.2.2.1	purine nucleosidase	-1,09	-1,05	-1,05	1,01	-1,10	-1,06	-1,17
_1159	0		hypothetical protein	1,00	-1,03	1,06	1,23	1,39	1,47	2,07
_1160	0		MazG family protein	-1,05	1,04	-1,01	-1,07	-1,33	-1,35	-1,25
_1161	0	3.5.1.32	hippurate hydrolase	1,02	1,01	-1,06	-1,03	1,20	1,18	1,07
_1162	0		acriflavin resistance protein	1,04	1,00	1,02	1,01	1,31	1,43	1,32
_1163	0		RND family efflux transporter MFP subunit	-1,00	-1,00	1,09	1,19	1,36	1,36	1,31
_1164	0		hypothetical protein	1,07	1,08	-1,00	-1,00	-1,31	-1,74	-1,10
_1165	0		Pyrrolo-quinoline quinone	1,07	1,01	-1,04	-1,31	-1,30	-1,47	-1,15
_1166	engA		GTP-binding protein EngA	1,02	1,02	-1,12	-1,26	-1,26	-1,38	-1,02
_1167	0		peptidase M48 Ste24p	1,04	-1,05	1,08	1,15	1,06	1,11	1,02
_1168	0		aminotransferase class I and II	1,00	1,07	1,04	-1,12	-1,33	-1,68	-1,21
_1169	amiC	3.5.1.28	N-acetylmuramoyl-L-alanine amidase	1,00	1,01	1,02	1,01	-1,00	-1,08	1,05
_1170	0		methyltransferase type 11	-1,15	-1,05	1,08	1,10	-1,06	1,01	-1,07
_1171	0	2.4.1.129	peptidoglycan glycosyltransferase	-1,06	-1,02	-1,04	-1,27	-1,05	-1,03	-1,02
_1172	prfB		peptide chain release factor 2	1,08	1,07	-1,03	-1,06	-1,14	-1,60	-1,16
_1173	0		NMT1/THI5-like domain-containing protein	1,05	1,01	-1,10	-1,01	-1,23	-1,22	-1,14
_1174	0		hypothetical protein	-1,04	-1,04	-1,02	-1,03	-1,02	-1,14	-1,18
_1175	0		hypothetical protein	1,06	1,03	-1,07	-1,16	-1,34	-1,70	-1,02
_1176	0		peptidase M23B	1,12	1,07	-1,04	-1,22	1,21	-1,18	1,25

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_1177	0		hypothetical protein	1,04	1,01	-1,09	-1,16	-1,15	-1,44	-1,09
_1178	0		alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	-1,07	-1,07	1,06	1,14	1,09	1,11	1,05
_1179	0		hypothetical protein	1,03	-1,01	1,06	-1,04	1,15	1,20	1,18
_1180	queA	2.4.99.17	S-adenosyl methionine:tRNA ribosyltransferase-isomerase	1,06	1,05	-1,06	-1,02	-1,16	-1,44	1,01
_1181	0		hypothetical protein	-1,09	-1,07	-1,03	-1,14	-1,19	-1,12	-1,31
_1182	hemA2	2.3.1.37	5-aminolevulinate synthase	1,20	1,77	2,49	2,98	4,78	2,96	2,13
_1183	0		hypothetical protein	-1,03	-1,03	-1,14	-1,08	1,09	1,10	-1,17
_1184	ispG	1.17.7.1	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase	-1,03	1,00	1,04	-1,09	1,08	1,03	1,07
_1185	ksgA	2.1.1.182	16S rRNA (adenine1518-N6/adenine1519-N6)-dimethyltransferase	-1,07	-1,03	-1,02	1,00	-1,05	-1,09	-1,20
_1186	pdxA	1.1.1.262	4-hydroxy threonine-4-phosphate dehydrogenase	1,04	-1,01	-1,01	-1,08	-1,23	-1,29	-1,08
_1187	0		SurA domain protein	-1,01	-1,01	-1,03	1,09	-1,17	-1,23	-1,06
_1188	ostA		organic solvent tolerance protein	1,01	-1,02	1,06	-1,08	-1,07	-1,03	-1,06
_1189	0		permease YjgP/YjgQ family protein	1,00	-1,01	1,09	-1,03	-1,01	1,03	-1,14
_1190	0		permease YjgP/YjgQ family protein	-1,03	1,00	1,06	1,00	1,10	1,07	-1,06
_1191	pepA1	3.4.11.1	leucyl aminopeptidase	-1,10	-1,03	1,06	1,05	-1,21	-1,31	-1,33
_1192	holC		DNA polymerase III subunit chi	-1,01	-1,05	1,01	-1,01	-1,04	-1,02	-1,07
_1193	0		cytochrome P450	-1,00	-1,03	-1,08	-1,02	-1,64	-1,44	-1,65
_1194	0		TRAP transporter, 4TM/12TM fusion protein	-1,02	-1,00	-1,25	-1,61	-5,15	-3,08	-2,81
_1195	0		TRAP transporter solute receptor	-1,11	-1,02	-1,20	-1,44	-4,82	-3,14	-3,67
_1196	dctD		two component, sigma54 specific, Fis family transcriptional regulator	1,03	-1,04	-1,01	1,08	1,05	1,11	1,16
_1197	dctB		integral membrane sensor signal transduction histidine kinase	1,00	-1,01	1,04	1,15	1,34	1,45	1,36
_1198	0		beta-lactamase	1,02	-1,04	-1,01	1,03	1,08	1,33	1,22
_1199	suhB1	3.1.3.25	inositol-phosphate phosphatase	1,10	1,11	-1,12	-1,42	-1,56	-2,4	-1,38
_1200	0		rhomboid family protein	1,04	1,02	-1,03	1,11	1,05	1,26	1,25
_1201	0		TPR repeat-containing protein	-1,10	-1,06	1,05	-1,16	1,06	1,26	-1,21
_1202	0		heat shock protein DnaJ domain-containing protein	-1,01	1,01	1,01	1,22	-1,01	-1,19	-1,47
_1203	0		BolA family protein	-1,02	-1,00	1,01	1,12	-1,04	-1,14	-1,16
_1204	0		hypothetical protein	-1,09	-1,04	-1,01	1,08	-1,04	1,17	-1,07
_1205	0		hypothetical protein	-1,07	-1,05	-1,06	-1,15	-1,50	-1,16	-1,04
_1206	0		hypothetical protein	1,04	-1,02	-1,06	-1,15	-1,33	-1,40	-1,08
_1207	gatB	6.3.5.-	Glutamyl-tRNA(Gln) amidotransferase subunit A 1	1,08	1,09	-1,07	-1,11	-1,35	-1,76	-1,37
_1208	0		hypothetical protein	-1,02	1,00	-1,05	-1,11	-1,11	-1,00	-1,19
_1209	coxC		putative integral membrane sensor protein	-1,04	-1,08	-1,11	-1,03	-1,19	-1,20	-1,42
_1210	coxM	1.2.99.2	carbon-monoxide dehydrogenase (acceptor)	-1,30	-1,46	-1,35	-1,12	-1,18	1,11	-1,13
_1211	coxS	1.2.99.2	carbon-monoxide dehydrogenase (acceptor)	1,01	-1,10	1,02	1,12	1,01	1,21	1,01
_1212	coxL2	1.2.99.2	carbon-monoxide dehydrogenase (acceptor)	1,05	-1,01	-1,03	-1,07	1,12	1,13	1,23
_1213	coxD		ATPase	-1,00	-1,00	-1,03	-1,23	-1,03	1,02	1,21
_1214	coxE		VWA containing CoxE family protein	1,06	-1,06	-1,16	1,14	1,09	1,22	1,11
_1215	coxF		hypothetical protein	1,07	-1,04	-1,04	1,05	1,19	1,15	1,27
_1216	panE	1.1.1.169	2-dehydropantoate 2-reductase	-1,01	-1,00	-1,08	-1,10	-1,36	-1,60	-1,44
_1217	0		AMP-dependent synthetase and ligase	1,00	1,02	-1,13	-1,16	-1,83	-2,08	-1,77
_1218	0		hypothetical protein	-1,03	-1,04	-1,11	-1,37	-1,37	1,06	-1,33
_1219	0		hypothetical protein	1,10	1,05	-1,05	-1,38	-1,01	1,04	1,02
_1220	0		hypothetical protein	1,05	-1,03	-1,16	-1,23	-1,13	-1,12	-1,18
_1221	0		XRE family transcriptional regulator	1,07	-1,01	-1,11	-1,22	-1,04	-1,00	1,04
_1222	0		short-chain dehydrogenase/reductase SDR	-1,04	1,00	1,12	1,06	-1,11	-1,15	-1,18
_1223	pepN	3.4.11.2	membrane alanyl aminopeptidase	-1,04	-1,01	1,04	1,18	1,11	-1,01	-1,02
_1224	0		hypothetical protein	-1,02	-1,06	-1,02	1,11	1,06	1,14	1,14
_1225	0	4.1.99.3	deoxy ribodipyrimidine photo-lyase	-1,11	-1,08	1,00	1,18	1,12	1,11	1,05
_1226	0		hypothetical protein	1,05	-1,02	-1,04	1,03	1,14	1,34	1,06
_1227	glcB	2.3.3.9	malate synthase	-1,24	-1,09	-1,21	-1,61	-2,07	-2	-1,70
_1228	0		hypothetical protein	1,00	-1,03	-1,14	-1,21	-1,41	-1,38	-1,10
_1229	0		peptidase C26	1,03	1,01	-1,05	-1,17	-1,05	-1,24	-1,08
_1230	0	3.7.1.3	kynureninase	-1,01	-1,05	-1,09	-1,14	-1,17	1,10	1,03
_1231	0		beta-lactamase domain-containing protein	-1,04	-1,06	-1,03	1,01	1,03	-1,02	-1,20
_1232	0		isoprenylcysteine carboxyl methyltransferase family protein	1,02	1,01	1,05	-1,14	-1,02	-1,03	1,03

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_1233	pntA	1.6.1.2	NAD(P)+ transhydrogenase (AB-specific)	1,17	1,19	-1,03	-1,14	-1,14	-1,79	-1,06
_1234	pntB	1.6.1.2	NAD(P)+ transhydrogenase (AB-specific)	1,02	1,05	-1,10	-1,18	-2,01	-2,44	-1,50
_1235	xylB1	2.7.1.17	xylulokinase	1,09	-1,01	-1,12	-1,08	-1,39	-1,48	-1,14
_1236	dmsC		DMSO reductase anchor subunit (DmsC)	-1,01	1,01	1,16	1,09	1,13	1,20	1,05
_1237	dmsB	1.8.99.-	4Fe-4S ferredoxin	-1,05	-1,02	1,05	1,13	1,16	1,02	1,15
_1238	dmsA2	1.8.99.-	molybdopterin oxidoreductase Fe4S4 region	-1,04	-1,03	1,13	-1,04	1,23	1,09	-1,00
_1239	lacZ	3.2.1.23	beta-galactosidase	1,02	-1,02	-1,07	-1,18	1,07	1,11	1,09
_1240	0		SMP-30/gluconolaconase/LRE domain-containing protein	-1,08	-1,06	1,05	1,10	-1,08	1,08	-1,38
_1241	dgoA	4.1.2.21	2-dehydro-3-deoxy-6-phosphogalactonate aldolase	-1,13	-1,06	1,08	1,14	-1,18	-1,32	-1,23
_1242	dgoK	2.7.1.58	2-dehydro-3-deoxygalactonokinase	-1,03	-1,06	1,03	1,15	-1,14	-1,16	-1,22
_1243	0		short-chain dehydrogenase/reductase SDR	-1,03	-1,00	1,01	1,03	-1,13	1,10	1,01
_1244	ilvD2	4.2.1.9	dihydroxy-acid dehydratase	1,01	-1,02	1,02	-1,19	-1,03	-1,03	-1,02
_1245	melA	3.2.1.22	alpha-galactosidase	1,04	-1,02	-1,10	-1,13	-1,02	-1,02	1,02
_1246	0		binding-protein-dependent transport systems inner membrane component	1,01	-1,03	-1,12	-1,02	-1,16	1,02	-1,08
_1247	0		binding-protein-dependent transport systems inner membrane component	1,05	-1,01	-1,10	-1,09	-1,19	-1,14	-1,11
_1248	0		extracellular solute-binding protein	-1,08	-1,08	-1,25	-1,29	-1,69	-1,30	-1,55
_1249	0		IclR family transcriptional regulator	1,03	-1,02	-1,10	1,02	-1,02	1,05	1,14
_1250	0	3.6.3.-	ABC transporter-like protein	-1,00	1,01	-1,00	-1,18	-1,23	-1,24	-1,15
_1251	0		hypothetical protein	-1,03	-1,01	1,03	-1,02	1,19	1,49	1,62
_1252	0		hypothetical protein	1,04	-1,05	1,08	1,20	1,12	1,24	1,11
_1253	0		ArsR family transcriptional regulator	-1,01	1,02	-1,12	-1,09	-1,06	-1,15	-1,16
_1254	0	1.2.1.12	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)	1,02	-1,03	-1,05	1,01	-1,05	-1,12	-1,07
_1255	0		major facilitator transporter	-1,03	-1,02	-1,02	-1,19	-1,11	-1,06	-1,01
_1256	0		exopolysaccharide synthesis ExoD	1,05	-1,03	1,09	1,06	1,21	1,32	1,26
_1257	0		hypothetical protein	1,03	1,00	1,00	1,04	1,02	1,11	1,15
_1258	0		short-chain dehydrogenase/reductase SDR	1,07	1,06	-1,09	-1,11	-1,28	-1,49	-1,07
_1259	0	3.6.3.4	Cu2+-exporting ATPase	1,00	1,00	-1,09	-1,08	-1,04	-1,11	1,11
_1260	0		MerR family transcriptional regulator	1,03	-1,02	-1,03	1,07	-1,06	1,02	1,15
_1261	gltS		sodium/glutamate symporter	1,03	1,03	-1,07	-1,01	-1,17	-1,40	-1,15
_1262	0		acriflavin resistance protein	-1,03	-1,06	1,02	-1,05	1,07	1,11	-1,14
_1263	0		RND family efflux transporter MFP subunit	-1,09	-1,05	-1,05	1,01	-1,04	1,09	-1,09
_1264	0		Ion transport 2 domain-containing protein	-1,06	-1,04	1,08	1,00	-1,01	1,04	-1,07
_1265	idhA	1.1.1.18	inositol 2-dehydrogenase	-1,04	1,01	1,05	1,09	1,01	1,02	1,00
_1266	fbaA	4.1.2.13	Fructose-bisphosphate aldolase	-1,03	-1,02	1,14	-1,13	-1,12	1,03	-1,04
_1267	iolB		hypothetical protein	1,01	-1,03	-1,02	-1,03	1,18	1,23	1,11
_1268	iolC	2.7.1.92	5-dehydro-2-deoxygluconokinase	-1,12	-1,02	1,09	1,10	1,05	1,07	-1,18
_1269	iolD		thiamine pyrophosphate protein central region	-1,07	1,01	1,02	-1,05	1,14	1,22	1,02
_1270	0	1.1.1.18	inositol 2-dehydrogenase	1,00	-1,01	-1,02	1,17	1,12	-1,02	1,09
_1271	0		xylose isomerase domain-containing protein	-1,06	1,01	-1,01	1,03	-1,10	-1,20	-1,02
_1272	0	1.1.1.18	inositol 2-dehydrogenase	1,04	-1,02	-1,03	-1,08	-1,22	-1,15	-1,13
_1273	0	5.1.1.1	Alanine racemase	-1,02	-1,03	1,15	1,15	1,16	1,19	1,00
_1274	0		periplasmic binding protein/LacI transcriptional regulator	-1,06	-1,07	-1,18	-1,26	-1,99	-1,68	-2,4
_1275	0	3.6.3.17	Monosaccharide-transporting ATPase	1,03	-1,06	-1,10	-1,52	-1,53	-1,60	-1,67
_1276	0	3.6.3.17	Monosaccharide-transporting ATPase	-1,02	-1,02	-1,01	-1,05	-1,10	-1,09	-1,14
_1277	0		hypothetical protein	1,03	-1,04	-1,03	1,01	-1,05	-1,09	-1,02
_1278	0		phytanoyl-CoA dioxygenase	1,04	-1,02	-1,06	-1,17	-1,06	1,02	1,00
_1279	iolB2		myo-inositol catabolism IolB domain-containing protein	1,01	-1,05	1,15	-1,02	1,02	1,02	1,12
_1280	0		aminotransferase class V	-1,00	1,06	1,05	-1,02	-1,27	-1,81	-1,38
_1281	fdhB	1.2.1.2	formate dehydrogenase	1,01	-1,01	1,17	1,28	1,20	1,09	-1,09
_1282	fdhA	1.2.1.2	formate dehydrogenase	1,00	1,00	1,04	1,05	1,02	1,08	-1,20
_1283	fhs	6.3.4.3	Formate-tetrahydrofolate ligase	-1,04	1,02	-1,07	-1,13	-1,17	-1,21	-1,27
_1284	0		chorismate mutase related enzyme	1,08	1,05	1,03	-1,05	-1,09	-1,13	-1,03
_1285	folD	3.5.4.9	methenyl tetrahydrofolate cyclohydrolase	1,09	1,05	1,01	1,05	-1,10	-1,23	1,03
_1286	0		hypothetical protein	1,05	1,08	1,07	1,14	1,19	-1,42	1,05
_1287	0		protein of unknown function DUF395 YeeE/YedE	1,05	1,03	-1,25	-1,50	-2,05	-1,41	1,22
_1288	0	3.5.1.32	hippurate hydrolase	1,05	1,04	-1,10	-1,27	-1,24	-1,19	-1,01
_1289	0	6.3.5.2	GMP synthase (glutamine-hydrolysing)	1,09	1,04	-1,11	-1,20	-1,22	-1,23	-1,03

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_1290	moaA	4.1.99.18	cyclic pyranopterin monophosphate synthase	-1,07	-1,06	-1,16	-1,30	-1,43	-1,62	-1,76
_1291	0		DNA alkylation repair enzyme	1,02	-1,04	-1,14	1,01	-1,53	-1,46	-1,31
_1292	0		pyridoxamine 5'-phosphate oxidase-related FMN-binding	1,04	-1,02	-1,05	-1,07	-1,48	-1,71	-1,01
_1293	glmS	2.6.1.16	Glutamine-fructose-6-phosphate transaminase (isomerizing)	1,05	1,05	-1,13	-1,18	-1,25	-1,32	1,04
_1294	glmU	2.3.1.157	glucosamine-1-phosphate N-acetyltransferase	1,05	1,05	-1,16	-1,20	-1,01	-1,15	1,16
_1295	0	3.1.3.18	phosphoglycolate phosphatase	1,01	1,02	-1,14	-1,23	-1,15	-1,37	-1,03
_1296	0		DegT/DnrJ/EryC1/StrS aminotransferase	-1,08	-1,05	-1,05	-1,21	-1,17	-1,25	-1,21
_1297	ivd		acyl-CoA dehydrogenase domain-containing protein	-1,08	-1,04	-1,25	-1,50	-1,42	-1,25	-1,36
_1298	0		hypothetical protein	-1,12	-1,08	1,00	-1,09	-1,37	-1,32	-1,32
_1299	0		OmpW family protein	1,58	4,39	7,21	9,63	17	9,66	14,1
_1300	mccB	6.4.1.4	methylcrotonoyl-CoA carboxylase	-1,01	-1,02	-1,02	-1,00	1,11	1,05	1,07
_1301	mccA	6.4.1.4	methylcrotonoyl-CoA carboxylase	-1,06	-1,04	-1,08	-1,04	-1,07	-1,15	-1,13
_1302	0		glutathione S-transferase domain-containing protein	-1,01	-1,05	-1,04	1,04	-1,19	-1,17	-1,20
_1303	mvaB	4.1.3.4	Hydroxymethyl glutaryl-CoA lyase	1,00	-1,09	-1,03	1,10	-1,09	-1,17	-1,12
_1304	mvaA	4.2.1.18	methylglutaconyl-CoA hydratase	-1,04	-1,02	-1,03	-1,08	-1,24	1,01	-1,17
_1305	0		17 kDa surface antigen	-1,04	-1,02	-1,00	-1,22	-1,25	-1,08	-1,47
_1306	0		hypothetical protein	-1,11	-1,08	1,02	-1,04	-1,13	1,16	-1,24
_1307	nuoA	1.6.5.3, 1.6.99.5	NADH:ubiquinone reductase (H+-translocating),NADH dehydrogenase (quinone)	1,04	1,22	1,36	1,48	1,55	1,45	1,33
_1308	nuoB	1.6.99.5	NADH dehydrogenase (quinone)	1,01	1,17	1,26	1,24	1,58	1,29	1,48
_1309	nuoC	1.6.99.5	NADH dehydrogenase (quinone)	1,01	1,12	1,18	1,35	1,48	1,32	1,43
_1310	0		hypothetical protein	1,04	1,10	1,10	1,16	1,36	1,27	1,47
_1311	nuoD	1.6.99.5	NADH dehydrogenase (quinone)	-1,01	1,05	1,15	1,17	1,28	1,22	1,41
_1312	0		hypothetical protein	-1,02	1,03	1,18	1,58	1,40	1,32	1,55
_1313	nuoE	1.6.5.3, 1.6.99.5	NADH:ubiquinone reductase (H+-translocating),NADH dehydrogenase (quinone)	-1,01	1,01	1,21	1,39	1,21	1,31	1,43
_1314	0		hypothetical protein	-1,04	-1,00	1,15	1,27	1,06	1,02	1,03
_1315	0		hypothetical protein	1,01	-1,00	1,06	1,28	1,06	1,22	1,19
_1316	nuoF	1.6.5.3, 1.6.99.5	NADH:ubiquinone reductase (H+-translocating),NADH dehydrogenase (quinone)	-1,02	1,00	1,08	1,00	1,13	1,15	1,22
_1317	0		hypothetical protein	1,01	1,00	1,11	1,26	1,24	1,20	1,49
_1318	0		hypothetical protein	1,03	-1,02	1,09	1,12	1,18	1,20	1,32
_1319	0		hypothetical protein	1,03	1,01	-1,00	1,03	1,23	1,31	1,15
_1320	nuoG	1.6.5.3, 1.6.99.5	NADH:ubiquinone reductase (H+-translocating),NADH dehydrogenase (quinone)	1,00	1,01	1,04	1,17	1,09	1,17	1,20
_1321	nuoH	1.6.99.5	NADH dehydrogenase (quinone)	1,03	1,17	1,28	1,54	1,53	1,39	1,85
_1322	nuoI	1.6.99.5	NADH dehydrogenase (quinone)	1,04	1,10	1,11	1,18	1,62	1,22	1,8
_1323	0		carboxymuconolactone decarboxylase	1,02	1,15	1,17	1,28	1,8	1,34	1,83
_1324	nuoJ	1.6.99.5	NADH dehydrogenase (quinone)	-1,01	1,04	1,14	1,35	1,40	1,25	1,58
_1325	0		hypothetical protein	1,02	1,05	1,10	1,35	1,22	1,28	1,56
_1326	nuoK	1.6.99.5	NADH dehydrogenase (quinone)	1,01	1,09	1,12	1,41	1,39	1,40	1,75
_1327	nuoL	1.6.99.5	NADH dehydrogenase (quinone)	-1,03	1,07	1,18	1,13	1,28	1,20	1,59
_1328	nuoM	1.6.5.3, 1.6.99.5	NADH:ubiquinone reductase (H+-translocating),NADH dehydrogenase (quinone)	-1,02	1,04	1,06	1,09	1,29	1,20	1,66
_1329	nuoN	1.6.99.5	NADH dehydrogenase (quinone)	-1,03	1,05	1,21	1,43	1,30	1,17	1,68
_1330	0	6.3.4.15	Biotin-[acetyl-CoA-carboxylase] ligase	1,06	-1,01	1,02	1,13	1,47	1,58	1,87
_1331	0	2.7.1.33	pantothenate kinase	-1,01	1,01	-1,02	-1,32	-1,01	1,15	1,45
_1332	0		beta-lactamase domain-containing protein	-1,03	1,01	-1,07	1,06	-1,19	-1,05	1,02
_1333	rhlE		DEAD/DEAH box helicase domain-containing protein	1,11	1,11	1,02	1,07	-1,12	-1,43	1,10
_1334	0		TPR repeat-containing protein	1,03	1,03	1,11	1,43	1,30	1,22	1,29
_1336	prfC		peptide chain release factor 3	1,10	1,08	-1,15	-1,46	-1,34	-1,47	-1,06
_1337	0		hypothetical protein	-1,04	-1,06	-1,29	-1,36	-1,70	-1,27	-1,40
_1338	uspA1		UspA domain-containing protein	1,65	2,55	6,15	10,3	13,6	9,14	5,14
_1339	0	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase	1,02	1,03	-1,14	-1,24	-1,46	-1,72	-1,65
_1340	0		Na+/solute symporter	-1,00	1,00	-1,09	-1,05	-1,43	-1,64	-1,36
_1341	0	3.6.3.30	Fe3+-transporting ATPase	1,02	1,06	1,09	1,13	1,14	-1,04	1,04
_1342	0		helix-turn-helix type 11 domain-containing protein	-1,07	1,01	-1,11	-1,19	-1,16	1,08	-1,01
_1343	0		sec-independent translocation protein mttA/Hcf106	-1,00	1,02	1,04	-1,09	-1,23	-1,60	-1,30
_1344	tatB		twin-arginine translocation protein, TatB subunit	1,02	-1,01	-1,02	-1,13	-1,34	-1,55	-1,29
_1345	tatC		Sec-independent protein translocase, TatC subunit	-1,02	-1,01	-1,03	-1,51	-1,29	-1,28	-1,24
_1346	0		hypothetical protein	-1,05	-1,00	-1,03	-1,12	-1,40	-1,21	-1,44

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_1347	0		hypothetical protein	1,04	-1,01	1,03	1,01	-1,01	1,12	1,20
_1348	0		multiple antibiotic resistance (MarC)-related protein	1,09	1,14	-1,11	1,01	-1,24	-1,86	1,07
_1349	0		ABC transporter related	1,12	1,05	-1,18	-1,17	-1,11	-1,23	1,11
_1350	ndk	2.7.4.6	Nucleoside-diphosphate kinase	1,07	1,11	-1,09	-1,46	-1,79	-2,43	-1,35
_1351	0		hypothetical protein	-1,04	-1,04	-1,18	-1,04	-1,16	-1,09	1,42
_1352	0		TfoX domain-containing protein	-1,09	-1,21	-1,10	1,01	1,06	1,50	1,37
_1353	0		extracellular solute-binding protein	-1,03	-1,03	-1,06	-1,17	-1,26	-1,31	-1,58
_1354	0		binding-protein-dependent transport systems inner membrane component	-1,03	-1,02	-1,00	1,10	-1,28	-1,33	-1,36
_1355	0		binding-protein-dependent transport systems inner membrane component	-1,00	-1,06	-1,01	1,01	-1,07	-1,14	-1,13
_1356	0		hypothetical protein	-1,02	-1,02	-1,02	1,03	-1,04	-1,01	-1,21
_1357	0		ABC transporter related	1,02	-1,01	1,02	-1,04	1,00	1,05	-1,27
_1358	0		short-chain dehydrogenase/reductase SDR	-1,04	-1,01	1,00	1,13	-1,09	1,03	-1,16
_1359	0		hypothetical protein	1,03	1,05	1,30	1,60	1,76	2,03	1,87
_1360	0		hypothetical protein	-1,02	-1,04	1,03	1,06	1,19	1,19	1,09
_1361	dld1	1.1.2.4	D-lactate dehydrogenase (cytochrome)	-1,08	-1,05	1,05	-1,15	-1,02	-1,18	-1,24
_1362	0		putative oxidoreductase	-1,07	-1,07	-1,00	-1,22	-1,10	1,14	-1,47
_1363	pyrD1	1.3.1.2	dihydropyrimidine dehydrogenase (NADP+)	-1,03	-1,03	1,00	1,11	-1,03	1,17	-1,28
_1364	0		hypothetical protein	1,04	-1,00	1,04	1,15	1,34	1,34	1,73
_1365	0		TetR family transcriptional regulator	-1,09	-1,04	1,10	1,06	1,09	1,02	-1,06
_1366	0	2.6.1.18	Beta-alanine-pyruvate transaminase	-1,05	-1,09	1,02	1,13	1,11	1,24	-1,17
_1367	amaB	3.5.1.87	N-carbamoyl-L-amino-acid hydrolase	1,01	-1,04	1,00	-1,13	-1,00	1,25	-1,07
_1368	0		hypothetical protein	1,02	-1,00	1,03	-1,05	-1,30	1,01	-1,22
_1369	0		class II aldolase/adducin family protein	-1,02	-1,01	-1,01	1,09	-1,15	1,03	-1,27
_1370	dht	3.5.2.2	dihydropyrimidinase	1,01	-1,03	1,01	-1,06	-1,31	-1,08	-1,28
_1371	0		ABC transporter related	1,01	-1,01	-1,05	-1,08	-1,15	1,02	-1,12
_1372	0		binding-protein-dependent transport systems inner membrane component	1,03	-1,02	1,01	1,10	-1,02	1,10	-1,01
_1373	0		binding-protein-dependent transport systems inner membrane component	-1,06	-1,02	-1,03	1,09	-1,02	1,23	-1,22
_1374	0		NMT1/THI5-like domain-containing protein	-1,12	-1,10	-1,02	1,03	-1,89	-1,93	-2,76
_1375	0	4.1.1.17	ornithine decarboxylase	1,21	1,08	-1,16	-1,29	-1,27	-1,74	-1,34
_1376	0	3.5.2.10	creatininase	-1,03	1,02	1,11	1,23	1,11	1,17	1,20
_1377	0		2OG-Fe(II) oxygenase	1,03	1,00	-1,00	-1,07	1,18	1,36	1,24
_1378	0	1.6.5.2	NAD(P)H dehydrogenase (quinone)	1,02	1,06	1,13	1,28	1,47	1,58	1,34
_1379	0	1.6.5.2	NAD(P)H dehydrogenase (quinone)	1,00	-1,03	-1,07	-1,01	-1,50	-1,61	-1,35
_1380	0		FAD linked oxidase domain-containing protein	1,01	-1,02	-1,11	-1,08	-1,42	-1,41	-1,28
_1381	0		cytosine deaminase	1,02	1,01	-1,00	-1,17	-1,41	-1,58	-1,34
_1382	0		binding-protein-dependent transport systems inner membrane component	-1,00	-1,03	-1,02	-1,04	-1,18	-1,02	-1,33
_1383	0		ABC transporter related	1,03	-1,05	-1,10	-1,06	-1,17	1,04	-1,07
_1384	0		permease protein of ABC transporter	1,00	-1,07	-1,05	-1,15	-1,13	1,06	-1,26
_1385	0		endoribonuclease L-PSP	-1,04	-1,05	1,04	1,03	1,03	-1,00	1,01
_1386	0		hypothetical protein	-1,01	-1,01	-1,00	-1,22	1,10	1,07	1,18
_1387	clpX		ATP-dependent protease ATP-binding subunit ClpX	-1,05	-1,03	1,03	1,05	-1,11	-1,15	-1,24
_1388	clpP	3.4.21.92	Endopeptidase Clp	-1,05	-1,03	-1,02	-1,15	-1,24	-1,41	-1,44
_1389	0		deoxyribodipyrimidine photo-lyase, putative	-1,06	1,03	1,10	1,09	-1,03	-1,06	1,22
_1390	0	1.6.99.3, 1.6.5.3	NADH dehydrogenase,NADH:ubiquinone reductase (H+-translocating)	1,02	1,13	1,38	1,40	1,8	1,43	1,56
_1391	0		hypothetical protein	1,03	1,02	1,08	1,35	1,33	1,24	1,12
_1392	0		hypothetical protein	1,01	-1,00	1,10	1,27	1,24	1,15	1,16
_1393	0		hypothetical protein	-1,08	-1,02	-1,07	-1,04	-1,02	1,06	-1,18
_1394	aat	2.3.2.6	leucyltransferase	1,02	-1,04	-1,11	-1,04	1,06	1,19	1,17
_1395	accC	6.3.4.14	Biotin carboxylase	1,05	1,01	-1,11	-1,40	-1,27	-1,60	-1,19
_1396	accB		acetyl-CoA carboxylase, biotin carboxyl carrier protein	1,03	1,07	-1,03	-1,03	-1,21	-1,55	-1,14
_1397	0		phospholipase/lecithinase/hemolysin-like protein	-1,26	-1,16	-1,14	-1,31	-2,08	-1,50	-2,31
_1398	0		hypothetical protein	-1,05	-1,07	-1,06	-1,34	-1,64	-1,42	-1,70
_1399	acsA	6.2.1.1	acetate-CoA ligase	-1,02	1,09	1,10	1,24	1,77	1,16	1,82
_1400	0		ABC transporter related	-1,06	-1,09	-1,25	-1,28	-1,31	-1,22	-1,01
_1401	0		ABC transporter related	-1,02	-1,11	-1,15	-1,22	-1,38	-1,37	-1,11
_1402	0		inner-membrane translocator	-1,11	-1,13	-1,28	-1,18	-1,65	-1,30	-1,28
_1403	0		inner-membrane translocator	-1,04	-1,15	-1,15	-1,05	-1,29	-1,39	-1,36

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_1404	0		branched-chain amino acid ABC transporter, periplasmic binding protein, putative	-1,28	-1,28	-1,45	-1,79	-2,06	-1,73	-1,81
_1405	0		XRE family transcriptional regulator	-1,01	1,02	1,03	1,00	1,09	1,22	1,28
_1406	0		response regulator receiver protein	-1,12	-1,09	-1,06	1,00	-1,30	-1,20	-1,83
_1407	0		hypothetical protein	-1,07	-1,10	1,04	-1,02	-1,15	-1,12	-1,62
_1408	0	2.7.13.3	histidine kinase	-1,07	-1,05	1,03	1,04	1,01	-1,08	-1,48
_1409	0		hypothetical protein	1,09	-1,00	1,01	1,11	1,74	1,64	1,74
_1410	0		hypothetical protein	-1,00	-1,00	-1,04	-1,14	-1,04	-1,34	-1,13
_1411	0		TraR/DksA family transcriptional regulator	1,61	2,91	5,63	8,82	12,2	7,57	4,98
_1412	0		hypothetical protein	1,75	3,32	7,3	11,9	16,4	10,3	6,62
_1413	0		extracellular solute-binding protein	-1,12	-1,06	1,09	1,40	1,23	1,12	-1,26
_1414	0		binding-protein-dependent transport systems inner membrane component	1,02	-1,06	-1,05	-1,21	-1,13	1,05	-1,12
_1415	0		binding-protein-dependent transport systems inner membrane component	1,00	-1,05	-1,02	1,06	-1,09	1,01	-1,15
_1416	0		ABC transporter related	-1,09	-1,05	-1,04	-1,13	-1,13	-1,01	-1,18
_1417	0		hypothetical protein	-1,04	-1,05	-1,06	1,06	-1,16	1,07	-1,13
_1418	0		hypothetical protein	1,12	1,01	-1,12	-1,00	-1,10	-1,32	1,10
_1419	0		hypothetical protein	1,06	1,07	-1,11	-1,18	-1,69	-2,33	-1,77
_1420	0		hypothetical protein	1,05	1,01	1,03	1,09	1,59	1,41	1,46
_1421	0		ribose ABC transporter, substrate-binding protein	1,00	-1,05	1,03	1,10	1,07	-1,09	-1,08
_1422	rbsA3	3.6.3.17	Monosaccharide-transporting ATPase	1,05	-1,05	1,04	1,04	1,16	1,07	1,10
_1423	rbsB2		inner-membrane translocator	-1,04	1,05	1,03	1,05	1,04	1,06	1,14
_1424	rbsC1		inner-membrane translocator	1,03	-1,04	-1,02	-1,07	1,12	1,23	1,23
_1425	0	1.2.1.3	aldehyde dehydrogenase (NAD+)	1,02	-1,02	1,11	1,03	1,03	-1,04	1,06
_1426	0	4.2.1.2	fumarate hydratase	-1,06	-1,02	1,14	1,15	1,06	1,19	-1,18
_1427	citF	2.8.3.10, 4.1.3.6	citrate CoA-transferase,citrate (pro-3S)-lyase	-1,04	1,01	1,10	-1,06	1,04	1,12	1,04
_1428	0	1.1.99.1	choline dehydrogenase	-1,03	-1,01	1,01	-1,13	-1,09	-1,04	-1,29
_1429	fabG	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase	-1,00	-1,01	1,04	1,08	1,08	1,15	1,11
_1430	0	1.2.1.3	aldehyde dehydrogenase (NAD+)	1,07	-1,01	-1,03	1,05	1,11	1,20	1,18
_1431	0		LysR family transcriptional regulator	-1,12	-1,06	-1,00	1,16	-1,02	1,09	1,05
_1432	0		L-carnitine dehydratase/bile acid-inducible protein F	1,03	-1,02	-1,05	1,07	1,10	1,28	1,24
_1433	0		hypothetical protein	-1,09	-1,08	1,07	1,12	1,12	1,20	-1,03
_1434	0		Xaa-Pro dipeptidase	1,00	-1,02	1,00	-1,04	1,08	1,14	1,14
_1435	0		alpha/beta hydrolase fold	-1,04	1,00	1,01	1,18	-1,06	-1,05	-1,11
_1436	0		binding-protein-dependent transport systems inner membrane component	-1,00	1,07	1,03	-1,03	1,08	1,11	1,11
_1437	0	3.6.3.32	Quaternary-amine-transporting ATPase	-1,05	-1,01	1,12	-1,00	1,10	1,03	1,08
_1438	0		substrate-binding region of ABC-type glycine betaine transport system	-1,04	-1,05	-1,02	1,08	1,16	1,21	1,14
_1439	0	4.4.1.15, 3.5.99.7	D-cysteine desulfhydrase,1-aminocyclopropane-1-carboxylate deaminase	-1,04	-1,05	1,19	-1,09	1,12	1,22	1,18
_1440	0		LysR family transcriptional regulator	-1,09	-1,01	1,06	-1,31	-1,06	1,47	1,13
_1441	0		hypothetical protein	-1,02	-1,06	-1,13	-1,05	-1,14	1,10	-1,20
_1442	0		peroxidase	-1,02	-1,07	-1,16	-1,18	-1,44	-1,26	-1,65
_1443	0		TRAP transporter solute receptor TAXI family protein	-1,12	-1,16	-1,21	-1,41	-2,45	-2,12	-2,75
_1444	0		TRAP transporter, 4TM/12TM fusion protein	-1,05	-1,10	-1,13	-1,42	-1,48	-1,45	-1,74
_1445	uspG		UspA domain-containing protein	-1,04	-1,09	-1,10	-1,12	-1,35	-1,37	-1,56
_1446	0		hypothetical protein	-1,05	-1,06	-1,06	-1,12	-1,41	-1,09	-1,64
_1447	0		transposase	-1,01	-1,02	1,04	-1,12	-1,02	1,10	1,05
_1448	0		HTH-type transcriptional regulator ZntR	-1,08	-1,01	1,06	1,23	1,16	1,29	1,07
_1449	0		TonB-dependent receptor	1,00	-1,00	1,22	1,07	3,28	4,25	3,83
_1450	0		NnrS family protein	1,02	-1,02	1,12	1,27	4,84	4,88	3,5
_1451	ssuB2		ABC transporter related	-1,11	-1,06	1,45	1,92	5,53	5,19	4,14
_1452	ssuC2		binding-protein-dependent transport systems inner membrane component	1,09	1,05	1,45	1,73	6,44	6,18	4,21
_1453	ssuA2		putative sulfonate/nitrate transport system substrate-binding protein	1,07	1,16	1,98	4,09	11,5	9,82	7,66
_1454	0		hypothetical protein	1,24	1,25	2,74	7,97	16,4	11,9	7,56
_1455	0		transposase	1,03	-1,01	1,00	1,15	1,15	1,16	1,29
_1456	0		integrase catalytic region	-1,06	-1,00	-1,09	1,01	1,10	1,26	1,24
_1457	0	3.1.21.5	type III site-specific deoxyribonuclease	-1,01	-1,01	-1,00	1,11	1,23	1,19	1,35
_1458	0		phage integrase family site specific recombinase	-1,04	-1,01	-1,07	1,03	-1,15	-1,03	-1,39

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_1459	0		hypothetical protein	-1,02	1,02	1,05	-1,01	1,07	1,12	1,17
_1460	rplU		50S ribosomal protein L21/unknown domain fusion protein	1,14	1,11	-1,13	-1,32	-1,73	-2,48	-1,29
_1461	rpmA		50S ribosomal protein L27	1,07	1,07	-1,17	-1,36	-1,96	-2,42	-1,43
_1462	0		amino acid transporter LysE	-1,00	1,03	-1,22	-1,06	-1,57	-2,33	-1,66
_1463	0		GCN5-related N-acetyltransferase	-1,04	-1,05	-1,18	-1,13	-1,25	-1,86	-1,51
_1464	0		GCN5-related N-acetyltransferase	-1,04	-1,04	-1,13	1,01	-1,14	-1,26	-1,26
_1465	0		GCN5-related N-acetyltransferase	-1,02	-1,02	-1,01	1,11	1,05	-1,25	1,01
_1466	obgE		GTPase ObgE	1,05	1,07	-1,00	1,04	-1,12	-1,58	-1,12
_1467	proB	2.7.2.11	glutamate 5-kinase	-1,01	1,07	-1,06	-1,10	-1,15	-1,31	-1,22
_1468	0		hypothetical protein	1,04	-1,01	-1,11	-1,27	-1,14	-1,07	-1,10
_1469	proA	1.2.1.41	glutamate-5-semialdehyde dehydrogenase	1,07	1,06	-1,09	-1,41	-1,41	-1,84	-1,18
_1470	0		hypothetical protein	-1,02	-1,06	1,00	1,10	-1,32	-1,52	-1,33
_1471	0		hypothetical protein	1,07	1,01	-1,08	-1,13	1,01	1,04	1,09
_1472	0		phospholipid/glycerol acyltransferase	1,02	1,03	-1,02	1,01	1,05	-1,05	1,05
_1473	0		phospholipid/glycerol acyltransferase	-1,15	-1,03	1,01	-1,12	-1,17	-1,18	-1,02
_1474	0	6.1.1.-	glutamyl-tRNA synthetase	1,04	1,02	1,04	-1,00	-1,04	1,01	1,14
_1475	gid	2.1.1.74	methyl enetetrahydrofolate-tRNA-(uracil54-C5)-methyltransferase (FADH2-oxidizing)	1,09	1,06	1,12	1,02	-1,11	-1,08	-1,05
_1476	gyrA	5.99.1.3	DNA topoisomerase (ATP-hydrolysing)	-1,02	1,03	1,02	1,04	1,11	1,14	1,04
_1477	0		Usg family protein	1,19	-1,05	-1,00	1,02	2,02	2,29	1,49
_1478	0		disulphide bond formation protein DsbB	-1,04	1,02	1,06	-1,16	-1,10	-1,10	-1,17
_1479	0		exopolysaccharide synthesis ExoD	-1,05	-1,04	-1,05	-1,06	-1,11	-1,00	1,00
_1480	0		TRAP dicarboxylate transporter- DctP subunit	-1,05	-1,07	-1,13	-1,46	-1,76	-1,39	-1,79
_1481	0		hypothetical protein	-1,01	-1,02	-1,15	-1,27	-1,30	-1,35	-1,18
_1482	0		TRAP dicarboxylate transporter, DctM subunit	1,03	-1,00	-1,06	-1,13	-1,34	-1,56	-1,16
_1483	0		hypothetical protein	1,01	1,01	-1,04	-1,15	1,05	1,05	1,93
_1484	0		hypothetical protein	1,02	-1,06	-1,02	1,17	1,16	1,26	1,15
_1485	0		FAD dependent oxidoreductase	1,08	-1,06	-1,06	-1,06	-1,01	1,24	1,03
_1486	0		BCCT transporter	-1,05	-1,00	-1,12	-1,33	-1,93	-1,84	-1,85
_1487	0		oligopeptide/dipeptide ABC transporter, ATPase subunit	-1,02	1,00	-1,04	1,06	-1,30	-1,37	-1,19
_1488	0		binding-protein-dependent transport systems inner membrane component	-1,04	-1,03	1,03	1,10	-1,39	-1,42	-1,32
_1489	0		binding-protein-dependent transport systems inner membrane component	-1,01	-1,02	-1,01	-1,15	-1,62	-1,53	-1,54
_1490	0		extracellular solute-binding protein	-1,10	-1,07	-1,17	-1,31	-1,66	-1,8	-1,76
_1491	0		AraC family transcriptional regulator	-1,02	-1,02	1,03	1,09	1,11	1,30	1,07
_1492	miaA	2.5.1.75	tRNA dimethylallyl transferase	1,02	-1,01	1,05	1,04	-1,04	1,04	1,04
_1493	pyrH	2.7.4.22	UMP kinase	1,02	1,01	-1,04	1,02	1,01	-1,15	-1,09
_1494	frr		ribosome recycling factor	1,03	1,04	-1,09	-1,28	-1,26	-1,58	-1,19
_1495	uppS	2.5.1.31	ditrans,polycis-undecaprenyl-diphosphate synthase [(2E,6E)-farnesyl-diphosphate specific]	-1,01	-1,03	-1,05	-1,23	-1,10	-1,02	1,18
_1496	cdsA1	2.7.7.41	phosphatidate cytidylyltransferase	-1,04	-1,03	1,08	1,02	-1,08	1,08	1,33
_1497	dxr	1.1.1.267	1-deoxy-D-xylulose-5-phosphate reductoisomerase	1,00	1,01	-1,02	-1,11	-1,11	-1,08	-1,00
_1498	ecfE	3.4.24.-	putative membrane-associated zincmetalloprotease"	1,03	-1,00	-1,11	-1,21	-1,05	1,05	1,32
_1499	yaeT		surface antigen (D15)	1,03	1,02	-1,09	-1,39	-1,23	-1,49	-1,18
_1500	0		outer membrane chaperone Skp (OmpH)	1,01	-1,01	-1,04	1,04	-1,20	-1,17	-1,11
_1501	fabZ	4.2.1.59	3-hydroxyacyl-[acyl-carrier-protein] dehydratase	1,09	1,10	-1,10	-1,28	-1,41	-2,14	-1,32
_1502	lpxA	2.3.1.129	acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase	1,06	1,04	-1,21	-1,44	-1,79	-1,98	-1,43
_1503	0		hypothetical protein	1,05	-1,01	-1,10	-1,24	-1,41	-1,51	-1,25
_1504	lpxB	2.4.1.182	lipid-A-disaccharide synthase	1,06	1,00	-1,09	-1,42	-1,60	-1,42	-1,25
_1505	0		hypothetical protein	-1,12	-1,05	1,05	-1,08	-1,12	-1,22	-1,38
_1506	mnmA	2.8.1.-	Putative sulfurtransferase DsrE	1,02	1,02	-1,11	-1,16	1,03	-1,09	1,04
_1507	0		hypothetical protein	1,07	1,01	1,10	1,04	1,49	1,58	1,85
_1508	ctrA		two component transcriptional regulator	-1,02	-1,03	-1,12	-1,29	1,03	1,21	1,24
_1509	ligA	6.5.1.2	DNA ligase (NAD+)	1,00	1,00	-1,07	-1,17	-1,14	-1,35	-1,14
_1510	recG	3.6.1.-	ATP-dependent DNA helicase RecG	1,00	-1,05	1,09	1,10	-1,19	-1,19	-1,05
_1511	0	3.4.17.19	Carboxypeptidase Taq	1,03	1,02	1,03	-1,22	-1,33	-1,27	-1,09
_1512	0			1,05	1,08	1,09	1,10	-1,02	-1,22	1,06
_1513	0		tRNA/rRNA methyltransferase (SpoU)	1,09	1,05	-1,08	1,00	-1,12	-1,39	-1,03
_1514	0		thiamine monophosphate synthase	1,06	1,13	1,01	1,11	-1,08	-1,36	1,14

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_1515	hisI	3.5.4.19	phosphoribosyl-AMP cyclohydrolase	1,12	1,05	-1,05	-1,24	-1,01	-1,23	1,10
_1516	0		NifU domain-containing protein	-1,03	-1,01	-1,00	-1,03	-1,00	1,13	-1,06
_1517	0		inner-membrane translocator	-1,00	-1,02	-1,07	-1,01	-1,47	-1,48	-1,51
_1518	0		inner-membrane translocator	-1,06	-1,03	-1,02	1,06	-1,63	-1,78	-1,92
_1519	0		hypothetical protein	-1,02	-1,03	-1,12	-1,23	-1,66	-1,67	-1,63
_1520	livF2		ABC transporter related	1,00	1,00	-1,10	-1,32	-1,41	-1,55	-1,38
_1521	0		ABC transporter related	1,02	-1,03	-1,26	-1,49	-2,15	-2,25	-2,12
_1522	0		extracellular ligand-binding receptor	-1,12	-1,11	-1,16	-1,33	-2,71	-2,4	-2,71
_1523	yliI		glucose sorbosone dehydrogenase	1,07	1,01	1,06	1,09	1,00	1,11	1,11
_1524	0		hypothetical protein	-1,04	-1,01	1,11	-1,08	-1,02	-1,01	1,15
_1525	0		AraC family transcriptional regulator	-1,09	-1,05	1,06	1,16	1,12	1,14	-1,11
_1526	aroH	2.5.1.54	3-deoxy-7-phosphoheptulonate synthase	1,05	1,08	-1,02	-1,01	-1,09	-1,63	-1,38
_1527	0		hypothetical protein	-1,01	-1,04	-1,12	-1,11	-1,06	-1,01	1,08
_1528	0		hypothetical protein	1,03	-1,00	-1,07	-1,07	-1,08	1,06	-1,00
_1529	gmk	2.7.4.8	guanylate kinase	1,05	1,08	-1,10	-1,02	-1,22	-1,65	-1,13
_1530	0		hexapaptide repeat-containing transferase	1,06	1,07	-1,06	-1,24	-1,51	-1,89	-1,29
_1531	0		hypothetical protein	-1,05	-1,05	-1,05	-1,09	1,04	-1,03	-1,35
_1532	phoR	2.7.13.3	histidine kinase	1,02	1,03	-1,00	1,26	1,08	-1,19	1,12
_1533	0		phosphate ABC transporter, periplasmic phosphate-binding protein	1,01	1,02	-1,16	-1,37	-2,78	-3,04	-2,12
_1534	pstC		phosphate ABC transporter, inner membrane subunit PstC	-1,03	1,04	-1,24	-1,26	-3,27	-3,41	-2,46
_1535	pstA		phosphate ABC transporter, inner membrane subunit PstA	1,00	1,02	-1,09	-1,04	-1,99	-2,12	-1,84
_1536	pstB	3.6.3.27	Phosphate-transporting ATPase	-1,03	-1,02	-1,07	-1,26	-1,40	-1,56	-1,48
_1537	phoU		phosphate uptake regulator, PhoU	-1,01	1,02	-1,10	-1,04	-1,62	-1,97	-1,66
_1538	phoB		two component transcriptional regulator	1,03	-1,06	-1,06	-1,03	-1,53	-1,83	-1,47
_1539	0		CaCA family Na(+)/Ca(+) antiporter	1,00	-1,02	1,02	-1,14	1,14	1,20	1,25
_1540	0		2-alkenal reductase	1,03	-1,00	-1,05	1,06	-1,03	1,18	1,14
_1541	0		amidohydrolase 3	-1,09	-1,05	-1,01	1,07	-1,01	1,01	-1,16
_1542	0		hypothetical protein	-1,07	-1,00	1,14	-1,01	1,06	1,21	1,08
_1543	0		patatin	1,03	1,06	1,04	1,00	1,04	-1,11	1,07
_1544	0	1.1.1.30	3-hydroxybutyrate dehydrogenase	-1,03	1,09	1,07	1,01	1,11	-1,22	-1,11
_1545	0		extracellular solute-binding protein	-1,12	-1,01	-1,03	1,13	1,02	1,02	-1,07
_1546	0		hypothetical protein	1,05	1,02	-1,10	-1,05	1,01	-1,01	1,21
_1547	0		ribokinase-like domain-containing protein	1,08	1,02	-1,08	-1,18	-1,26	-1,27	-1,14
_1548	rpsB		30S ribosomal protein S2	1,12	1,13	-1,17	-1,56	-2,03	-3,64	-1,78
_1549	tsf		elongation factor Ts	1,03	1,11	-1,23	-1,58	-3,38	-5,11	-2,7
_1550	0		LuxR family transcriptional regulator	1,02	1,01	1,01	-1,09	-1,04	1,22	1,03
_1551	0	4.2.1.10	3-dehydroquinate dehydratase	-1,02	-1,04	-1,07	-1,05	1,02	1,21	1,03
_1552	0		type III effector Hrp-dependent outers	-1,10	-1,02	-1,06	1,07	-1,20	-1,17	-1,44
_1553	0		putative aldolase	-1,04	1,01	-1,01	1,01	-1,16	-1,36	-1,43
_1554	0	5.3.1.22	Hydroxypyruvate isomerase	-1,04	1,00	-1,01	-1,08	-1,15	-1,07	-1,24
_1555	0		XRE family transcriptional regulator	-1,08	-1,06	1,03	1,13	1,05	1,03	-1,21
_1556	0		AMP-dependent synthetase and ligase	1,02	1,02	-1,01	-1,03	-1,15	-1,20	1,01
_1557	0		DSBA oxidoreductase	1,09	1,01	-1,19	-1,31	-1,48	-1,71	-1,24
_1558	0		hypothetical protein	1,01	1,04	1,19	1,48	2,87	4,38	4,32
_1559	0		Bcr/CflA subfamily drug resistance transporter	1,00	1,02	-1,07	-1,03	-1,28	-1,43	-1,10
_1560	0		hypothetical protein	-1,02	-1,03	1,10	1,15	1,33	1,46	1,30
_1561	mfd		transcription-repair coupling factor	1,08	1,04	-1,16	-1,15	-1,35	-1,51	-1,08
_1562	0		hypothetical protein	1,04	1,06	-1,03	1,03	-1,13	-1,39	-1,15
_1563	hemB1	4.2.1.24	porphobilinogen synthase	-1,04	1,01	-1,02	-1,00	-1,22	-1,33	-1,25
_1564	0		twin-arginine translocation pathway signal	1,02	1,02	-1,03	-1,23	-1,09	-1,19	-1,11
_1565	0	3.5.1.11	penicillin amidase	1,02	1,03	-1,08	-1,16	-1,21	-1,27	-1,09
_1566	hflX		GTP-binding protein HSR1-related	1,06	-1,07	1,01	-1,07	-1,05	1,13	-1,01
_1568	trkH		cation transporter	-1,04	-1,07	-1,04	1,01	1,02	1,01	1,02
_1569	trkA		potassium transporter peripheral membrane component	1,01	1,03	-1,07	-1,22	-1,14	-1,17	-1,03
_1570	0		hypothetical protein	-1,06	-1,04	1,08	1,06	-1,04	-1,01	-1,30
_1571	0		hypothetical protein	-1,05	-1,07	1,05	-1,03	1,06	1,14	-1,09
_1572	ntrX		two component, sigma54 specific, Fis family transcriptional regulator	-1,02	1,03	1,01	-1,07	-1,42	-1,20	-1,07
_1573	ntrY	2.7.13.3	histidine kinase	1,02	-1,02	-1,00	-1,05	-1,01	1,19	1,11

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_1574	ntrC		two component, sigma54 specific, Fis family transcriptional regulator	-1,01	-1,06	1,10	1,06	1,19	1,22	1,21
_1575	ntrB	2.7.13.3	histidine kinase	1,04	1,05	-1,00	-1,13	1,23	1,43	1,24
_1576	dus			1,02	1,03	1,11	1,32	1,30	1,28	1,23
_1577	ispDF	4.6.1.12	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	1,06	1,05	-1,04	-1,11	-1,29	-1,63	-1,22
_1578	0		phosphatidylglycerophosphatase A	1,04	1,02	-1,02	-1,10	-1,42	-1,68	-1,12
_1579	0		CinA domain-containing protein	-1,03	-1,03	-1,01	-1,03	-1,27	-1,40	-1,11
_1580	0		cyclase/dehydrase	1,10	1,14	1,21	1,31	1,73	1,36	1,75
_1581	hpt	2.4.2.8	hypoxanthine phosphoribosyl transferase	-1,08	-1,00	1,03	-1,03	-1,06	-1,11	-1,16
_1582	0		hypothetical protein	1,02	-1,03	-1,02	1,15	1,04	1,09	1,06
_1583	lipA	2.8.1.8	lipoyl synthase	1,15	1,10	1,25	1,67	3,27	1,66	2,75
_1584	0		hypothetical protein	1,00	-1,01	-1,01	1,01	1,01	-1,22	-1,43
_1585	0		hypothetical protein	1,00	-1,00	-1,10	1,15	1,04	1,02	1,15
_1586	mttb		trimethylamine methyltransferase	-1,01	-1,04	1,13	1,03	1,08	1,04	1,12
_1587	guaA	6.3.5.2	GMP synthase (glutamine-hydrolysing)	1,04	1,05	-1,13	-1,43	-1,37	-1,93	-1,30
_1588	0		hypothetical protein	1,05	1,01	-1,02	-1,06	-1,30	-1,51	-1,35
_1589	0		hypothetical protein	1,02	-1,02	1,04	-1,22	-1,26	-1,28	-1,18
_1590	0		membrane protein involved in aromatic hydrocarbon degradation	-1,35	-1,27	-1,41	-1,71	-2,71	-2,11	-2,51
_1591	0		hypothetical protein	-1,13	-1,03	1,00	-1,04	-1,12	-1,30	-1,08
_1592	0		hypothetical protein	1,18	1,19	-1,18	-1,05	-1,56	-2,21	-1,36
_1593	metA	2.3.1.46	homoserine O-succinyl transferase	1,06	1,05	-1,19	-1,40	-1,40	-1,54	-1,22
_1595	0		hypothetical protein	-1,01	-1,04	-1,09	-1,49	-1,18	-1,04	-1,17
_1596	0		TetR family transcriptional regulator	-1,01	1,00	1,01	1,00	-1,13	1,02	-1,29
_1597	potA1	3.6.3.31	Polyamine-transporting ATPase	-1,05	-1,02	1,01	-1,06	-1,15	-1,13	-1,15
_1598	0		binding-protein-dependent transport systems inner membrane component	-1,06	-1,07	-1,07	-1,11	-1,06	-1,15	-1,12
_1599	potB		binding-protein-dependent transport systems inner membrane component	-1,00	-1,03	-1,06	-1,00	-1,00	-1,06	-1,15
_1600	0		antibiotic biosynthesis monooxygenase	1,02	1,05	1,14	1,08	-1,25	-1,59	-1,19
_1601	rpsI		30S ribosomal protein S9	1,09	1,11	-1,20	-1,64	-2,14	-4,21	-2,27
_1602	rplM		50S ribosomal protein L13	1,15	1,14	-1,20	-1,59	-2	-4	-2,14
_1603	0		thioesterase superfamily protein	-1,10	1,00	1,08	1,13	-1,07	-1,16	-1,38
_1604	0		enoyl-CoA hydratase	-1,06	-1,04	-1,06	-1,13	-1,52	-1,74	-1,63
_1605	0		lytic transglycosylase catalytic	-1,02	1,01	1,06	1,05	1,24	1,11	1,16
_1606	ssb		single-strand binding protein	-1,02	-1,02	-1,10	-1,20	-1,38	-1,51	-1,42
_1607	0		hypothetical protein	-1,01	-1,02	-1,10	-1,06	-1,13	-1,07	-1,27
_1608	aroB	4.2.3.4	3-dehydroquinate synthase	1,05	1,07	-1,10	-1,09	-1,32	-1,52	-1,26
_1609	aroK	2.7.1.71	shikimate kinase	-1,01	1,00	-1,04	1,03	-1,11	-1,28	-1,03
_1610	0		hypothetical protein	1,00	-1,03	-1,04	1,05	-1,06	-1,17	-1,05
_1611	xerD		integrase family protein	1,00	1,01	-1,01	-1,19	-1,30	-1,15	-1,17
_1612	0		hypothetical protein	-1,02	-1,03	1,02	1,13	1,28	1,30	1,10
_1613	0		hypothetical protein	1,04	1,04	-1,01	-1,24	-1,17	-1,43	-1,19
_1614	yjgR		protein of unknown function DUF853 NPT hydrolase putative	-1,03	1,00	-1,01	1,14	1,14	1,17	1,15
_1615	0		invasion associated locus B family protein	1,08	1,05	-1,30	-1,79	-1,78	-2,72	-1,34
_1616	0		Beta-ketoacyl synthase	1,06	1,08	-1,01	1,04	-1,15	-1,08	-1,29
_1617	0		phosphopantetheine-binding	1,06	1,08	-1,02	-1,02	-1,16	-1,24	-1,07
_1618	lpxD	2.3.1.-	UDP-3-O-[3-hydroxymyristoyl] glucosamineN-acyltransferase"	-1,01	-1,01	-1,03	-1,13	1,12	1,03	1,07
_1619	0		peptidoglycan binding domain-containing protein	-1,05	1,00	1,10	1,07	1,71	1,41	1,37
_1620	0		hypothetical protein	1,06	1,07	1,02	-1,16	1,01	1,15	1,29
_1621	0	2.7.1.11	6-phospho fructokinase	-1,00	-1,00	-1,07	-1,02	-1,09	-1,05	1,47
_1622	0		hypothetical protein	1,08	1,02	1,02	1,01	1,10	-1,24	1,85
_1623	sufS	2.8.1.7, 4.4.1.16	cysteine desulfurase,selenocysteine lyase	1,01	-1,02	-1,03	1,03	-1,04	-1,12	1,08
_1624	0		hypothetical protein	1,00	-1,02	1,05	1,19	1,00	-1,10	1,16
_1625	0		hypothetical protein	-1,05	-1,09	-1,14	-1,05	-1,82	-1,69	-1,26
_1626	sufD		SufBD protein	-1,03	-1,07	-1,19	-1,33	-2,42	-2,28	-1,21
_1627	sufC		FeS assembly ATPase SufC	-1,04	-1,07	-1,25	-1,21	-2,24	-2,08	-1,13
_1628	0		hypothetical protein	-1,00	-1,10	-1,26	-1,58	-1,82	-1,87	-1,15
_1629	0		hypothetical protein	1,00	-1,13	-1,27	-1,13	-1,8	-1,63	-1,05
_1630	0		hypothetical protein	1,01	-1,10	-1,21	-1,19	-1,54	-1,66	1,08

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_1631	sufB		cysteine desulfurase activator complex subunit SufB	-1,06	-1,12	-1,30	-1,39	-1,51	-1,57	1,07
_1632	nifS	2.8.1.7	cysteine desulfurase	-1,01	-1,06	-1,27	-1,47	-1,31	-1,62	-1,02
_1633	iscR		BadM/Rrf2 family transcriptional regulator	-1,00	-1,08	-1,30	-1,16	-1,29	-1,41	1,32
_1634	0		hypothetical protein	1,11	1,15	-1,08	-1,18	-1,43	-1,91	-1,17
_1635	0		hypothetical protein	1,12	1,10	-1,10	-1,60	-1,64	-1,85	-1,25
_1636	0		hypothetical protein	1,03	1,02	1,14	1,23	1,20	1,09	1,16
_1637	0		hypothetical protein	-1,06	1,01	-1,02	1,02	-1,04	-1,12	1,04
_1638	emrE		small multidrug resistance protein	-1,04	1,03	1,08	1,15	-1,03	-1,00	-1,18
_1639	0		hypothetical protein	-1,11	-1,08	1,03	-1,11	-1,13	1,01	-1,38
_1640	0		hypothetical protein	-1,08	-1,06	-1,00	-1,39	-1,06	1,05	-1,16
_1641	0		hypothetical protein	-1,07	-1,02	-1,06	-1,08	-1,62	-1,94	-1,55
_1642	alaS	6.1.1.7	Alanine-tRNA ligase	1,06	1,09	-1,05	-1,18	-1,21	-1,94	-1,15
_1643	recA		recombinase A	1,02	-1,02	-1,08	-1,17	-1,11	-1,02	1,04
_1644	0	2.7.13.3	histidine kinase	1,03	-1,03	-1,05	-1,22	1,22	1,04	1,04
_1645	rsmB2		Fmu (Sun) domain-containing protein	1,03	1,02	-1,00	-1,02	-1,41	-1,67	-1,31
_1646	guaB	1.1.1.205	IMP dehydrogenase	1,22	1,15	-1,02	-1,08	-1,28	-2,26	-1,35
_1647	hpcH	4.1.2.-	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase	-1,06	-1,01	-1,05	1,02	-1,03	-1,19	-1,36
_1648	malK	3.6.3.19	maltose-transporting ATPase	-1,02	-1,03	-1,08	-1,23	-1,35	-1,59	-1,85
_1649	0	3.2.1.20	alpha-glucosidase	1,02	-1,08	-1,05	1,05	-1,19	-1,47	-1,56
_1650	0		binding-protein-dependent transport systems inner membrane component	-1,01	-1,10	-1,15	-1,10	-1,83	-2,05	-1,93
_1651	0		binding-protein-dependent transport systems inner membrane component	-1,04	-1,13	-1,25	-1,35	-2,1	-2,04	-2,15
_1652	0		extracellular solute-binding protein	-1,06	-1,12	-1,34	-1,59	-2,4	-2,07	-2,79
_1653	0		LacI family transcription regulator	-1,12	-1,11	-1,03	-1,02	-1,06	1,01	-1,25
_1654	bglA	3.2.1.21	beta-glucosidase	1,04	-1,03	-1,10	-1,37	-1,11	1,16	-1,24
_1655	glk	2.7.1.2	glucokinase	-1,27	-1,14	-1,11	-1,17	-1,83	-1,37	-1,73
_1656	0		ABC-3 protein	1,02	1,03	1,12	1,27	1,02	-1,33	-1,13
_1657	0		ABC-3 protein	1,09	1,06	1,10	1,27	-1,01	-1,14	-1,12
_1658	0		ABC transporter related	1,07	1,19	1,13	1,05	1,03	-1,34	-1,05
_1659	0		periplasmic solute binding protein	1,12	1,16	1,17	1,43	1,06	-1,41	-1,07
_1660	0		BadM/Rrf2 family transcriptional regulator	1,73	3,15	4,42	5,29	8,77	6,06	3,69
_1661	0		response regulator receiver/ANTAR domain-containing protein	1,00	1,01	1,03	-1,08	1,09	1,07	1,18
_1662	0		putative nitrate transport protein	-1,03	1,01	-1,00	-1,07	1,08	1,08	1,15
_1663	0		nitrate transporter substrate-binding	-1,01	-1,03	1,01	1,04	1,13	1,05	1,15
_1664	0		binding-protein-dependent transport systems inner membrane component	1,01	1,09	1,03	-1,00	1,16	1,14	1,21
_1665	0		nitrate ABC transporter, ATPase subunits C and D	-1,06	-1,06	1,04	1,15	1,03	1,08	-1,04
_1666	0		globin	1,09	-1,00	-1,04	1,16	1,44	1,70	1,45
_1667	nasD	1.7.1.4	nitrite reductase [NAD(P)H]	1,01	1,01	1,09	1,23	1,21	1,20	1,36
_1668	nasE	1.7.1.4	nitrite reductase [NAD(P)H]	1,01	-1,05	1,04	1,23	1,13	1,09	1,24
_1669	nasA	1.7.99.4	nitrate reductase	-1,10	1,08	1,16	1,05	-1,03	1,20	1,03
_1670	0		hypothetical protein	-1,05	1,02	1,03	1,29	1,03	1,11	1,21
_1671	cysG	2.1.1.107, 4.99.1.4, 1.3.1.76	uroporphyrinogen-III C-methyltransferase,sirohydrochlorin ferrochelatase,precorrin-2 dehydrogenase	1,13	1,02	1,03	-1,16	1,13	1,17	1,24
_1672	0	2.1.1.166	23S rRNA (uridine2552-2-O)-methyltransferase	-1,00	-1,01	-1,10	-1,14	-1,19	-1,11	-1,11
_1673	0	3.6.1.11, 3.6.1.40	exopolyphosphatase,guanosine-5-triphosphate,3-diphosphate phosphatase	1,01	-1,00	-1,07	-1,02	-1,04	1,01	1,07
_1675	0		MetF protein-like protein	-1,22	-1,27	-1,46	-1,61	-1,44	-1,62	-1,47
_1676	0		HAD family hydrolase	-1,06	-1,18	-1,37	-1,35	-1,51	-1,57	-1,33
_1677	0		methyltetrahydrofolate:corrinoid/iron-sulfur protein methyltransferase	-1,10	-1,23	-1,30	-1,22	-1,73	-1,81	-1,55
_1678	0		hypothetical protein	-1,07	-1,08	1,02	-1,04	1,14	1,03	1,07
_1679	0		hypothetical protein	1,02	-1,03	1,01	1,01	1,04	1,08	-1,05
_1680	0		ferredoxin	-1,75	-1,85	-1,97	-2,22	-2,86	-2,78	-2,12
_1681	0		thioesterase superfamily protein	1,12	1,07	-1,07	1,03	-1,28	-1,53	-1,06
_1682	pgi	5.3.1.9	Glucose-6-phosphate isomerase	-1,06	-1,05	1,12	1,08	-1,30	-1,38	-1,22
_1683	0	3.1.1.31	6-phospho gluconolactonase	-1,05	-1,11	1,08	1,28	-1,33	-1,25	-1,32
_1684	zwf	1.1.1.49	glucose-6-phosphate dehydrogenase	-1,89	-1,44	-1,16	1,06	-2,81	-2,57	-3,08
_1685	0		radical SAM domain-containing protein	1,04	1,09	1,05	1,12	1,09	-1,27	1,35
_1686	0		transglutaminase domain-containing protein	1,04	1,04	1,01	1,05	1,27	1,48	1,17

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_1687	0		HNH endonuclease	-1,06	-1,06	1,12	1,34	1,43	1,77	1,07
_1688	0		phospholipase/carboxylesterase	1,06	1,12	1,19	1,08	1,21	-1,11	1,22
_1689	0		HhH-GPD family protein	-1,02	1,03	1,07	1,12	-1,00	1,07	1,16
_1690	cobK	1.3.1.54	precorrin-6A reductase	-1,01	-1,03	1,04	1,02	1,10	1,21	1,14
_1691	cbiD		cobalamin (vitamin B12) biosynthesis CbiD protein	-1,06	1,01	1,13	1,06	1,02	1,09	1,16
_1692	cobA1	2.1.1.107	uroporphyrinogen-III C-methyltransferase	1,07	1,09	1,17	1,24	1,53	1,23	1,44
_1693	cobB		cobyrinic acid A,C-diamide synthase	-1,02	-1,01	1,05	-1,03	1,18	1,04	1,33
_1694	0		major facilitator transporter	1,04	1,10	1,27	1,59	1,58	1,31	1,81
_1695	0		hypothetical protein	-1,01	-1,00	-1,01	-1,28	-1,61	-1,70	-1,31
_1696	0	2.3.3.13, 2.3.1.182	2-isopropylmalate synthase,(R)-citramalate synthase	1,02	-1,00	-1,06	-1,32	-1,66	-1,83	-1,45
_1697	0		hypothetical protein	1,01	-1,00	-1,22	-1,67	-2,13	-2,34	-1,66
_1698	cysS	6.1.1.16	Cysteine-tRNA ligase	1,06	1,05	-1,15	-1,23	-1,19	-1,74	-1,09
_1699	0		hypothetical protein	-1,01	1,02	1,07	1,24	1,14	-1,04	1,64
_1700	0		short-chain dehydrogenase/reductase SDR	-1,08	1,01	-1,18	-1,07	-1,05	-1,01	-1,23
_1701	0		ABC-3 protein	-1,03	-1,05	-1,02	1,14	-1,13	-1,03	1,34
_1702	znuC	3.6.3.-	zinc import ATP-binding protein	-1,02	-1,01	-1,01	1,03	-1,12	1,02	1,31
_1703	0		ferric uptake regulator family protein	-1,01	-1,01	1,10	1,13	1,01	1,02	1,38
_1704	0		periplasmic solute binding protein	-1,03	-1,00	-1,06	-1,28	-1,48	-1,37	-1,00
_1705	0		hypothetical protein	1,03	-1,02	1,04	1,19	1,07	1,06	1,41
_1707	0		putative hemolysin	-1,06	-1,01	1,10	-1,01	1,13	1,01	1,17
_1708	0		NERD domain-containing protein	-1,04	1,01	1,03	-1,02	1,04	-1,00	-1,04
_1709	mscS		MscS mechanosensitive ion channel	1,11	1,11	-1,12	-1,18	-1,43	-1,72	-1,24
_1710	0		glutaredoxin-like protein	-1,04	-1,01	1,00	-1,00	-1,25	-1,35	-1,15
_1711	0		hypothetical protein	-1,04	-1,02	-1,03	-1,05	-1,29	-1,28	-1,22
_1712	0		BolA family protein	-1,06	-1,01	-1,04	-1,02	-1,23	-1,30	-1,23
_1713	purL	6.3.5.3	phosphoribosylformyl glycinamidine synthase	1,12	1,13	-1,06	-1,05	-1,32	-1,66	-1,10
_1714	0		ABC transporter related	1,08	1,03	-1,11	-1,03	-1,10	-1,14	1,11
_1715	0		sulfotransferase	-1,09	-1,04	1,03	-1,14	-1,06	-1,01	-1,23
_1716	0		hypothetical protein	1,11	1,04	-1,00	-1,17	-1,18	-1,45	1,00
_1717	0		hypothetical protein	1,01	1,04	1,05	-1,17	-1,01	-1,01	1,20
_1718	rpmF		50S ribosomal protein L32	1,17	1,13	-1,17	-1,40	-1,65	-2,55	-1,47
_1719	plsX	2.3.1.n2	putative glycerol-3-phosphate acyltransferase PlsX	1,12	1,07	-1,15	-1,20	-1,43	-1,82	-1,35
_1720	fabH	2.3.1.180	beta-ketoacyl-[acyl-carrier-protein] synthase III	1,05	1,03	-1,09	-1,54	-1,82	-1,72	-1,42
_1721	ihfA		integration host factor subunit alpha	-1,02	-1,02	-1,04	-1,03	-1,35	-1,31	-1,65
_1722	0		MerR family transcriptional regulator	1,00	-1,02	1,00	-1,03	-1,40	-1,46	-1,50
_1723	0	3.5.4.13	dCTP deaminase	-1,04	-1,04	-1,11	-1,27	-1,39	-1,11	-1,41
_1724	0		segregation and condensation protein B	-1,01	-1,05	-1,06	-1,26	1,02	1,04	-1,08
_1725	0		chromosome segregation and condensation protein ScpA	-1,04	-1,08	1,02	1,01	-1,04	1,05	-1,08
_1726	nagZ	3.2.1.52	Beta-N-acetylhexosaminidase	-1,01	1,00	-1,08	-1,12	-1,01	1,09	1,06
_1727	0		sporulation domain-containing protein	-1,02	-1,03	-1,02	1,10	1,04	-1,18	-1,08
_1728	argS	6.1.1.19	Arginine-tRNA ligase	1,15	1,10	-1,17	-1,42	-1,52	-2,21	-1,40
_1729	0		putative deoxyguanosinetriphosphate triphosphohydrolase	-1,02	-1,02	-1,12	-1,12	-1,02	1,01	1,05
_1730	0		iron-sulfur cluster assembly accessory protein	-1,03	-1,02	1,02	-1,06	1,04	1,27	1,11
_1731	0		hypothetical protein	1,11	1,05	-1,14	-1,19	-1,16	-1,45	1,26
_1732	hemK	2.1.1.-	putative protein methyltransferase	-1,01	-1,00	-1,14	-1,36	-1,62	-1,64	-1,38
_1733	prfA		peptide chain release factor 1	1,16	1,07	-1,07	-1,19	-1,16	-1,40	1,02
_1734	0		hypothetical protein	1,01	-1,00	-1,04	-1,03	-1,20	-1,05	-1,09
_1735	speB	3.5.3.11	agmatinase	-1,00	-1,03	-1,11	-1,16	-1,32	-1,10	-1,34
_1736	0		hypothetical protein	-1,08	-1,01	-1,03	-1,06	-1,32	-1,22	-1,48
_1737	0		hypothetical protein	-1,07	-1,02	-1,03	-1,23	-1,24	-1,30	-1,44
_1738	tktA	2.2.1.1	transketolase	1,12	1,14	-1,12	-1,44	-2,14	-3,5	-1,69
_1739	0		hypothetical protein	-1,05	-1,03	1,08	1,02	1,10	1,37	1,08
_1740	gap2	1.2.1.12	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)	1,72	1,69	1,29	-1,22	1,72	1,56	2,58
_1741	0		hypothetical protein	1,07	1,16	-1,04	-1,32	1,15	1,21	1,48
_1742	gap1	1.2.1.12	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)	-1,70	-1,30	-1,19	1,00	-3,05	-2,36	-2,96
_1743	0		GCN5-related N-acetyltransferase	-1,01	1,01	-1,04	-1,14	1,02	-1,00	1,16
_1744	coaD	2.7.7.3	Pantetheine-phosphate adenylyltransferase	-1,02	-1,01	-1,00	-1,12	-1,14	-1,15	-1,45
_1745	0		signal-transduction protein	-1,08	-1,03	1,06	1,16	-1,03	1,20	-1,04

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_1746	0		LysR family transcriptional regulator	-1,08	-1,00	1,05	1,02	1,08	1,18	-1,16
_1747	mmsA	1.2.1.27	Methylmalonate-semialdehyde dehydrogenase (acylating)	-1,03	1,01	1,04	-1,18	-1,16	-1,13	-1,17
_1748	0		hypothetical protein	-1,05	-1,07	-1,10	-1,25	-1,31	-1,10	-1,03
_1749	0			-1,03	-1,02	1,01	-1,17	-1,09	1,12	-1,08
_1750	0	1.3.99.-	acyl-CoA dehydrogenase	-1,05	-1,02	1,02	-1,13	-1,24	-1,16	-1,12
_1751	0		enoyl-CoA hydratase/isomerase	-1,02	-1,03	-1,05	-1,07	-1,22	-1,11	-1,24
_1752	mmsB	1.1.1.31	3-hydroxyisobutyrate dehydrogenase	-1,04	-1,03	1,00	1,10	-1,27	-1,16	-1,20
_1753	0	4.2.1.17	enoyl-CoA hydratase	-1,23	-1,18	-1,03	-1,00	-1,26	1,01	-1,19
_1755	0		hypothetical protein	-1,03	-1,05	-1,04	-1,08	1,14	1,17	1,26
_1757	0		hypothetical protein	1,05	1,01	1,05	1,05	1,13	1,12	1,28
_1758	ccmE		cytochrome c-type biogenesis protein CcmE	-1,02	1,07	1,18	1,31	1,34	1,14	1,20
_1759	argC	1.2.1.38	N-acetyl-gamma-glutamyl-phosphate reductase	-1,01	1,02	1,06	-1,05	-1,19	-1,31	-1,02
_1760	murI	5.1.1.3	Glutamate racemase	1,04	1,08	-1,02	-1,29	1,05	-1,18	1,02
_1761	0		phospholipid/glycerol acyltransferase	1,09	1,08	1,13	1,16	1,31	1,08	1,48
_1762	0	1.2.7.8	indolepyruvate ferredoxin oxidoreductase	1,13	1,03	-1,15	-1,35	1,40	1,05	1,9
_1763	0		LysR family transcriptional regulator	-1,13	-1,09	-1,18	-1,19	-2,05	-2,18	-1,97
_1764	0		esterase/lipase-like protein	1,04	1,03	-1,03	1,09	1,18	1,10	1,20
_1765	0		ABC transporter related	-1,02	1,04	1,18	1,27	1,47	1,31	1,29
_1766	0		peptidoglycan-binding LysM	-1,04	-1,04	1,05	1,07	1,05	1,17	-1,10
_1767	0		hypothetical protein	1,03	1,02	-1,08	-1,03	1,06	-1,03	1,04
_1768	eda	4.1.2.14, 4.1.3.16	2-dehydro-3-deoxy-phosphogluconate aldolase,4-Hydroxy-2-oxoglutarate aldolase	-1,00	-1,05	1,14	1,25	-1,14	1,01	-1,15
_1769	edd	4.2.1.12	phosphogluconate dehydratase	-1,97	-1,42	-1,07	1,16	-3,28	-3,18	-3,74
_1770	0		hypothetical protein	1,09	1,01	1,14	1,57	2,26	1,76	2,31
_1771	0		hypothetical protein	1,08	1,02	-1,02	-1,05	-1,13	-1,37	1,12
_1772	0		hypothetical protein	-1,02	-1,08	-1,01	1,10	-1,03	-1,06	1,08
_1773	0		peptidase M48 Ste24p	1,02	-1,02	1,01	1,11	1,22	1,46	1,66
_1774	0		hypothetical protein	1,05	1,00	-1,01	-1,01	1,09	1,18	1,13
_1775	0	2.7.7.42	[glutamate-ammonia-ligase] adenylyltransferase	-1,02	-1,03	-1,04	-1,14	1,09	1,09	-1,03
_1776	0		hypothetical protein	-1,02	1,02	-1,05	1,14	1,13	1,43	1,42
_1777	lon	3.4.21.53	Endopeptidase La	-1,04	-1,01	1,01	-1,02	-1,04	1,23	1,22
_1778	0		hypothetical protein	-1,07	-1,06	-1,14	-1,50	-1,09	1,10	-1,31
_1779	ilvI	2.2.1.6	acetolactate synthase	-1,08	-1,03	-1,26	-1,58	-1,85	-2,27	-1,91
_1780	0		hypothetical protein	-1,04	-1,02	-1,15	-1,24	-1,60	-1,66	-1,59
_1781	ilvH		acetolactate synthase 3 regulatory subunit	-1,00	-1,02	-1,18	-1,32	-1,97	-1,86	-1,86
_1782	0		Rieske (2Fe-2S) domain-containing protein	-1,03	1,01	-1,00	1,11	-1,01	1,12	1,08
_1783	0		hypothetical protein	-1,03	-1,01	1,08	1,11	1,17	-1,12	-1,10
_1784	0		ECF subfamily RNA polymerase sigma-24 factor	-1,01	-1,00	-1,00	-1,00	-1,12	1,07	1,04
_1785	nrdJ	1.17.4.1	Ribonucleoside-diphosphate reductase	-1,01	-1,03	-1,14	-1,38	-1,55	1,02	-1,45
_1786	0		hypothetical protein	-1,03	-1,04	-1,03	-1,15	1,11	1,19	1,34
_1787	0		hypothetical protein	1,00	-1,05	-1,10	-1,10	1,03	1,18	-1,07
_1788	0		cold-shock DNA-binding domain-containing protein	-1,06	-1,04	-1,07	-1,15	-1,29	-1,16	-1,42
_1789	pdxH	1.4.3.5	pyridoxal 5-phosphate synthase	1,12	1,11	-1,15	-1,16	-1,43	-1,9	-1,26
_1790	fabI2	1.3.1.9	enoyl-[acyl-carrier-protein] reductase (NADH)	1,16	1,13	1,07	-1,03	1,12	-1,58	1,22
_1791	0		lysine exporter protein LysE/YggA	1,04	1,01	1,03	-1,09	-1,25	-1,55	-1,03
_1792	0		lysine exporter protein LysE/YggA	-1,02	-1,01	1,06	1,04	-1,17	-1,26	-1,09
_1793	gpt	2.4.2.22	xanthine phosphoribosyl transferase	1,00	1,04	-1,00	-1,15	-1,26	-1,53	-1,23
_1794	0		hypothetical protein	-1,00	-1,00	1,03	-1,10	-1,25	-1,26	-1,13
_1795	0	5.2.1.8	Peptidylprolyl isomerase	1,08	1,05	-1,05	-1,16	-1,50	-1,91	-1,35
_1796	trpE	4.1.3.27	anthranilate synthase	1,03	1,03	-1,05	-1,20	-1,27	-1,56	-1,26
_1797	0		protein of unknown function DUF610, YibQ	-1,04	-1,03	-1,01	1,12	1,02	1,06	-1,10
_1798	trpG	4.1.3.27	anthranilate synthase	1,03	1,06	-1,03	-1,12	-1,22	-1,56	-1,18
_1799	trpD	2.4.2.18	anthranilate phosphoribosyl transferase	1,05	-1,00	-1,02	-1,08	-1,21	-1,37	-1,21
_1800	trpC	4.1.1.48	indole-3-glycerol-phosphate synthase	1,00	1,01	-1,03	-1,28	-1,48	-1,71	-1,26
_1801	moaC		molybdenum cofactor biosynthesis protein C	1,00	1,00	-1,05	-1,13	-1,44	-1,38	-1,32
_1802	moeA1		molybdenum cofactor synthesis domain-containing protein	-1,07	-1,01	1,04	-1,15	-1,48	-1,69	-1,49
_1803	lexA	3.4.21.88	Repressor LexA	1,06	1,02	-1,02	-1,06	1,12	-1,04	1,25
_1804	0		ComEC/Rec2-related protein	1,06	1,00	-1,02	1,07	1,57	1,71	1,50
_1805	gltX	6.1.1.17	Glutamate-tRNA ligase	1,11	1,07	-1,11	-1,20	-1,29	-1,55	1,00
_1806	gltA2	2.3.3.1	citrate (Si)-synthase	-1,05	1,10	1,00	-1,29	-1,45	-1,38	1,09

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_1807	0		UspA domain-containing protein	1,01	-1,05	-1,03	1,02	-1,13	1,37	1,04
_1808	0		amino acid carrier protein	-1,01	-1,06	-1,03	1,01	-1,18	1,18	-1,06
_1809	uvrA		excinuclease ABC subunit A	1,09	-1,02	1,05	1,17	1,08	1,04	1,18
_1810	0		major facilitator transporter	1,01	-1,03	1,04	-1,16	-1,13	-1,22	1,07
_1811	lpdV	1.8.1.4	dihydrolipoyl dehydrogenase	1,13	1,10	1,11	1,07	1,06	-1,20	1,01
_1812	0		hypothetical protein	-1,07	-1,04	-1,05	-1,20	-1,18	-1,35	-1,53
_1813	0		major facilitator transporter	1,02	-1,00	-1,14	-1,16	-1,08	-1,15	-1,13
_1814	0		hypothetical protein	1,01	1,02	-1,06	-1,08	-1,03	-1,08	1,08
_1815	0		LuxR family transcriptional regulator	-1,06	-1,01	1,04	-1,00	1,01	1,09	-1,08
_1816	0		MscS mechanosensitive ion channel	-1,07	-1,07	1,05	1,09	1,10	1,19	-1,11
_1817	0		pirin domain-containing protein	-1,07	-1,03	-1,02	-1,04	-1,17	-1,31	1,02
_1818	0		hypothetical protein	1,02	1,09	-1,07	-1,10	-1,07	-1,10	1,02
_1819	0		LuxR family transcriptional regulator	1,08	1,04	1,01	-1,03	-1,11	-1,05	-1,11
_1820	0	3.1.3.70	mannosyl-3-phosphoglycerate phosphatase	1,00	-1,02	-1,01	1,04	-1,04	-1,05	1,03
_1822	0		arsenical-resistance protein	-1,02	1,04	1,15	1,25	1,52	1,58	1,57
_1823	0		hypothetical protein	-1,02	1,03	-1,08	-1,04	-1,29	-1,21	-1,28
_1824	0	2.4.1.7	sucrose phosphorylase	1,01	-1,00	-1,06	1,06	-1,08	-1,20	1,03
_1825	pta1	2.3.1.8	phosphate acetyltransferase	-1,01	1,02	1,06	1,15	1,02	1,05	1,24
_1826	0		protein of unknown function DUF861 cupin_3	-1,03	-1,01	1,04	1,18	1,01	1,21	1,09
_1827	0		hypothetical protein	1,00	1,05	-1,07	1,15	1,06	1,11	1,22
_1828	xcs	2.3.3.15	sulfoacetaldehyde acetyltransferase	-1,05	1,02	1,07	-1,01	-1,10	1,06	-1,12
_1829	0		FAD dependent oxidoreductase	1,00	1,00	-1,04	1,21	1,14	1,06	1,26
_1830	0		hypothetical protein	-1,01	-1,04	1,03	1,08	1,08	1,09	1,17
_1831	0		UspA domain-containing protein	1,03	-1,02	-1,01	1,14	1,16	1,30	1,27
_1832	siaT		TRAP dicarboxylate transporter, DctM subunit	1,03	1,00	1,01	1,17	1,12	1,17	1,05
_1833	0		tripartite ATP-independent periplasmic transporter DctQ	-1,04	1,01	-1,02	1,03	1,06	1,19	1,06
_1834	0		TRAP dicarboxylate transporter- DctP subunit	-1,01	1,00	1,07	1,01	1,10	1,13	1,19
_1835	0		transcriptional regulator	-1,06	-1,07	-1,09	-1,12	-1,05	1,28	-1,09
_1836	0		hypothetical protein	1,08	1,01	-1,02	-1,15	1,21	1,21	1,38
_1837	0		carbohydrate kinase, YjeF related protein	-1,03	-1,04	-1,01	-1,08	-1,08	-1,01	1,06
_1838	0		nitrogen regulatory protein P-II	1,05	1,06	-1,08	-1,17	-1,09	-1,25	-1,10
_1839	glnA	6.3.1.2	Glutamate-ammonia ligase	-1,02	1,05	1,02	-1,28	-1,28	-1,75	-1,38
_1840	0		OsmC family protein	-1,05	-1,05	1,07	1,07	-1,10	-1,12	1,02
_1841	0		hypothetical protein	-1,06	-1,03	1,01	-1,25	-1,09	1,11	-1,08
_1842	purB	4.3.2.2	adenylosuccinate lyase	1,13	1,27	1,11	1,01	1,12	-1,48	1,38
_1843	0		hypothetical protein	-1,06	-1,04	-1,12	-1,41	-1,66	1,00	-1,41
_1844	0		TPR repeat-containing protein	1,05	-1,02	-1,16	-1,29	-1,42	-1,13	-1,37
_1845	0		flagellar motor switch protein FliG	1,09	-1,00	-1,02	1,04	1,36	1,45	1,51
_1846	0		hypothetical protein	1,06	1,03	-1,01	1,15	1,03	1,03	1,30
_1847	0		hypothetical protein	-1,12	-1,05	1,08	1,05	1,01	1,18	-1,22
_1848	0		putative ScnA-like protein	-1,06	-1,12	-1,01	1,09	1,04	1,16	-1,03
_1849	nthA	4.2.1.84	nitrile hydratase	-1,07	-1,03	-1,04	-1,29	1,16	1,15	-1,01
_1850	0		hypothetical protein	1,06	-1,01	1,11	1,04	-1,11	-1,14	1,26
_1851	acnA	4.2.1.3	aconitate hydratase	-1,01	1,02	-1,17	-1,22	-1,49	-1,47	-1,40
_1852	0		redoxin domain-containing protein	-1,03	1,01	1,06	1,25	1,17	1,37	1,43
_1853	ccmC		heme exporter protein CcmC	1,02	1,10	1,25	1,44	1,85	1,58	1,73
_1854	ccmB		heme exporter protein CcmB	1,06	1,08	1,05	-1,16	1,02	-1,06	1,27
_1855	ccmA	3.6.3.41	heme-transporting ATPase	1,10	1,10	-1,01	1,06	1,03	-1,13	1,22
_1856	0		hypothetical protein	-1,02	-1,01	-1,05	-1,06	-1,38	-1,13	-1,11
_1857	0		hypothetical protein	1,01	-1,04	-1,07	-1,16	-1,39	-1,13	-1,02
_1858	secF		preprotein translocase subunit SecF	1,01	1,01	-1,11	-1,70	-1,70	-1,53	-1,38
_1859	secD		preprotein translocase subunit SecD	-1,02	-1,00	-1,10	-1,18	-1,70	-1,51	-1,27
_1860	yajC		preprotein translocase, YajC subunit	1,04	1,03	-1,10	-1,27	-1,58	-1,55	-1,27
_1861	0		hypothetical protein	-1,03	-1,04	-1,01	1,18	1,15	1,32	1,05
_1862	0		pentapeptide repeat-containing protein	-1,03	-1,01	1,02	1,02	1,27	1,50	1,24
_1863	serS	6.1.1.11	Serine-tRNA ligase	1,06	1,06	-1,08	-1,36	-1,45	-1,63	-1,15
_1864	0		lytic murein transglycosylase	-1,01	-1,03	-1,02	-1,17	-1,11	-1,12	-1,08
_1865	0		hypothetical protein	-1,02	-1,02	-1,02	1,10	1,13	1,33	-1,15
_1866	0		hypothetical protein	-1,05	-1,04	1,16	1,00	1,25	1,36	-1,05
_1867	glnT	6.3.1.2	Glutamate-ammonia ligase	-1,00	-1,01	1,10	1,10	1,19	1,35	1,37
_1868	0		ferredoxin-dependent glutamate synthase	-1,04	1,02	1,11	1,13	1,10	1,17	1,27

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_1869	0		glutamate synthase alpha subunit	1,01	-1,03	-1,07	1,07	1,20	1,39	1,30
_1870	0		glutamine amidotransferase class-II	-1,03	-1,00	-1,04	1,07	1,11	1,34	1,22
_1871	0		XRE family transcriptional regulator	1,02	1,02	1,00	1,02	-1,12	-1,03	-1,00
_1872	0		hypothetical protein	-1,03	-1,10	-1,30	-1,48	-2,19	-1,9	-2,51
_1873	0		cytochrome c class I	1,01	-1,03	-1,15	-1,27	-1,41	-1,58	-1,59
_1874	0		TetR family transcriptional regulator	1,01	-1,02	-1,04	1,08	1,01	1,10	1,06
_1875	0		hypothetical protein	-1,03	1,00	-1,03	-1,10	-1,06	-1,07	1,10
_1876	0		glutaredoxin 3	-1,01	-1,04	1,03	1,10	-1,04	-1,03	1,17
_1877	0		hypothetical protein	-1,03	-1,02	-1,05	1,02	1,03	1,19	-1,07
_1878	0		nonspecific acid phosphatase	1,01	-1,01	-1,07	-1,47	-1,08	1,05	1,02
_1879	0		hypothetical protein	1,10	-1,02	-1,08	-1,01	-1,24	-1,27	-1,19
_1880	0		hypothetical protein	-1,03	1,02	-1,02	-1,09	-1,14	-1,24	-1,13
_1881	0		hypothetical protein	-1,06	-1,06	1,13	1,14	1,44	1,17	1,04
_1882	0		GCN5-related N-acetyltransferase	-1,09	-1,07	1,13	1,23	1,13	-1,04	-1,02
_1883	0		ATPase central domain-containing protein	1,07	1,05	-1,12	-1,17	-1,40	-1,86	-1,28
_1884	0		TraR/DksA family transcriptional regulator	1,11	1,11	-1,00	1,01	-1,17	-1,93	-1,11
_1885	0		monooxygenase FAD-binding	1,03	-1,03	1,04	1,44	1,44	1,08	1,01
_1886	0		exodeoxyribonuclease III Xth	1,02	1,05	-1,01	-1,24	-1,17	-1,36	-1,25
_1887	0		ribonuclease D	1,02	1,04	-1,07	1,03	1,09	-1,05	1,19
_1888	purN	2.1.2.2	phosphoribosyl glycinamide formyltransferase	1,08	1,01	-1,17	-1,21	-1,32	-1,36	-1,02
_1889	purM	6.3.3.1	phosphoribosylformyl glycinamidine cyclo-ligase	1,16	1,16	-1,15	-1,17	-1,33	-1,87	-1,13
_1890	0		Sel1 domain-containing protein	-1,06	-1,01	1,04	1,07	1,15	1,27	1,37
_1891	0		globin	1,00	1,06	1,18	1,19	1,19	1,01	1,15
_1892	0		hypothetical protein	-1,06	-1,04	1,03	-1,11	-1,08	1,14	1,22
_1894	0		two component LuxR family transcriptional regulator	-1,03	-1,02	-1,03	-1,13	1,02	1,08	-1,04
_1895	0		hemolysin-type calcium-binding region	1,01	1,00	-1,06	1,08	1,06	1,20	1,48
_1896	algD	1.1.1.132	GDP-mannose 6-dehydrogenase	1,02	-1,07	-1,06	1,03	1,26	1,14	2,39
_1897	algA	2.7.7.22, 5.3.1.8, 2.7.7.13	mannose-1-phosphate guanylyltransferase (GDP),Mannose-6-phosphate isomerase,mannose-1-phosphate guanylyltransferase	-1,12	-1,11	-1,13	-1,03	1,40	1,16	1,79
_1898	0		alginate synthesis-related protein	-1,08	1,01	-1,03	1,11	1,05	1,05	1,24
_1899	0		multidrug resistance efflux pump-like protein	-1,20	-1,16	-1,22	-1,25	1,23	1,13	1,64
_1900	algC	5.4.2.8, 5.4.2.2	phosphomannomutase,phosphoglucomutase	-1,00	1,02	-1,03	-1,13	-1,11	-1,56	1,02
_1901	0		hypothetical protein	-1,01	-1,00	-1,08	-1,15	1,33	1,15	1,8
_1902	0		membrane bound O-acyl transferase MBOAT family protein	-1,08	-1,02	-1,05	1,07	1,08	1,17	1,38
_1903	0		hypothetical protein	1,03	1,09	-1,03	-1,09	1,11	1,11	1,29
_1904	0		hypothetical protein	-1,06	-1,01	1,01	1,08	1,01	-1,01	-1,03
_1905	0		integrase family protein	1,05	1,05	-1,04	-1,22	-1,11	-1,15	1,21
_1906	0		prophage CP4-57 regulatory	1,00	-1,04	-1,00	1,15	1,02	1,14	1,20
_1907	0		hypothetical protein	-1,05	-1,03	-1,01	1,14	1,10	1,09	1,24
_1908	0		hypothetical protein	-1,02	-1,02	1,03	1,17	1,32	1,26	1,16
_1909	0		hypothetical protein	-1,02	-1,04	-1,01	-1,15	1,14	1,17	-1,02
_1910	0		hypothetical protein	-1,07	-1,00	1,14	1,16	1,06	1,33	1,12
_1911	0		hypothetical protein	1,03	-1,02	-1,09	1,03	1,12	1,18	1,22
_1912	0		hypothetical protein	-1,01	-1,02	1,01	1,06	1,21	1,20	1,23
_1915	0		hypothetical protein	-1,03	1,02	-1,07	-1,00	1,11	1,27	1,26
_1916	0		hypothetical protein	1,04	1,01	1,07	-1,05	1,27	1,23	1,22
_1919	0		hypothetical protein	-1,08	-1,08	-1,08	-1,15	-1,28	-1,11	-1,59
_1922	0		hypothetical protein	1,00	-1,03	-1,06	1,13	1,01	1,01	1,12
_1923	0		hypothetical protein	-1,05	-1,08	1,01	1,07	1,09	1,29	1,08
_1924	0		TRAP transporter solute receptor TAXI family protein	1,01	-1,05	1,05	1,02	1,12	1,30	1,06
_1925	0		AAA ATPase	1,03	-1,05	-1,01	-1,42	-1,14	-1,03	-1,37
_1926	priA		primosome assembly protein PriA	-1,00	-1,02	-1,04	-1,02	-1,01	-1,10	-1,08
_1927	tal	2.2.1.2	transaldolase	-1,13	-1,01	-1,13	-1,42	-3,05	-3,57	-2,27
_1928	0		hypothetical protein	1,01	-1,03	-1,12	-1,18	-1,18	-1,09	-1,20
_1930	0		hypothetical protein	1,01	1,06	-1,09	1,06	-1,23	-1,15	1,08
_1931	0		hypothetical protein	1,10	1,03	-1,01	1,05	-1,11	-1,36	-1,18
_1932	0		hypothetical protein	1,03	1,01	-1,12	-1,13	-1,85	-2	-1,57
_1933	ileS	6.1.1.5	Isoleucine-tRNA ligase	1,10	1,05	-1,18	-1,51	-1,63	-1,81	-1,39
_1934	0		hypothetical protein	-1,06	-1,06	-1,22	-1,65	-2,57	-2,56	-2,99

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_1935	0		cyclic nucleotide-regulated FAD-dependent pyridine nucleotide-disulphide oxidoreductase	-1,04	-1,02	-1,02	1,03	-1,13	-1,12	-1,07
_1936	0		hypothetical protein	-1,07	1,00	1,07	1,06	-1,23	-1,36	1,11
_1937	0		protein of unknown function DUF463 YcjX family protein	1,03	-1,00	-1,03	1,05	-1,03	-1,00	1,28
_1938	truA	5.4.99.12	tRNA pseudouridine38-40 synthase	1,07	1,07	1,03	1,03	-1,13	-1,22	-1,03
_1939	0		binding-protein-dependent transport systems inner membrane component	-1,05	-1,04	-1,00	1,03	1,02	1,02	-1,13
_1940	0		ABC transporter related	-1,05	-1,04	1,03	-1,02	-1,07	-1,08	-1,25
_1941	0		NMT1/THI5-like domain-containing protein	-1,12	-1,03	-1,06	-1,36	-1,49	-1,30	-1,73
_1942	0		GSCFA domain-containing protein	1,00	-1,01	1,04	1,04	1,08	1,06	1,05
_1943	codA	3.5.4.1	cytosine deaminase	-1,00	-1,02	-1,01	-1,02	-1,20	-1,16	-1,18
_1944	0		hypothetical protein	-1,01	1,01	1,09	-1,18	1,11	-1,07	1,01
_1945	0		inner-membrane translocator	1,07	1,02	-1,06	-1,15	-1,12	-1,06	-1,01
_1946	0		inner-membrane translocator	-1,07	-1,08	-1,11	-1,13	-1,26	-1,20	-1,24
_1947	rbsA4	3.6.3.17	Monosaccharide-transporting ATPase	-1,01	-1,01	-1,11	-1,27	-1,77	-1,53	-1,72
_1948	0		basic membrane lipoprotein	-1,04	-1,02	-1,16	-1,38	-1,82	-1,73	-1,71
_1949	0		hypothetical protein	-1,02	-1,02	-1,20	-1,62	-1,52	-1,42	-1,32
_1950	0		type I phosphodiesterase/nucleotide pyrophosphatase	1,01	1,11	1,23	1,36	1,68	1,46	1,63
_1951	0		secretion protein HlyD family protein	1,06	1,00	1,01	-1,03	1,26	1,48	1,43
_1952	0		hypothetical protein	-1,03	1,00	-1,04	-1,06	1,14	1,01	-1,07
_1953	0		putative secreted hydrolase	-1,02	-1,01	-1,03	-1,03	-1,04	-1,06	1,01
_1954	0		short-chain dehydrogenase/reductase SDR	-1,01	1,00	-1,04	-1,09	-1,09	1,04	-1,13
_1955	0		short-chain dehydrogenase/reductase SDR	1,01	1,00	1,03	-1,02	-1,07	-1,13	1,01
_1956	0		NAD-dependent epimerase/dehydratase	1,04	1,00	-1,02	1,00	-1,31	-1,72	-1,30
_1957	0		TPR repeat-containing protein	-1,02	-1,00	-1,04	-1,03	-1,57	-1,87	-1,63
_1958	0		NAD-dependent epimerase/dehydratase	-1,01	1,01	1,02	1,14	-1,05	-1,12	-1,11
_1960	0		type I phosphodiesterase/nucleotide pyrophosphatase	1,02	1,02	1,03	1,05	-1,21	-1,39	-1,12
_1961	0		hypothetical protein	1,01	1,03	1,06	1,26	-1,23	-1,76	-1,16
_1962	0		Beta-ketoacyl synthase	1,03	1,02	1,00	1,16	-1,35	-1,25	-1,14
_1963	0		Beta-ketoacyl synthase	1,07	1,03	-1,06	-1,26	-1,15	-1,15	1,10
_1964	0		FkbH like protein	1,01	1,00	-1,00	-1,02	1,29	1,19	1,16
_1965	0		hypothetical protein	-1,00	1,00	-1,04	1,11	1,22	1,22	1,28
_1966	lpdA	1.8.1.4	dihydrolipoyl dehydrogenase	1,04	1,09	1,06	1,23	1,31	1,37	1,97
_1967	aceF	2.3.1.12	Dihydrolipoyllysine-residue acetyltransferase	1,04	1,09	1,06	1,15	1,25	1,20	1,84
_1968	aceE	1.2.4.1	pyruvate dehydrogenase (acetyl-transferring)	1,15	1,12	1,08	1,44	3,03	1,60	2,43
_1970	0		TRAP dicarboxylate transporter, DctM subunit	-1,04	-1,00	1,06	-1,12	1,00	1,10	1,03
_1972	0		GntR domain-containing protein	-1,07	1,05	-1,04	-1,06	-1,16	-1,07	-1,16
_1973	0		ATPase	-1,05	-1,02	-1,08	1,08	1,05	1,13	1,23
_1974	0		hypothetical protein	1,07	1,01	-1,06	1,03	1,18	1,24	1,28
_1975	0		hypothetical protein	-1,09	-1,01	-1,03	-1,19	1,03	1,03	-1,11
_1976	0		ribokinase-like domain-containing protein	-1,17	-1,14	-1,03	-1,07	-1,10	1,05	-1,14
_1977	0		extracellular ligand-binding receptor	-1,04	-1,07	1,06	1,08	-1,19	-1,08	-1,11
_1978	0		inner-membrane translocator	1,02	1,02	-1,04	-1,00	-1,00	1,21	-1,06
_1979	0		inner-membrane translocator	1,04	-1,00	1,07	-1,17	-1,00	1,15	1,19
_1980	0		ABC transporter related	-1,06	1,01	-1,04	-1,18	1,06	1,09	1,12
_1981	0		ABC transporter related	-1,03	1,02	-1,02	1,06	-1,02	1,00	1,05
_1982	0		aldo/keto reductase	-1,02	-1,04	-1,03	1,05	1,01	1,21	1,12
_1983	0		hypothetical protein	-1,03	-1,01	-1,03	-1,02	1,04	1,22	1,00
_1985	0		aldo/keto reductase	-1,06	1,03	-1,00	-1,04	-1,01	1,08	1,09
_1986	icd	1.1.1.42	isocitrate dehydrogenase (NADP+)	-1,14	1,09	-1,06	-1,53	-2,53	-1,60	-1,38
_1987	0		hypothetical protein	-1,03	1,01	1,02	-1,09	1,01	-1,06	-1,07
_1988	0		hypothetical protein	-1,01	1,03	-1,05	-1,02	-1,18	-1,13	-1,21
_1989	0		secretion protein HlyD family protein	-1,01	1,03	-1,06	-1,02	-1,13	-1,24	-1,14
_1990	0		aminoglycoside phosphotransferase	-1,06	1,01	-1,07	1,24	-1,01	1,01	1,21
_1991	0		ABC transporter related	1,02	-1,02	1,00	1,11	-1,01	-1,02	-1,05
_1992	0		glycosyl transferase group 1	1,03	-1,03	-1,03	-1,12	-1,04	-1,04	-1,04
_1993	0		glycosyl transferase group 1	1,04	-1,03	1,08	1,10	-1,10	-1,12	-1,09
_1994	0		hypothetical protein	1,02	1,02	1,01	-1,05	-1,01	-1,00	1,01
_1995	0		hypothetical protein	-1,04	-1,02	-1,00	-1,33	-1,13	1,17	1,24
_1996	xylA	5.3.1.5	Xylose isomerase	1,02	-1,03	-1,04	1,09	-1,29	-1,31	-1,35
_1997	xylB2	2.7.1.17	xylulokinase	1,01	-1,05	-1,05	1,00	-1,38	-1,25	-1,28

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_1998	0		ABC transporter related	-1,04	-1,03	-1,08	-1,00	-1,29	-1,27	-1,24
_1999	xylH		inner-membrane translocator	-1,00	-1,05	-1,13	-1,19	-1,34	-1,24	-1,23
_2000	0	3.6.3.17	Monosaccharide-transporting ATPase	-1,09	-1,13	-1,16	-1,45	-2,35	-1,71	-2,61
_2001	0		ROK family protein	1,00	-1,05	-1,05	1,09	1,01	1,16	1,11
_2002	0		FG-GAP repeat-containing protein	-1,03	-1,02	-1,03	1,03	1,08	1,29	1,08
_2003	0		twin-arginine translocation pathway signal	1,03	-1,02	1,05	1,22	1,03	1,25	1,07
_2004	0		ferric reductase domain-containing protein	-1,01	-1,05	-1,04	1,09	-1,01	1,09	1,13
_2005	0		di-haem cytochrome c peroxidase	-1,06	-1,07	-1,04	-1,15	1,04	1,12	1,03
_2006	0		hypothetical protein	1,02	1,07	1,27	1,36	1,43	1,79	1,56
_2007	0		NUDIX hydrolase	-1,02	-1,04	1,07	1,15	1,02	1,29	1,24
_2008	0		DeoR family transcriptional regulator	-1,04	-1,03	-1,08	-1,16	-1,37	-1,17	-1,24
_2009	0		putative phosphonates-binding periplasmic protein	-1,04	-1,04	-1,18	-1,34	-2,55	-2,36	-2,48
_2010	phnC1	3.6.3.28	Phosphonate-transporting ATPase	-1,01	-1,06	-1,16	-1,29	-1,53	-1,38	-1,25
_2011	0		phosphonate ABC transporter, inner membrane subunit	-1,04	-1,04	-1,07	-1,24	-1,70	-1,62	-1,74
_2012	0		phosphonate ABC transporter, inner membrane subunit	1,01	-1,03	-1,09	-1,12	-1,52	-1,47	-1,51
_2013	0		hydrolase	1,01	-1,04	-1,01	1,09	-1,31	-1,31	-1,11
_2014	ugpB1		extracellular solute-binding protein	-1,03	-1,04	-1,11	-1,25	-2,08	-2,61	-2,58
_2015	ugpA4		binding-protein-dependent transport systems inner membrane component	-1,00	-1,02	-1,17	-1,17	-1,82	-2,01	-1,81
_2016	ugpE3		binding-protein-dependent transport systems inner membrane component	1,02	1,02	-1,15	-1,13	-1,77	-1,95	-1,70
_2017	ugpC4	3.6.3.20	glycerol-3-phosphate-transporting ATPase	1,00	-1,04	-1,04	-1,01	-1,57	-1,85	-1,51
_2018	0		hypothetical protein	1,05	1,00	1,03	1,00	-1,12	-1,30	-1,17
_2020	pgm	5.4.2.2	phosphoglucomutase	1,05	1,02	-1,02	1,32	1,44	-1,12	1,18
_2021	0		extracellular solute-binding protein	-1,03	-1,04	-1,02	1,03	3,39	3,83	2,21
_2022	0		hypothetical protein	-1,04	-1,05	-1,00	1,14	2,37	2,84	2,12
_2023	0		binding-protein-dependent transport systems inner membrane component	1,08	1,07	1,05	-1,06	1,22	-1,01	1,30
_2024	0		hypothetical protein	-1,05	-1,03	1,08	1,23	-1,01	-1,04	1,05
_2025	0		hypothetical protein	-1,04	-1,00	1,08	1,02	-1,21	-1,11	-1,29
_2026	0		LamB/YcsF family protein	-1,01	-1,02	1,07	-1,05	-1,01	1,11	-1,15
_2027	0		allophanate hydrolase subunit 2	-1,02	-1,05	1,10	1,04	1,13	1,13	1,00
_2028	0		allophanate hydrolase subunit 1	-1,13	-1,09	1,09	1,24	1,06	1,12	-1,20
_2029	0		LacI family transcription regulator	-1,04	-1,03	1,01	-1,10	-1,01	1,24	-1,07
_2030	0		hypothetical protein	-1,05	-1,06	-1,20	-1,26	-1,51	-1,48	-1,51
_2031	0		TRAP dicarboxylate transporter- DctP subunit	-1,05	-1,08	-1,29	-1,47	-1,45	-1,37	-1,47
_2032	0		tripartite ATP-independent periplasmic transporter DctQ	1,06	-1,02	-1,08	-1,08	-1,16	-1,26	-1,14
_2033	0		TRAP dicarboxylate transporter, DctM subunit	-1,02	-1,02	-1,09	1,06	-1,12	-1,10	-1,11
_2034	hisD2	1.1.1.23	histidinol dehydrogenase	-1,02	-1,01	-1,00	-1,12	-1,17	-1,13	-1,08
_2035	0		short-chain dehydrogenase/reductase SDR	-1,02	-1,01	1,09	1,05	1,02	-1,02	1,07
_2036	0		alcohol dehydrogenase	1,03	1,01	1,08	-1,16	-1,24	-1,20	-1,14
_2037	0		hypothetical protein	-1,03	1,01	1,01	-1,12	-1,47	-1,40	-1,40
_2038	0		Altronate dehydratase	-1,06	-1,01	1,00	1,13	-1,44	-1,36	-1,30
_2039	0		malate/L-lactate dehydrogenase	-1,03	-1,01	1,04	1,03	-1,10	-1,14	-1,03
_2040	0		UspA domain-containing protein	-1,09	-1,01	1,08	1,16	-1,17	-1,18	-1,21
_2042	tpa	2.6.1.77	taurine-pyruvate aminotransferase	1,01	-1,02	1,00	-1,02	-1,00	1,14	1,14
_2043	0		hypothetical protein	-1,03	-1,03	-1,08	-1,05	1,11	1,25	1,07
_2044	0		transcriptional regulator	-1,05	-1,03	1,07	1,15	1,36	1,44	1,17
_2045	xsc	2.3.3.15	sulfoacetaldehyde acetyltransferase	-1,03	-1,01	1,01	-1,06	-1,33	-1,14	-1,15
_2047	0		hypothetical protein	-1,01	1,02	1,01	-1,08	-1,35	-1,64	-1,32
_2048	0		hypothetical protein	1,04	1,02	-1,01	-1,09	-1,43	-1,72	-1,24
_2049	0		ABC transporter related	1,02	1,00	-1,07	-1,08	-1,33	-1,46	-1,15
_2050	0		hypothetical protein	1,01	1,03	-1,05	-1,22	-1,20	-1,27	1,09
_2051	0		hypothetical protein	1,01	-1,02	1,03	1,09	1,70	3,33	3,96
_2052	0		hypothetical protein	1,03	-1,02	1,03	1,18	2,12	3,12	4,25
_2053	0		hypothetical protein	1,01	-1,01	-1,09	-1,49	-1,26	-1,39	-1,15
_2054	0		histone deacetylase superfamily protein	1,09	-1,00	-1,04	1,08	1,07	1,33	1,24
_2055	0		glutathione peroxidase	1,03	-1,04	1,07	1,07	1,07	1,09	1,28
_2056	0		NUDIX hydrolase	-1,02	-1,00	1,10	1,39	1,45	1,24	-1,05
_2057	0		hypothetical protein	-1,04	1,01	1,10	1,25	1,10	1,27	1,08

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_2058	0		short-chain dehydrogenase/reductase SDR	1,07	1,03	1,02	1,05	-1,03	1,11	-1,06
_2059	0		hypothetical protein	1,04	1,02	-1,13	-1,12	1,00	1,02	-1,18
_2060	acnB	4.2.1.3	aconitate hydratase	-1,20	1,09	1,05	-1,67	-1,83	-1,15	-1,38
_2061	lysC	2.7.2.4	aspartate kinase	1,24	1,30	1,15	1,30	1,11	-1,73	1,23
_2062	ptsI	2.7.3.9	Phosphoenolpyruvate-protein phosphotransferase	1,03	-1,00	1,05	-1,08	1,05	-1,00	1,09
_2063	0		von Willebrand factor type A	-1,02	-1,07	1,11	1,15	1,31	1,75	1,35
_2064	0		GCN5-related N-acetyltransferase	1,07	1,04	-1,04	-1,09	-1,29	-1,51	-1,11
_2065	0		flavin reductase-like, FMN-binding	1,04	1,02	-1,01	-1,22	-1,23	-1,14	1,04
_2066	0		hypothetical protein	1,02	1,05	1,06	1,13	1,13	-1,17	1,14
_2067	0		sulphate transporter	1,12	1,09	-1,02	1,22	2,13	1,11	2,11
_2068	0	2.4.2.28	S-methyl-5-thioadenosine phosphorylase	1,02	1,01	1,11	1,16	1,54	-1,04	1,17
_2069	0		hypothetical protein	-1,21	-1,17	-1,04	-1,50	-1,17	1,13	-1,32
_2070	0		glyoxalase/bleomycin resistance protein/dioxygenase	-1,06	-1,07	-1,04	-1,04	-1,24	-1,05	-1,33
_2071	0		hypothetical protein	-1,02	-1,10	-1,16	-1,41	-1,68	-1,34	-1,8
_2072	0		gluconate 2-dehydrogenase (acceptor)	-1,02	-1,08	-1,11	-1,20	-1,61	-1,40	-1,70
_2073	0		hypothetical protein	1,01	1,01	-1,04	1,11	-1,01	1,07	1,06
_2074	apt	2.4.2.7	adenine phosphoribosyl transferase	-1,10	1,00	1,03	-1,08	-1,25	-1,17	-1,17
_2075	0		hypothetical protein	1,04	-1,00	-1,08	-1,25	-1,15	-1,14	-1,03
_2076	0		FAD linked oxidase domain-containing protein	1,01	1,03	1,02	1,14	-1,01	-1,19	1,30
_2077	0		hypothetical protein	-1,02	-1,03	1,05	1,15	1,05	1,44	1,21
_2078	tpiA	5.3.1.1	Triose-phosphate isomerase	1,00	-1,03	1,02	1,02	-1,07	1,11	-1,06
_2079	0		LysR family transcriptional regulator	-1,07	-1,03	1,07	-1,43	-1,14	1,17	-1,03
_2080	metF	1.5.1.20	methyl enetetrahydrofolate reductase [NAD(P)H]	-2	-2,21	-2,4	-2,33	-3,77	-2,85	-1,95
_2081	0		cytochrome c class I	1,01	-1,14	-1,30	-1,53	-2,51	-1,84	-2,37
_2082	0		L-sorbosone dehydrogenase, putative	-1,11	-1,19	-1,34	-1,54	-3,59	-2,46	-3,76
_2083	0		thioesterase superfamily protein	1,05	1,03	-1,19	-1,65	-1,74	-1,70	-1,59
_2084	0		hypothetical protein	1,03	1,03	-1,01	1,06	1,56	1,79	1,55
_2085	0		hypothetical protein	-1,24	-1,14	-1,30	-1,39	-2,04	-2,37	-1,35
_2086	coxL3	1.2.99.2	carbon-monoxide dehydrogenase (acceptor)	-1,02	-1,02	1,12	1,09	-1,11	-1,28	-1,08
_2087	valS	6.1.1.9	Valine-tRNA ligase	1,13	1,15	-1,04	-1,07	-1,09	-1,64	-1,01
_2088	0	2.6.1.9	histidinol-phosphate transaminase	1,12	1,05	-1,07	-1,12	-1,04	-1,20	1,00
_2089	0		hypothetical protein	1,02	-1,04	-1,01	1,17	-1,00	1,00	1,19
_2090	0	2.6.1.45	serine-glyoxylate transaminase	-1,01	1,01	-1,11	-1,16	-1,37	-1,48	-1,28
_2091	0		glycosyl transferase family protein	1,04	1,02	-1,04	-1,05	-1,17	-1,40	-1,09
_2092	0		glycine cleavage T protein (aminomethyl transferase)	1,04	1,03	-1,02	1,10	-1,16	-1,14	1,05
_2093	0		hypothetical protein	1,08	1,05	-1,08	-1,09	-1,22	-1,38	-1,22
_2094	efp		elongation factor P	1,27	1,25	-1,18	-1,34	-1,57	-2,47	-1,45
_2095	0		hypothetical protein	1,29	1,13	-1,05	-1,19	1,05	-1,02	1,42
_2096	cobQ		cobyric acid synthase	1,07	1,01	-1,06	-1,33	-1,45	-1,50	-1,25
_2097	0		hypothetical protein	-1,01	-1,03	1,07	1,16	1,11	1,16	1,03
_2098	0		TolC family type I secretion outer membrane protein	-1,01	1,00	-1,01	1,17	1,26	-1,19	-1,02
_2099	0		protein-L-isoaspartate(D-aspartate) O-methyltransferase	1,06	1,18	1,35	1,62	2,1	1,36	1,77
_2100	0		integrase family protein	1,02	-1,03	1,08	1,09	1,07	1,01	1,06
_2101	0		type III restriction enzyme, res subunit	-1,03	-1,01	1,07	1,10	1,04	1,14	1,09
_2102	0		DNA methylase N-4/N-6 domain-containing protein	-1,04	-1,02	1,02	-1,20	-1,08	1,20	1,03
_2103	0		transposase IS3/IS911 family protein	-1,03	-1,03	-1,02	-1,09	-1,38	-1,27	-1,21
_2104	0		integrase catalytic region	1,01	-1,00	-1,04	-1,27	-1,24	-1,10	-1,15
_2105	0		DNA methylase N-4/N-6 domain-containing protein	-1,07	-1,02	-1,06	-1,05	1,10	1,27	-1,06
_2106	0		XRE family transcriptional regulator	1,06	1,05	1,01	1,15	1,16	1,26	1,47
_2107	0		hypothetical protein	1,05	-1,01	-1,06	1,08	1,14	1,23	1,24
_2108	0		cyclic nucleotide-binding protein	1,04	1,04	1,08	1,28	1,31	1,33	1,59
_2109	0		alanine racemase domain-containing protein	-1,09	-1,07	1,10	-1,00	-1,01	-1,01	-1,10
_2110	0			1,09	1,04	-1,11	-1,06	-1,27	-1,84	-1,37
_2111	purU	3.5.1.10	formyl tetrahydrofolate deformylase	-1,05	-1,05	1,04	1,11	1,10	1,09	1,12
_2113	glyA	2.1.2.1	glycine hydroxymethyl transferase	1,06	1,01	1,00	1,02	1,15	1,20	1,23
_2114	0		sarcosine oxidase gamma subunit	-1,01	-1,02	1,05	1,10	1,20	1,38	1,15
_2115	soxA2	1.5.3.1	sarcosine oxidase	-1,06	1,02	1,06	-1,16	-1,31	-1,27	-1,21
_2116	0		sarcosine oxidase delta subunit family protein	1,03	-1,01	1,14	-1,02	1,11	1,13	1,20
_2117	soxB	1.5.3.1	sarcosine oxidase	-1,06	1,01	-1,00	-1,00	1,24	1,18	1,17
_2118	0		AraC family transcriptional regulator	-1,02	-1,01	-1,04	1,01	1,11	1,16	1,03
_2119	0		choline/carnitine/betaine transporter	-1,01	-1,01	-1,05	-1,16	1,01	1,12	-1,00

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_2120	potA2	3.6.3.31	Polyamine-transporting ATPase	-1,05	1,00	1,01	-1,08	1,05	1,15	1,13
_2121	0		binding-protein-dependent transport systems inner membrane component	1,09	1,01	-1,03	-1,26	1,10	-1,01	1,16
_2122	0		binding-protein-dependent transport systems inner membrane component	1,01	-1,01	-1,02	-1,08	1,17	1,21	1,20
_2123	0		extracellular solute-binding protein	-1,03	1,03	1,01	-1,05	1,00	1,06	1,15
_2124	0	3.5.2.10	creatininase	1,03	1,01	1,04	-1,02	1,16	1,27	1,18
_2125	0		LysR family transcriptional regulator	-1,03	-1,02	-1,06	1,08	1,12	1,16	1,11
_2126	0	3.5.3.3	creatinase	1,00	1,02	-1,05	1,02	1,01	1,09	-1,20
_2127	0		putative transcriptional regulator protein	-1,07	-1,02	-1,04	1,03	1,16	1,14	-1,03
_2128	0		paraquat-inducible protein A	-1,03	-1,03	1,02	1,03	1,13	1,26	1,08
_2129	0		DNA repair protein RadA	1,06	1,03	1,01	-1,12	-1,31	-1,54	-1,17
_2130	0		colicin V production protein	-1,01	1,02	-1,01	-1,13	-1,47	-1,9	-1,44
_2131	0		hypothetical protein	-1,13	-1,06	-1,14	-1,27	-1,35	-1,46	-1,16
_2132	purF	2.4.2.14	amidophosphoribosyl transferase	1,09	1,07	1,01	-1,07	-1,09	-1,31	1,17
_2133	0		hypothetical protein	1,04	1,03	-1,07	-1,05	-1,14	-1,17	1,26
_2134	0		BioY protein	-1,04	1,02	1,09	1,38	1,27	-1,00	1,17
_2135	0		short-chain dehydrogenase/reductase SDR	1,13	1,10	-1,08	-1,04	-1,06	-1,60	1,01
_2136	surE	3.1.3.5	5-nucleotidase	1,02	1,00	-1,04	-1,09	-1,19	-1,37	-1,21
_2137	pcm	2.1.1.77	protein-L-isoaspartate(D-aspartate) O-methyltransferase	-1,00	-1,01	1,03	1,10	-1,12	-1,20	-1,13
_2138	0		peptidase M23B	1,01	-1,03	1,01	1,16	-1,11	-1,01	-1,01
_2139	0		hypothetical protein	-1,02	1,01	-1,05	-1,06	-1,17	-1,43	-1,16
_2140	0		sodium/hydrogen exchanger	-1,07	-1,08	-1,01	1,06	1,03	1,05	-1,15
_2141	0		hypothetical protein	-1,04	-1,02	-1,04	-1,09	-1,19	-1,05	-1,31
_2142	0		ferric uptake regulator family protein	1,03	1,04	-1,02	-1,16	-1,24	-1,29	-1,10
_2143	0		pirin domain-containing protein	-1,02	1,02	1,02	1,01	-1,03	-1,21	-1,03
_2144	0	4.1.2.5	L-threonine aldolase	1,03	1,02	1,06	-1,09	1,07	1,16	-1,03
_2145	eno	4.2.1.11	phosphopyruvate hydratase	-1,16	-1,10	-1,26	-1,36	-1,95	-2,51	-1,61
_2146	0		PRC-barrel domain-containing protein	1,05	1,01	1,02	-1,10	1,14	1,22	1,34
_2147	0		hypothetical protein	1,07	1,00	1,05	1,14	1,39	1,70	1,53
_2148	0		hypothetical protein	-1,03	-1,07	1,05	1,12	1,07	1,15	1,05
_2149	0		hypothetical protein	-1,06	-1,04	-1,02	-1,05	1,04	1,24	1,17
_2150	anmK	2.7.1.170	Anhydro-N-acetylmuramic acid kinase	-1,06	-1,04	-1,04	-1,18	-1,04	-1,03	-1,24
_2151	tyrS	6.1.1.1	Tyrosine-tRNA ligase	1,19	1,16	-1,12	-1,46	-1,17	-1,88	-1,03
_2152	0		hypothetical protein	-1,02	-1,06	1,13	1,13	-1,15	-1,12	-1,18
_2153	0	5.2.1.8	Peptidylprolyl isomerase	-1,03	-1,01	-1,09	-1,28	-2,1	-2,65	-2,32
_2154	0	5.2.1.8	Peptidylprolyl isomerase	-1,05	-1,00	-1,10	-1,54	-2,12	-2,77	-2,37
_2155	pgk	2.7.2.3	phosphoglycerate kinase	1,08	1,03	-1,14	-1,42	-1,44	-1,76	-1,18
_2156	fda	4.1.2.13	Fructose-bisphosphate aldolase	1,38	1,29	1,05	1,00	1,41	-1,30	1,49
_2157	0		septum formation initiator	1,02	-1,03	1,05	1,02	1,06	1,30	1,17
_2158	pdhA1	1.2.4.1	pyruvate dehydrogenase (acetyl-transferring)	1,18	1,13	-1,01	-1,08	-1,11	-1,45	-1,44
_2159	pdhB2	1.2.4.1	pyruvate dehydrogenase (acetyl-transferring)	1,01	1,05	-1,08	-1,46	-1,95	-2,13	-2,27
_2160	pdhC1	2.3.1.12	Dihydrolipoyllysine-residue acetyltransferase	-1,04	-1,03	-1,12	-1,16	-2,41	-2,39	-2,54
_2161	cysE	2.3.1.30	serine O-acetyltransferase	-1,02	1,00	-1,01	1,04	1,02	-1,03	1,01
_2162	0		hypothetical protein	-1,03	1,03	1,31	1,74	1,66	1,10	1,19
_2163	0		hypothetical protein	-1,03	-1,01	1,11	1,12	1,11	-1,02	1,18
_2164	0		NlpC/P60 family phage cell wall peptidase	-1,07	-1,04	1,04	1,10	1,05	1,26	-1,06
_2165	0		hypothetical protein	-1,00	-1,01	1,00	1,15	1,16	1,19	1,19
_2166	0		hypothetical protein	-1,06	-1,00	-1,01	1,18	1,23	1,27	1,16
_2167	0		phage-related minor tail protein-like protein	1,05	-1,03	1,02	1,27	1,17	1,06	-1,06
_2168	0		hypothetical protein	-1,03	-1,04	-1,03	1,10	1,16	1,11	1,22
_2169	0		hypothetical protein	1,02	1,00	1,04	1,15	1,18	1,22	1,25
_2170	0		TP901-1 family phage major tail protein	1,03	-1,04	1,03	1,05	1,08	1,07	1,24
_2171	0		hypothetical protein	-1,14	-1,03	1,02	-1,03	1,13	1,03	1,30
_2172	0		phage head-tail adaptor, putative	-1,04	-1,02	1,13	1,01	1,14	1,06	1,20
_2173	0		hypothetical protein	-1,04	1,00	-1,01	1,04	1,14	1,07	1,23
_2174	0		HK97 family phage major capsid protein	-1,06	-1,01	1,19	-1,06	1,04	1,03	-1,10
_2175	0		HK97 family phage prohead protease	1,01	-1,01	1,13	1,10	1,17	1,05	1,25
_2176	0		hypothetical protein	1,06	1,00	-1,04	-1,05	1,20	1,21	1,32
_2177	0		HK97 family phage portal protein	-1,11	-1,02	1,01	1,17	1,18	1,04	1,02
_2178	0		hypothetical protein	-1,05	-1,02	-1,04	-1,03	1,03	1,06	1,12

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_2179	0		aminodeoxychorismate lyase	1,03	1,00	-1,00	-1,13	-1,52	-1,94	-1,32
_2180	fabF	2.3.1.179, 2.3.1.41	beta-ketoacyl-[acyl-carrier-protein] synthase II,beta-ketoacyl-[acyl-carrier-protein] synthase I	1,12	1,08	-1,09	-1,27	-1,57	-1,96	-1,25
_2181	acpP		acyl carrier protein	1,11	1,10	-1,10	-1,49	-2,92	-3,8	-1,68
_2182	0		3-oxoacyl-(acyl-carrier-protein) reductase	1,03	1,05	-1,02	-1,16	-1,58	-1,77	-1,18
_2183	fabD	2.3.1.39	[acyl-carrier-protein] S-malonyltransferase	1,02	1,06	-1,02	-1,07	-1,23	-1,30	1,00
_2184	0		cytochrome B561	-1,03	1,06	-1,00	-1,13	1,07	1,13	1,18
_2185	0		YceI family protein	-1,02	-1,03	-1,08	1,06	-1,19	-1,26	-1,13
_2186	rpsF		30S ribosomal protein S6	1,09	1,13	-1,23	-1,35	-2,09	-4,15	-1,98
_2187	rpsR		30S ribosomal protein S18	1,05	1,06	-1,22	-1,63	-2,36	-3,47	-1,98
_2188	rplI		50S ribosomal protein L9	1,04	1,06	-1,23	-1,77	-2,73	-4,71	-2,4
_2189	cpdB	3.1.4.16	2,3-cyclic-nucleotide 2-phosphodiesterase	-1,04	-1,04	1,06	1,06	1,08	1,17	-1,08
_2190	tig	5.2.1.8	Peptidylprolyl isomerase	1,11	1,13	-1,16	-1,37	-1,60	-2,49	-1,30
_2191	0		ETC complex I subunit region	-1,02	1,12	1,27	1,42	1,8	1,45	1,49
_2192	uvrB		excinuclease ABC subunit B	-1,11	-1,05	1,07	1,23	1,13	-1,07	-1,24
_2193	0		hypothetical protein	-1,14	-1,05	-1,01	1,02	-1,10	-1,07	-1,29
_2194	0		hypothetical protein	-1,01	1,00	1,02	1,03	-1,05	1,19	1,16
_2195	0		entericidin EcnAB	-1,22	-1,16	-1,04	1,17	-1,03	1,19	1,23
_2196	0		hypothetical protein	-1,01	-1,02	-1,14	-1,33	-1,47	-1,37	-1,17
_2197	0		putative ABC transporter ATP-binding protein	1,10	1,12	-1,12	-1,14	-1,20	-1,51	1,04
_2198	0		MOSC domain-containing protein	1,01	-1,02	-1,02	1,07	1,00	1,18	1,10
_2199	0		aspartate racemase	1,01	-1,01	1,05	1,05	-1,07	-1,19	1,09
_2200	0		regulatory protein TetR	-1,02	-1,00	-1,04	-1,01	-1,03	-1,08	-1,08
_2201	0		S-isoprenylcysteine methyltransferase-like protein	-1,03	-1,02	-1,11	-1,03	-1,03	-1,17	1,05
_2202	0		hypothetical protein	-1,04	-1,12	-1,02	1,10	1,06	1,31	1,02
_2203	nadD	2.7.7.18	Nicotinate-nucleotide adenylyltransferase	-1,00	-1,01	-1,01	-1,05	1,00	-1,05	1,05
_2204	0		hypothetical protein	1,00	-1,03	-1,08	-1,04	-1,02	-1,05	1,04
_2205	0		hypothetical protein	1,05	1,09	1,06	1,15	-1,03	-1,15	1,23
_2206	lysK	6.1.1.6	Lysine-tRNA ligase	1,18	1,17	-1,06	-1,39	-1,39	-1,98	-1,37
_2207	0		hypothetical protein	1,10	1,05	-1,14	-1,12	-1,43	-1,62	-1,20
_2208	0		D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase	-1,07	-1,04	1,19	1,19	1,09	1,12	-1,07
_2209	0		hypothetical protein	-1,00	1,00	-1,03	-1,08	-1,15	-1,25	1,04
_2210	0		hypothetical protein	-1,02	1,01	-1,07	-1,03	1,04	1,16	1,03
_2211	0		hypothetical protein	-1,04	-1,00	-1,04	-1,25	1,00	1,19	1,02
_2212	0		pyridoxamine 5'-phosphate oxidase-related FMN-binding	-1,08	-1,08	-1,09	-1,04	1,00	1,24	1,02
_2213	0		UspA domain-containing protein	1,24	1,65	3,26	7,34	12,7	7,07	3,94
_2214	0		antibiotic biosynthesis monooxygenase	1,04	1,19	2,08	4,49	6,19	3,83	1,85
_2215	0		hypothetical protein	-1,08	-1,03	1,07	1,23	1,38	1,40	1,12
_2216	0		cobyrinic acid ac-diamide synthase	-1,03	-1,02	1,01	1,03	-1,01	1,11	-1,07
_2217	0		hypothetical protein	-1,03	-1,02	1,03	1,03	1,18	1,39	1,37
_2218	0		thioesterase superfamily protein	1,01	-1,05	-1,01	1,02	1,02	1,07	1,07
_2219	0		cold-shock DNA-binding domain-containing protein	-1,04	-1,06	-1,17	-1,26	-1,88	-1,39	-1,13
_2220	0		conserved hypothetical protein	1,02	-1,01	-1,12	-1,06	-1,04	-1,15	1,02
_2221	0		ABC transporter related	-1,12	-1,08	-1,03	-1,06	-1,22	-1,08	-1,50
_2222	0		extracellular solute-binding protein	-1,06	-1,05	-1,02	-1,02	-1,46	-1,35	-1,67
_2223	0		binding-protein-dependent transport systems inner membrane component	-1,03	-1,06	1,04	-1,06	-1,29	-1,06	-1,45
_2224	0		polar amino acid ABC transporter, inner membrane subunit	1,01	-1,04	1,05	-1,13	-1,03	1,19	-1,07
_2225	0		glutamine amidotransferase class-I	-1,00	-1,07	1,07	1,24	1,26	1,38	1,03
_2226	0	6.3.1.2	Glutamate-ammonia ligase	1,00	-1,05	1,01	1,02	1,23	1,50	1,10
_2227	0		FAD dependent oxidoreductase	1,00	1,02	1,07	-1,09	1,02	1,34	1,23
_2228	0		DegT/DnrJ/EryC1/StrS aminotransferase	-1,10	-1,02	-1,35	-1,64	-1,67	-1,72	-1,15
_2229	0		LysR family transcriptional regulator	-1,01	1,00	1,01	-1,12	-1,18	-1,33	-1,29
_2230	0		polyhydroxyalkonate synthesis repressor, PhaR	1,01	1,05	1,03	-1,00	-1,09	-1,23	-1,25
_2231	0		hypothetical protein	1,15	1,30	1,28	1,55	3,29	1,82	3,75
_2232	0		hypothetical protein	1,16	1,26	1,10	1,35	2,44	1,18	2,9
_2233	phbC	2.3.1.-	poly-beta-hydroxybutyrate polymerase	1,06	1,20	1,49	2,29	3,07	2,07	2,28
_2234	0		polyhydroxyalkanoate depolymerase, intracellular	-1,03	1,03	1,01	1,11	1,29	1,15	1,14
_2235	0		methionine synthase vitamin-B12 independent	-1,06	1,01	1,02	1,01	-1,23	-1,32	-1,23
_2236	0		hypothetical protein	-1,01	-1,02	-1,03	1,05	-1,15	-1,02	-1,01

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_2237	0		hypothetical protein	-1,02	-1,02	-1,03	-1,18	-1,23	-1,06	-1,11
_2238	0		LacI family transcription regulator	-1,00	-1,00	-1,01	-1,15	-1,03	1,01	-1,02
_2239	0		short-chain dehydrogenase/reductase SDR	1,07	1,00	-1,07	1,02	-1,17	-1,14	-1,07
_2240	0		hypothetical protein	-1,04	-1,02	-1,09	1,05	-1,01	-1,03	1,06
_2241	0		hypothetical protein	-1,01	-1,03	-1,03	1,05	-1,19	-1,17	-1,31
_2242	hisD3	1.1.1.23	histidinol dehydrogenase	-1,12	-1,03	-1,08	-1,05	-1,42	-1,48	-2,03
_2243	0		alpha/beta hydrolase fold	1,00	1,01	-1,06	-1,02	1,00	-1,13	-1,06
_2244	0		hypothetical protein	-1,04	-1,04	-1,01	1,15	1,09	1,19	1,20
_2245	0		hypothetical protein	1,17	1,01	1,07	-1,06	1,48	1,58	1,59
_2248	0		putative aggregation factor core	1,02	-1,02	1,02	-1,07	1,26	1,27	1,24
_2249	nusB		NusB antitermination factor	1,08	1,01	-1,03	-1,15	-1,93	-2,83	-1,49
_2250	ribH	2.5.1.78	6,7-dimethyl-8-ribityllumazine synthase	1,05	1,04	-1,18	-1,39	-1,74	-2,44	-1,48
_2251	ribB	4.1.99.12	3,4-dihydroxy-2-butanone-4-phosphate synthase	1,20	1,20	-1,03	-1,14	-1,43	-2,64	-1,37
_2252	ribC	2.5.1.9	riboflavin synthase	1,07	1,02	-1,11	-1,16	-1,43	-1,77	-1,47
_2253	0		capsule polysaccharide biosynthesis protein	-1,02	-1,05	-1,03	1,05	1,17	1,04	-1,05
_2254	0		polysaccharide export protein	-1,07	-1,05	1,12	1,42	1,27	-1,10	-1,13
_2255	0		capsule polysaccharide biosynthesis protein	-1,00	-1,02	-1,04	-1,13	1,13	1,43	1,09
_2256	ribD	1.1.1.193	5-amino-6-(5-phosphoribosylamino) reductase	1,01	-1,05	1,03	-1,10	1,14	1,21	1,02
_2257	nrdR		transcriptional regulator NrdR	-1,04	1,03	1,04	1,29	1,30	1,08	-1,07
_2258	0		hypothetical protein	1,02	-1,02	-1,02	-1,17	1,03	1,12	-1,02
_2259	0		hypothetical protein	-1,06	-1,02	1,01	-1,12	-1,08	-1,09	-1,20
_2260	0		hypothetical protein	1,02	-1,03	-1,04	-1,00	-1,13	1,02	1,03
_2261	rpoD		RNA polymerase sigma factor RpoD	1,02	1,04	-1,03	1,01	-1,10	-1,17	1,02
_2262	dnaG	2.7.7.-	DNA primase	-1,02	-1,03	1,07	-1,01	1,01	1,16	1,09
_2263	0		sarcosine oxidase, gamma subunit, putative	-1,01	-1,01	1,07	-1,05	1,05	1,16	1,06
_2264	0	1.5.3.1	sarcosine oxidase	-1,05	-1,06	1,10	1,10	1,09	1,08	-1,12
_2265	0		sarcosine oxidase delta subunit heterotetrameric	-1,11	-1,06	1,03	1,06	-1,01	1,11	-1,25
_2266	0	1.5.3.1	sarcosine oxidase	-1,08	-1,08	1,00	1,13	1,14	1,08	-1,09
_2267	0		hypothetical protein	1,04	-1,02	1,01	1,29	1,61	1,55	1,94
_2268	0		TadE family protein	1,03	1,02	1,08	1,20	1,49	1,46	1,89
_2269	0		hypothetical protein	1,01	-1,02	-1,01	1,11	1,40	1,56	1,82
_2270	0		hypothetical protein	-1,13	-1,11	-1,05	-1,19	-1,22	1,05	-1,09
_2271	0		TetR family transcriptional regulator	-1,16	-1,12	-1,18	-1,66	-1,50	-1,15	-1,44
_2272	0		hypothetical protein	-1,09	-1,06	-1,06	-1,06	-1,15	-1,15	-1,16
_2273	0	1.1.1.3	homoserine dehydrogenase	1,12	1,11	-1,17	-1,29	-1,64	-2,21	-1,48
_2274	glpX	3.1.3.11	Fructose-bisphosphatase	1,02	1,02	-1,09	-1,22	-1,14	-1,58	-1,18
_2275	recJ			-1,03	-1,01	-1,06	-1,35	-1,40	-1,39	-1,01
_2276	0		hypothetical protein	-1,05	1,05	1,51	1,8	3,26	2,91	1,21
_2277	moeA2		molybdenum cofactor synthesis domain-containing protein	1,05	1,07	1,45	1,94	4,3	3,49	1,69
_2278	dmsA1	1.7.2.3	Trimethylamine-N-oxide reductase (cytochrome c)	1,16	1,30	2,46	5,54	11,7	6,56	3,4
_2279	0		two component transcriptional regulator	-1,03	-1,03	-1,02	1,06	1,02	1,04	1,06
_2280	0		multi-sensor hybrid histidine kinase	-1,03	-1,04	1,11	1,21	1,09	1,09	-1,02
_2281	0		TMAO reductase system periplasmic protein TorT	-1,07	-1,06	1,06	1,18	1,16	1,30	-1,03
_2282	0		AraC family transcriptional regulator	-1,07	-1,11	-1,04	-1,09	-1,13	-1,02	-1,23
_2283	pamO	1.14.13.92	phenylacetone monooxygenase	1,03	1,02	-1,08	1,01	1,05	1,25	1,03
_2284	0		beta-lactamase	-1,06	-1,04	-1,07	-1,06	-1,17	-1,19	-1,27
_2285	0		hypothetical protein	1,02	-1,02	1,02	1,07	1,12	1,26	1,05
_2286	0		MarR family transcriptional regulator	-1,06	-1,02	1,05	-1,24	1,15	-1,01	-1,03
_2287	0		TRAP transporter, 4TM/12TM fusion protein	-1,01	1,06	1,03	1,06	-1,07	1,02	-1,18
_2288	0		TRAP transporter solute receptor TAXI family protein	1,00	-1,01	-1,02	-1,18	-1,05	1,04	1,07
_2289	0		amidohydrolase	-1,02	-1,01	-1,04	-1,07	-1,05	1,01	-1,08
_2290	0		carbohydrate-selective porin OprB	-1,05	-1,02	1,04	1,07	-1,25	-1,30	-1,28
_2291	0		protein of unknown function DUF306 Meta and HslJ	-1,03	1,02	1,07	1,19	1,00	-1,03	-1,15
_2292	0		hypothetical protein	1,02	-1,00	-1,01	1,04	-1,00	-1,09	1,02
_2293	0		secretion protein HlyD family protein	1,03	1,01	1,01	-1,13	-1,29	-1,43	-1,26
_2294	0		Pyrrolo-quinoline quinone	1,07	1,05	-1,13	-1,06	-1,19	-1,26	1,02
_2295	0		amidohydrolase	1,18	1,21	-1,04	-1,27	-1,05	-1,86	-1,04
_2296	0		transposase IS4 family protein	-1,02	-1,03	-1,07	1,11	-1,02	1,03	1,08
_2297	0		IS5 family transposase OrfA	1,00	1,01	-1,01	-1,01	-1,02	-1,02	1,31
_2298	0		alanine racemase domain-containing protein	-1,02	-1,01	-1,02	1,03	-1,17	1,08	1,22
_2299	0		hypothetical protein	-1,04	1,00	1,01	1,09	-1,28	-1,11	1,41

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_2300	0		hypothetical protein	-1,06	-1,06	-1,07	-1,08	-1,05	1,04	1,12
_2301	0		hypothetical protein	-1,07	-1,02	-1,14	-1,31	1,02	1,19	1,56
_2302	0		hypothetical protein	1,05	1,02	-1,07	-1,02	2,32	10,4	9,74
_2303	0		NnrS family protein	1,03	-1,00	1,14	1,06	4,01	12,6	10,8
_2304	0		hemerythrin HHE cation binding domain-containing protein	1,05	-1,04	1,14	1,17	6,22	16,3	16,8
_2305	0		globin	1,01	1,02	1,07	1,35	4,48	8,98	6,11
_2306	0		BadM/Rrf2 family transcriptional regulator	1,03	-1,01	-1,13	1,18	3,82	8,45	7,85
_2307	0		hypothetical protein	-1,08	-1,03	-1,02	-1,04	2,89	5,93	5,69
_2308	0		hypothetical protein	-1,01	-1,00	1,03	-1,03	2,6	5,7	6
_2309	0	3.5.3.1	arginase	1,02	1,03	-1,08	1,01	1,03	1,33	1,87
_2310	0	4.3.1.12	ornithine cyclodeaminase	-1,03	1,03	-1,03	-1,20	-1,08	1,13	1,45
_2311	putA	1.5.99.8, 1.5.1.12	proline dehydrogenase,1-pyrroline-5-carboxylate dehydrogenase	1,01	-1,01	-1,02	1,05	1,02	1,07	1,08
_2312	0		hypothetical protein	1,07	1,00	-1,01	1,12	1,18	1,35	1,21
_2313	0		threonyl/alanyl tRNA synthetase SAD	-1,01	1,02	-1,09	-1,09	-1,34	-1,60	-1,42
_2314	0		pyridoxal-5'-phosphate-dependent protein beta subunit	1,06	1,06	-1,02	-1,10	-1,24	-1,57	-1,15
_2315	0		NUDIX hydrolase	1,00	-1,07	1,04	-1,05	-1,02	-1,03	1,32
_2316	0		hypothetical protein	1,00	-1,02	-1,03	-1,17	1,03	-1,02	1,31
_2317	cfa	2.1.1.79	Cyclopropane-fatty-acyl-phospholipid synthase	1,06	1,06	-1,13	-1,13	-1,13	-1,50	-1,11
_2318	phrB	4.1.99.3	deoxy ribodipyrimidine photo-lyase	1,01	-1,03	1,07	-1,08	-1,05	1,07	1,13
_2319	0		quinone oxidoreductase putative YhdH/YhfP	-1,01	-1,02	-1,00	1,03	-1,32	-1,39	-1,54
_2320	dmdA	2.1.2.10	aminomethyl transferase	1,02	-1,04	-1,05	1,02	-1,22	-1,11	-1,18
_2321	0		DinB family protein	1,02	-1,01	-1,01	-1,07	-1,48	-1,52	-1,49
_2322	0		hypothetical protein	1,02	1,00	-1,09	-1,05	-1,16	-1,15	-1,12
_2323	0		hypothetical protein	-1,14	-1,01	1,03	-1,03	-1,30	-1,38	-1,69
_2324	0		regulatory protein GntR HTH	1,02	1,01	1,01	1,06	1,03	1,09	-1,02
_2325	0		spermidine/putrescine ABC transporter, periplasmic spermidine/putrescine-binding protein	-1,10	-1,04	1,10	-1,08	-1,44	-1,70	-1,92
_2326	0		hypothetical protein	1,02	1,01	-1,11	-1,06	-1,20	-1,24	-1,21
_2327	0		hypothetical protein	-1,01	-1,06	-1,06	-1,33	-1,13	1,03	-1,06
_2328	0		tail collar domain-containing protein	-1,01	-1,03	-1,09	-1,28	-1,45	-1,29	-1,33
_2329	0		tail collar domain-containing protein	1,01	-1,02	-1,13	-1,07	-1,41	-1,30	-1,29
_2330	0		hypothetical protein	-1,04	-1,04	-1,05	-1,03	1,07	1,09	-1,04
_2331	0		antibiotic biosynthesis monooxygenase	1,02	-1,02	1,02	1,03	1,15	1,25	1,17
_2332	0		chromate transporter	1,02	1,00	-1,03	1,04	1,08	1,23	1,05
_2333	0		hypothetical protein	-1,06	-1,06	-1,02	1,12	1,06	1,07	-1,31
_2334	fumC	4.2.1.2	fumarate hydratase	1,00	1,15	1,23	-1,10	-1,43	-1,30	1,06
_2335	0		arylsulfate sulfotransferase-like protein	-1,03	-1,03	1,01	1,15	-1,27	-1,33	-1,49
_2336	0		hypothetical protein	-1,04	-1,01	-1,02	1,19	1,37	1,51	-1,09
_2337	0		cytochrome P450	-1,08	1,00	1,05	-1,17	-1,05	-1,01	1,03
_2338	0		hypothetical protein	-1,05	-1,03	1,02	1,17	-1,02	-1,14	-1,12
_2339	0		SirA family protein	-1,00	1,01	1,06	-1,04	-1,08	-1,32	-1,04
_2340	0		ribonuclease	1,04	-1,01	-1,21	-1,64	-1,54	-1,57	-1,40
_2341	0		TRAP C4-dicarboxylate transport system permease DctM subunit	1,02	-1,01	-1,11	-1,27	-1,8	-1,81	-1,72
_2342	0		TRAP-type mannitol/chloroaromatic compound transport system small permease component-like protein	-1,04	-1,06	-1,03	-1,41	-2,11	-2,2	-2,05
_2343	0		TRAP dicarboxylate transporter- DctP subunit	-1,11	-1,07	-1,17	-1,37	-3,06	-3,05	-2,96
_2344	0		integral membrane sensor signal transduction histidine kinase	-1,06	-1,03	-1,04	1,00	1,05	1,10	-1,02
_2345	0		two component LuxR family transcriptional regulator	1,00	1,00	1,08	-1,07	-1,14	-1,41	-1,12
_2346	tgt	2.4.2.29	tRNA-guanosine34 transglycosylase	1,09	1,07	1,01	-1,15	-1,12	-1,05	1,10
_2347	0		LysR family transcriptional regulator	1,02	-1,01	1,04	1,04	1,27	1,44	1,34
_2348	0		FeS assembly SUF system protein	-1,04	1,05	1,05	1,29	1,39	1,43	1,37
_2349	0		iron-sulfur cluster assembly accessory protein	-1,01	1,02	-1,06	-1,09	1,20	1,22	1,34
_2350	0		molybdopterin binding domain-containing protein	-1,01	-1,01	-1,01	-1,06	1,05	1,02	-1,30
_2351	0		hypothetical protein	-1,01	-1,03	-1,04	-1,03	-1,19	-1,17	-1,45
_2352	0		hypothetical protein	1,01	-1,01	1,06	1,14	1,18	1,43	1,10
_2353	0		hypothetical protein	-1,01	1,02	-1,01	-1,10	1,13	1,34	1,29
_2354	0		major facilitator transporter	1,01	1,01	1,14	1,14	1,04	-1,05	1,19

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_2355	0		VWA containing CoxE family protein	-1,03	-1,06	-1,01	-1,11	-1,09	-1,10	-1,26
_2356	0		ATPase	-1,08	-1,08	-1,03	-1,10	-1,35	-1,34	-1,62
_2357	0	1.3.8.6	glutaryl-CoA dehydrogenase	-1,04	1,02	-1,05	-1,20	-1,18	-1,36	-1,07
_2358	0		lysine exporter protein LysE/YggA	-1,04	-1,02	-1,00	1,10	-1,06	-1,24	1,04
_2359	0		hypothetical protein	-1,04	1,02	1,18	-1,09	-1,06	-1,01	1,08
_2360	ureG		urease accessory protein UreG	-1,03	-1,00	1,07	1,09	1,13	1,27	1,60
_2361	0		carboxymuconolactone decarboxylase	-1,05	1,03	1,03	-1,31	1,16	1,36	2
_2362	ureF		urease accessory protein UreF	-1,10	-1,04	1,13	1,02	1,26	1,42	1,16
_2363	ureE		UreE urease accessory domain-containing protein	1,16	-1,03	1,31	1,58	2,72	1,99	3,02
_2364	0		hypothetical protein	1,20	1,03	1,40	4,35	7,87	3,29	6,23
_2365	ureC	3.5.1.5	urease	1,09	-1,01	-1,10	-1,01	1,27	1,37	1,96
_2366	0		hypothetical protein	1,04	1,05	1,21	1,41	2,64	2,45	3,23
_2367	0		alginate regulatory protein AlgP	-1,01	1,06	1,19	1,14	2,36	1,94	2,79
_2368	ureB	3.5.1.5	urease	-1,07	1,05	1,23	1,57	2,43	2,36	2,23
_2369	ureA	3.5.1.5	urease	1,02	1,06	1,28	1,41	2,47	2,05	2,37
_2370	ureD		urease accessory protein UreD	1,02	1,07	1,29	1,99	2,96	1,85	2,36
_2371	pyrC2	3.5.2.3	dihydroorotase	1,04	1,05	-1,12	-1,37	-1,15	-1,31	-1,06
_2372	pyrE	2.4.2.10	orotate phosphoribosyl transferase	1,17	1,06	-1,08	-1,07	-1,32	-1,68	-1,10
_2373	dnaB	3.6.1.-	replicative DNA helicase	-1,01	1,01	-1,04	1,22	1,06	-1,22	-1,32
_2374	0		putative methyl-accepting chemotaxis sensory transducer	1,02	-1,03	1,10	1,14	1,17	1,14	1,18
_2375	0		hypothetical protein	-1,05	-1,04	1,08	1,07	1,07	1,31	1,02
_2376	0		hypothetical protein	-1,03	1,00	-1,08	1,02	-1,08	-1,14	-1,17
_2377	0		hypothetical protein	-1,02	-1,04	-1,19	-1,27	-1,56	-1,22	-1,73
_2378	alr	5.1.1.1	Alanine racemase	1,05	1,05	-1,04	-1,23	-1,17	-1,26	-1,00
_2379	0		hypothetical protein	-1,01	1,02	-1,02	-1,11	-1,39	-1,43	-1,44
_2380	0		ABC transporter related	1,05	-1,01	-1,07	-1,05	-1,37	-1,48	-1,13
_2381	lipB	2.3.1.181	lipoyl(octanoyl) transferase	1,02	1,04	-1,03	-1,01	-1,12	-1,22	-1,19
_2382	0		hypothetical protein	1,02	1,03	-1,07	-1,09	-1,22	-1,30	-1,11
_2383	ctaD	1.9.3.1	cytochrome-c oxidase	-1,01	1,05	-1,22	-1,57	-2,3	-2,19	1,11
_2384	0		integral membrane protein-like protein	-1,01	1,01	-1,17	-1,62	-1,96	-1,69	1,03
_2385	0		TraR/DksA family transcriptional regulator	1,01	1,00	-1,11	-1,09	-1,17	-1,03	1,10
_2386	0		GatB/YqeY	1,04	1,03	-1,05	-1,02	-1,17	-1,10	1,05
_2387	carA	6.3.5.5	Carbamoyl-phosphate synthase (glutamine-hydrolysing)	1,05	1,13	-1,01	-1,31	-1,30	-1,56	-1,14
_2388	0		glycosyl transferase family protein	1,03	-1,00	-1,10	-1,50	1,19	1,25	1,05
_2389	0		GntR family transcriptional regulator	-1,06	-1,02	-1,05	-1,05	-1,31	-1,13	-1,59
_2390	0		pyrimidine 5'-nucleotidase	1,04	1,06	-1,04	-1,05	-1,04	-1,36	1,13
_2391	0		hypothetical protein	1,23	1,26	1,40	2,08	4,36	1,85	3,7
_2392	0		2-octaprenyl-6-methoxyphenyl hydroxylase	-1,00	1,04	1,02	1,05	1,43	1,18	1,44
_2393	0		aminotransferase family protein, putative	1,08	1,19	1,28	1,25	1,71	1,39	1,45
_2394	0		AsnC family transcriptional regulator	-1,04	-1,01	-1,01	-1,12	-1,05	-1,07	-1,01
_2395	0		AsnC family transcriptional regulator	1,09	1,01	-1,04	1,01	1,10	-1,01	1,07
_2396	ilvC	1.1.1.86	ketol-acid reductoisomerase	1,08	1,01	-1,19	-1,05	1,22	-2,6	-1,43
_2397	glmM	5.4.2.10	phosphoglucosamine mutase	1,01	1,04	-1,11	-1,45	-1,38	-1,59	-1,19
_2398	folP	2.5.1.15	dihydropteroate synthase	1,09	1,06	-1,14	-1,17	-1,49	-1,89	-1,26
_2399	0		dihydroneopterin aldolase	1,04	1,04	-1,10	-1,16	-1,21	-1,25	-1,08
_2400	0		cell wall hydrolase SleB	1,19	1,20	1,12	1,29	1,53	-1,27	1,35
_2401	0	2.7.9.1	pyruvate, phosphate dikinase	-1,05	1,06	1,22	1,23	-1,15	-1,32	1,00
_2402	glyS	6.1.1.14	glycine-tRNA ligase	1,03	1,03	-1,03	-1,52	-1,81	-2,13	-1,42
_2403	0		hypothetical protein	1,03	1,06	1,04	-1,11	-1,24	-1,59	-1,08
_2404	glyQ	6.1.1.14	glycine-tRNA ligase	1,12	1,08	-1,07	-1,10	-1,11	-1,38	1,03
_2405	0		peptidoglycan binding domain-containing protein	-1,09	-1,01	1,11	1,10	1,14	-1,05	1,06
_2406	trkG		cation transporter	1,03	-1,01	-1,09	-1,15	-1,10	1,01	-1,01
_2407	0		glutathione S-transferase domain-containing protein	-1,07	-1,05	-1,02	-1,02	-1,00	1,13	-1,17
_2410	0		O-succinylhomoserine sulfhydrylase	1,11	1,06	-1,16	-1,37	-1,39	-1,71	1,03
_2411	0	3.5.4.16	GTP cyclohydrolase I	-1,29	-1,33	-1,40	-1,31	1,08	-1,23	1,17
_2412	0		chloride channel core	-1,08	1,00	1,08	1,18	1,30	1,42	1,30
_2413	recN		DNA repair protein RecN	1,05	1,01	1,02	-1,11	-1,06	-1,18	1,04
_2414	0		competence lipoprotein ComL, putative	1,04	1,05	-1,07	-1,01	-1,04	-1,13	1,13
_2415	lpxC	3.5.1.-	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosaminedeacetylase"	-1,02	-1,01	-1,23	-1,72	-1,32	-1,25	-1,12

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_2416	ftsZ		cell division protein FtsZ	-1,02	-1,04	-1,16	-1,12	-1,04	1,06	1,16
_2417	ftsA		cell division protein FtsA	1,02	-1,01	1,04	-1,16	-1,05	-1,02	-1,01
_2418	0		cell division protein FtsQ	-1,00	-1,02	-1,04	-1,01	-1,02	1,03	1,02
_2419	ddl	6.3.2.4	D-Alanine-D-alanine ligase	-1,02	-1,05	-1,04	1,01	-1,14	1,04	-1,10
_2420	murB	1.3.1.98	UDP-N-acetylmuramate dehydrogenase	1,04	1,01	-1,03	-1,23	-1,12	-1,23	1,01
_2421	0		hypothetical protein	1,02	-1,01	-1,06	-1,16	-1,32	-1,29	-1,11
_2422	murC	6.3.2.8	UDP-N-acetylmuramate-L-alanine ligase	-1,01	-1,02	-1,06	-1,14	-1,47	-1,25	-1,11
_2423	murG	2.4.1.227	undecaprenyl diphospho-muramoylpentapeptide beta-N-acetylglucosaminyl transferase	-1,00	-1,03	-1,07	-1,09	-1,17	-1,07	1,06
_2424	0		cell division protein FtsW	-1,01	-1,04	-1,06	1,03	1,10	1,22	1,18
_2425	0		hemolysin-type calcium-binding region	-1,02	-1,03	1,05	1,17	1,09	1,11	-1,06
_2426	0		peptidase S8 and S53 subtilisin kexin sedolisin	-1,01	-1,11	1,09	1,06	-1,19	-1,07	1,00
_2427	0		hypothetical protein	-1,02	1,01	-1,01	-1,09	-1,09	-1,16	-1,07
_2428	0		ECF subfamily RNA polymerase sigma-24 factor	1,04	1,01	-1,02	-1,11	-1,03	-1,08	-1,03
_2429	0		carbohydrate kinase FGGY	-1,10	-1,06	-1,01	1,13	-1,06	-1,02	-1,39
_2430	0	5.1.3.n3	L-rhamnose 1-epimerase	-1,02	-1,03	-1,08	1,15	-1,07	-1,02	-1,21
_2431	0		monosaccharide-transporting ATPase	-1,00	-1,03	-1,04	1,17	-1,17	-1,07	-1,10
_2432	0		monosaccharide-transporting ATPase	-1,10	-1,05	-1,04	-1,02	-1,29	-1,08	-1,20
_2433	rbsA1	3.6.3.17	Monosaccharide-transporting ATPase	-1,01	-1,07	-1,11	-1,57	-1,34	-1,13	-1,23
_2434	0		rhamnose ABC transporter, periplasmic rhamnose-binding protein	-1,09	-1,12	-1,21	-1,28	-2,02	-1,69	-2,03
_2435	0		DeoR family transcriptional regulator	-1,13	-1,09	-1,15	-1,10	-1,26	-1,12	-1,36
_2436	0		short chain dehydrogenase	-1,05	-1,07	-1,15	-1,08	-1,31	-1,12	-1,06
_2437	rhaA	5.3.1.14	L-Rhamnose isomerase	1,01	-1,02	-1,10	-1,09	-1,31	-1,18	-1,33
_2438	0		amidohydrolase 2	1,02	1,03	-1,00	1,05	-1,06	1,10	1,01
_2439	0		hypothetical protein	1,02	-1,03	1,01	1,17	1,02	1,07	1,20
_2440	0		hypothetical protein	1,06	-1,01	1,06	1,13	1,01	-1,12	-1,05
_2441	0		hypothetical protein	1,00	1,00	-1,05	-1,15	-1,04	-1,10	-1,10
_2442	aldH1	1.2.1.4	aldehyde dehydrogenase (NADP+)	-1,00	-1,01	-1,02	1,11	-1,01	1,08	1,06
_2443	0		6-phosphogluconate dehydrogenase NAD-binding	1,03	-1,04	1,03	1,05	1,03	1,00	1,05
_2444	pdxA	1.1.1.262	4-hydroxy threonine-4-phosphate dehydrogenase	-1,01	-1,02	1,00	1,08	-1,06	-1,04	-1,12
_2445	0		GntR family transcriptional regulator	1,00	-1,03	-1,02	1,06	-1,05	-1,11	1,03
_2446	0	4.2.1.43, 4.3.3.7	2-dehydro-3-deoxy-L-arabinonate dehydratase,4-hydroxy-tetrahydro dipicolinate synthase	-1,01	-1,01	-1,05	-1,06	1,00	-1,07	1,01
_2447	0		mandelate racemase/muconate lactonizing protein	-1,09	-1,02	-1,02	1,07	1,04	1,12	-1,40
_2448	0		hypothetical protein	1,00	-1,02	1,02	1,19	1,07	1,04	-1,20
_2449	0		hypothetical protein	-1,01	-1,00	-1,19	-1,26	-1,14	-1,05	-1,06
_2450	0		hypothetical protein	-1,06	-1,07	-1,12	-1,06	-1,48	-1,56	-1,37
_2451	murD	6.3.2.9	UDP-N-acetylmuramoyl-L-alanine-D-glutamate ligase	-1,03	1,04	-1,04	-1,03	-1,21	-1,27	-1,37
_2452	0		glycoside hydrolase family protein	-1,01	-1,02	-1,01	-1,03	1,09	1,11	-1,00
_2453	0		hypothetical protein	-1,02	1,00	1,16	-1,01	1,08	1,10	1,02
_2454	0		hypothetical protein	-1,11	-1,04	1,01	-1,07	-1,04	1,31	-1,07
_2455	0		ATPase central domain-containing protein	-1,02	-1,03	1,01	1,04	1,17	1,20	1,16
_2456	0		hypothetical protein	-1,04	-1,01	-1,04	1,04	1,05	1,26	-1,11
_2457	0		hypothetical protein	1,01	-1,01	1,00	1,08	1,15	1,32	1,10
_2458	0		hypothetical protein	1,01	1,02	1,01	-1,17	-1,13	1,27	-1,38
_2459	0		hypothetical protein	-1,02	-1,08	-1,04	1,12	-1,03	1,09	-1,06
_2460	0		GPW/gp25 family protein	-1,04	-1,01	-1,07	-1,15	-1,04	1,24	-1,20
_2461	0		PAAR repeat-containing protein	1,02	1,02	-1,07	-1,01	-1,13	1,10	-1,22
_2462	0		Rhs element Vgr protein	-1,00	-1,01	-1,02	1,06	-1,03	1,18	-1,38
_2463	0		hypothetical protein	-1,04	-1,05	-1,05	1,01	-1,16	1,10	-1,27
_2464	0		phage tail protein	1,01	-1,02	-1,02	1,04	-1,33	1,11	-1,44
_2465	0		phage tail protein	-1,03	-1,05	-1,06	-1,05	-1,65	1,12	-1,96
_2466	0		hypothetical protein	-1,06	-1,09	-1,05	-1,11	-1,49	1,06	-1,82
_2467	0		mucin-associated surface protein (MASP)	-1,08	-1,05	-1,04	-1,12	-1,23	1,32	-1,64
_2468	0		hypothetical protein	-1,06	-1,08	1,05	-1,08	1,11	1,25	-1,03
_2469	mraY	2.7.8.13	Phospho-N-acetylmuramoyl-pentapeptide-transferase	1,03	1,01	-1,05	1,02	-1,08	1,02	1,02
_2470	murF	6.3.2.10	UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine ligase	-1,02	-1,01	1,05	1,16	-1,14	1,05	-1,13
_2471	murE	6.3.2.13	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-2,6-diaminopimelate ligase	-1,01	-1,01	-1,03	-1,15	-1,11	-1,04	-1,01
_2472	ftsI2	2.4.1.129	peptidoglycan glycosyltransferase	1,01	1,01	1,08	1,02	-1,06	1,06	-1,03
_2473	0		putative FtsL	-1,01	-1,02	1,06	1,10	-1,01	1,17	1,02

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_2474	mraW	2.1.1.199	16S rRNA (cytosine1402-N4)-methyltransferase	-1,02	-1,02	1,09	-1,02	1,06	1,06	1,02
_2475	0		cell division protein MraZ	1,01	1,01	-1,09	-1,20	-1,00	-1,14	1,04
_2476	0		septum formation inhibitor-activating ATPase-like protein	-1,02	-1,01	1,03	1,05	1,03	1,09	-1,02
_2477	0		AsnC family transcriptional regulator	1,01	1,03	-1,03	-1,15	-1,18	-1,27	-1,50
_2478	0		lysine exporter protein LysE/YggA	1,02	-1,02	-1,08	-1,06	1,17	1,23	1,44
_2479	0		LysR family transcriptional regulator	1,06	1,01	1,05	-1,10	-1,17	-1,25	-1,00
_2480	0		short-chain dehydrogenase/reductase SDR	1,02	1,01	1,04	1,03	1,10	1,13	1,24
_2481	0		hypothetical protein	-1,07	-1,01	-1,13	1,16	1,12	1,37	1,34
_2482	0		ethyl tert-butyl ether degradation EthD	-1,10	-1,05	1,02	-1,11	-1,31	-1,32	-1,69
_2483	uvrD	3.6.4.12	DNA helicase	-1,08	-1,07	-1,03	1,01	-1,08	-1,08	-1,04
_2484	lldD1	1.1.2.3	L-lactate dehydrogenase (cytochrome)	1,07	1,06	1,02	-1,11	-1,09	-1,38	-1,07
_2485	0	6.4.1.1	pyruvate carboxylase	-1,00	1,03	-1,08	-1,27	-1,07	-1,25	-1,22
_2486	0		hypothetical protein	1,00	1,02	1,00	1,16	-1,05	1,08	1,07
_2487	0		cobalamin synthesis protein P47K	-1,10	1,01	-1,07	1,21	1,01	1,18	1,02
_2488	0		XRE family transcriptional regulator	1,02	-1,02	-1,05	1,05	1,15	1,31	1,94
_2489	0	2.6.1.45	serine-glyoxylate transaminase	1,34	1,19	1,19	1,27	1,66	1,57	1,79
_2490	citE1	4.1.3.34	citryl-CoA lyase	1,06	1,05	-1,09	-1,33	-1,70	-1,37	-1,66
_2491	sucC2	6.2.1.5	Succinate-CoA ligase (ADP-forming)	-1,02	-1,05	-1,13	-1,45	-2,31	-1,64	-2,34
_2492	sucD2	6.2.1.5	Succinate-CoA ligase (ADP-forming)	-1,03	-1,03	1,04	-1,20	-1,81	-1,15	-2,17
_2493	0		hypothetical protein	-1,02	-1,02	-1,11	-1,15	-1,69	-1,23	-1,93
_2494	0		acyl-CoA transferase/carnitine dehydratase-like protein	-1,03	-1,05	-1,10	-1,31	-1,62	-1,22	-1,74
_2495	0		cytochrome B561	-1,01	1,02	1,01	1,14	1,25	1,30	1,37
_2496	0		signal transduction protein	-1,17	-1,05	1,13	1,14	-1,01	1,13	1,10
_2497	0		two component transcriptional regulator	1,01	1,02	1,07	-1,05	1,03	1,10	1,16
_2498	0		integral membrane sensor signal transduction histidine kinase	-1,03	1,09	1,11	1,07	1,14	1,02	1,15
_2499	0		OmpA/MotB domain-containing protein	-1,01	-1,04	1,02	1,13	1,01	-1,12	1,01
_2501	0		ABC transporter related	-1,03	1,06	-1,12	1,00	1,06	1,14	1,22
_2502	0		HlyD family type I secretion membrane fusion protein	-1,03	-1,02	-1,06	-1,13	1,17	1,27	1,24
_2503	0		hemolysin-type calcium-binding region	1,00	-1,01	-1,11	1,11	1,15	1,17	-1,01
_2504	0		hypothetical protein	-1,04	1,03	-1,09	-1,12	1,10	1,13	1,16
_2505	0		hypothetical protein	1,03	1,01	-1,12	1,10	-1,01	1,01	1,10
_2506	0		hypothetical protein	1,01	-1,02	1,13	-1,22	1,03	1,04	1,22
_2509	0		integrase catalytic region	-1,03	-1,02	1,00	1,01	1,03	1,08	1,21
_2511	0		hypothetical protein	-1,01	1,01	1,05	1,07	1,04	1,33	1,25
_2512	dusA		tRNA-dihydrouridine synthase A	1,04	1,04	-1,01	-1,03	1,06	-1,01	-1,01
_2513	0		hypothetical protein	-1,00	-1,01	1,10	-1,09	-1,06	1,08	-1,24
_2514	0		hypothetical protein	-1,05	-1,04	1,17	1,04	1,15	1,28	1,04
_2515	0		sulfate transporter	1,01	1,00	-1,03	1,10	1,04	1,04	1,01
_2516	0		hypothetical protein	1,06	-1,02	1,07	1,24	1,16	1,23	1,33
_2517	0		beta-lactamase domain-containing protein	-1,00	1,05	-1,04	-1,12	-1,03	1,01	-1,07
_2518	0		protein of unknown function DUF395 YeeE/YedE	1,01	-1,01	1,08	1,08	-1,18	-1,07	-1,14
_2519	0		protein of unknown function DUF395 YeeE/YedE	-1,08	1,00	1,09	-1,09	-1,01	-1,06	-1,02
_2520	0		hypothetical protein	-1,05	1,04	-1,03	-1,15	-1,17	1,01	-1,08
_2521	0		Crp/FNR family transcriptional regulator	-1,07	-1,05	1,08	-1,12	-1,04	-1,04	-1,09
_2522	0	1.11.1.15	peroxiredoxin	-1,05	-1,04	1,03	1,03	1,09	1,17	1,02
_2523	0		LysR family transcriptional regulator	1,05	-1,02	-1,18	-1,14	-1,21	-1,15	-1,03
_2524	0		C4-dicarboxylate transporter/malic acid transport protein	1,00	1,03	-1,10	-1,17	-1,02	1,15	1,05
_2525	0		hypothetical protein	-1,04	-1,01	-1,04	-1,05	1,07	1,13	1,14
_2526	0		FAD-dependent pyridine nucleotide-disulphide oxidoreductase	-1,10	1,00	1,12	1,20	1,13	1,05	1,16
_2527	0		hypothetical protein	-1,06	-1,01	1,01	-1,12	-1,04	1,18	1,18
_2528	0		CRP/FNR family transcriptional regulator	1,09	-1,02	-1,01	1,22	1,25	1,11	1,35
_2529	0		hypothetical protein	-1,08	1,01	1,01	-1,07	1,14	1,25	1,15
_2530	0		aldehyde oxidase and xanthine dehydrogenase, molybdopterin binding	1,02	1,01	-1,01	1,03	1,11	1,16	1,35
_2531	0		hypothetical protein	1,08	-1,01	-1,06	1,15	1,16	1,20	1,35
_2532	0		twin-arginine translocation pathway signal	1,00	1,04	-1,00	-1,05	1,03	1,07	-1,11
_2533	0		hypothetical protein	-1,00	1,01	1,05	1,08	1,18	1,32	1,10
_2534	0		integral membrane protein	-1,05	-1,02	-1,01	1,06	1,08	1,22	1,14

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_2535	0		permease	-1,01	-1,00	-1,07	-1,12	1,16	1,30	1,24
_2536	0		hypothetical protein	1,01	1,02	-1,04	-1,04	-1,04	1,19	1,06
_2537	0	4.1.1.55	4,5-Dihydroxy phthalate decarboxylase	1,06	-1,01	-1,04	-1,12	-1,08	1,18	-1,03
_2538	0		fumarylacetoacetate (FAA) hydrolase	-1,05	-1,01	-1,08	-1,35	-1,06	1,05	-1,06
_2539	0		GntR domain-containing protein	-1,07	-1,02	1,05	1,02	-1,05	1,07	1,06
_2540	0		hypothetical protein	1,04	-1,00	-1,04	-1,07	1,14	1,16	1,23
_2541	0		GntR domain-containing protein	1,01	-1,01	-1,02	-1,17	-1,01	-1,09	-1,20
_2542	0		5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase	-1,09	-1,04	1,03	1,09	-1,22	-1,11	-1,10
_2543	0		NMT1/THI5-like domain-containing protein	-1,03	-1,05	-1,12	-1,11	-1,17	-1,11	-1,30
_2544	0		ABC transporter related	-1,02	1,01	-1,10	-1,38	-1,19	1,05	-1,22
_2545	0		binding-protein-dependent transport systems inner membrane component	-1,01	-1,04	-1,02	1,05	-1,06	1,04	-1,14
_2546	0		malate/L-lactate dehydrogenase	-1,02	-1,03	-1,06	-1,26	-1,04	1,08	-1,00
_2547	0		hypothetical protein	1,04	-1,02	1,01	-1,01	1,06	1,11	-1,03
_2548	0		hypothetical protein	-1,03	1,01	1,14	1,06	1,17	1,16	1,32
_2549	0		cell surface receptor IPT/TIG domain-containing protein	1,07	-1,01	-1,07	-1,00	1,13	1,14	1,14
_2550	0		hypothetical protein	-1,05	1,01	1,02	1,06	1,02	1,12	1,09
_2551	0		hypothetical protein	-1,01	-1,01	-1,05	1,21	1,06	1,07	1,22
_2552	0		hypothetical protein	-1,02	-1,01	1,01	-1,18	1,15	1,18	1,21
_2553	0		hypothetical protein	-1,03	1,03	1,03	1,15	1,04	-1,03	1,14
_2554	0		hypothetical protein	-1,05	1,03	1,17	1,11	1,00	-1,06	1,13
_2555	0		hypothetical protein	1,00	1,06	-1,00	1,03	1,18	1,26	-1,02
_2556	0		hypothetical protein	-1,05	1,03	-1,02	1,25	1,03	1,09	1,31
_2557	0		hypothetical protein	1,02	-1,03	-1,04	1,11	1,14	1,26	1,35
_2558	0		hypothetical protein	-1,04	1,02	-1,04	1,10	1,06	1,25	-1,02
_2559	0		ATPase central domain-containing protein	-1,02	1,01	1,03	1,10	1,23	1,16	1,16
_2560	0		hypothetical protein	1,07	1,02	1,07	1,16	1,12	1,11	1,24
_2561	0		hypothetical protein	-1,12	1,01	-1,01	1,13	1,08	1,31	1,11
_2562	0		hypothetical protein	-1,02	1,01	1,03	1,09	1,48	1,46	1,38
_2563	0		phage tail protein	1,03	1,03	-1,07	1,03	1,01	1,35	1,18
_2564	0		tail sheath protein	-1,02	1,00	1,03	1,13	1,10	1,08	1,24
_2565	0		two component LuxR family transcriptional regulator	-1,04	-1,03	-1,02	1,03	1,08	1,23	-1,12
_2566	0		transketolase central region	-1,06	-1,03	1,08	-1,00	-1,02	1,00	-1,14
_2567	0		multi-sensor signal transduction histidine kinase	-1,05	-1,08	-1,12	-1,07	-1,12	-1,08	-1,20
_2568	0		two component LuxR family transcriptional regulator	-1,07	-1,02	1,01	-1,10	-1,24	-1,11	-1,47
_2569	0		putative ammonia monooxygenase	-1,03	-1,01	-1,08	-1,02	-1,10	-1,01	1,34
_2570	0		GntR family transcriptional regulator	1,02	-1,01	-1,06	1,05	1,04	-1,07	1,48
_2571	0		RNA methyltransferase	1,07	1,02	-1,11	-1,24	-1,28	-1,42	-1,19
_2572	0		hypothetical protein	1,00	1,01	-1,01	-1,22	1,11	1,09	1,15
_2573	0		hypothetical protein	-1,02	1,04	-1,11	-1,18	-1,18	-1,08	1,05
_2574	0		CoA-binding domain-containing protein	-1,07	-1,06	1,00	1,06	-1,01	1,17	-1,01
_2575	hisE	3.6.1.31	phosphoribosyl-ATP diphosphatase	1,02	-1,00	-1,08	-1,16	-1,15	-1,25	-1,02
_2576	hisF	4.1.3.-	imidazole glycerol phosphate synthase subunitHisF"	1,13	1,04	-1,12	-1,21	-1,26	-1,73	-1,09
_2577	0		putative RNA methylase	1,04	1,08	1,08	1,13	-1,09	-1,19	1,09
_2578	hisA	5.3.1.16	1-(5-phospho ribosyl)-5-[(5-phosphoribosylamino) carboxamide isomerase	1,12	1,10	-1,10	-1,17	-1,55	-2,32	-1,29
_2579	0		hypothetical protein	-1,48	-1,46	-1,35	-1,59	-2,85	-1,60	-2,14
_2580	hrpB		ATP-dependent helicase HrpB	1,03	1,01	-1,05	-1,01	-1,34	-1,45	-1,19
_2581	0		hypothetical protein	-1,01	-1,03	1,04	1,10	1,10	1,39	1,22
_2582	0			1,07	1,08	1,12	1,09	1,32	1,09	1,37
_2583	rpmB		50S ribosomal protein L28	1,20	1,17	-1,06	-1,17	-1,39	-1,9	-1,19
_2584	0		hypothetical protein	-1,03	1,15	1,42	1,55	1,51	2,71	2,35
_2585	0		hypothetical protein	1,02	1,13	1,31	1,43	1,36	2,93	3,19
_2586	0		HpcH/HpaI aldolase	-1,01	-1,06	-1,03	1,08	-1,14	-1,29	-1,20
_2587	0		exonuclease of the beta-lactamase fold involved in RNA processing-like protein	-1,03	-1,02	1,07	1,04	-1,01	1,05	1,08
_2588	0		alpha/beta hydrolase domain-containing protein	-1,01	-1,00	1,03	-1,08	1,06	1,36	1,10
_2589	0	6.5.1.1	DNA ligase (ATP)	1,01	1,03	-1,05	1,00	1,11	1,09	1,07
_2590	0		integrase family protein	-1,07	-1,06	1,11	1,18	-1,02	-1,07	-1,02
_2591	0		BadM/Rrf2 family transcriptional regulator	1,07	1,04	-1,04	-1,09	-1,37	-1,43	-1,09
_2592	0		cobalamin synthesis protein P47K	1,00	1,02	-1,09	-1,12	-1,19	-1,21	-1,11

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_2593	0		hypothetical protein	-1,06	-1,05	-1,08	-1,05	-1,00	-1,01	-1,11
_2595	0		extracellular solute-binding protein	-1,01	-1,02	-1,09	1,04	-1,06	-1,06	-1,04
_2596	0		ABC transporter related	-1,11	-1,05	1,08	1,20	-1,14	-1,27	-1,25
_2597	0		ABC transporter related	-1,07	-1,01	-1,04	-1,04	-1,06	-1,03	1,10
_2598	0		binding-protein-dependent transport systems inner membrane component	-1,08	-1,03	-1,01	1,12	-1,08	-1,08	1,05
_2599	0		binding-protein-dependent transport systems inner membrane component	-1,10	-1,05	1,00	1,03	-1,08	-1,10	1,01
_2600	0		hypothetical protein	1,05	1,01	-1,08	-1,18	1,03	1,11	1,19
_2601	0		AraC family transcriptional regulator	-1,05	-1,07	1,11	1,17	1,08	1,18	-1,02
_2602	0		acyl-CoA dehydrogenase domain-containing protein	-1,03	1,02	1,06	-1,02	1,14	1,19	1,19
_2603	0		pepF/M3 family oligoendopeptidase	1,03	1,01	-1,10	-1,36	-1,10	-1,09	-1,07
_2604	0		hypothetical protein	1,01	-1,01	1,00	-1,08	-1,04	1,02	-1,08
_2605	0		hypothetical protein	-1,05	-1,02	1,04	-1,07	-1,16	-1,01	-1,28
_2606	0		zinc finger CDGSH-type domain-containing protein	-1,03	-1,02	1,03	-1,17	-1,03	1,10	1,08
_2607	0		hypothetical protein	-1,04	-1,05	1,02	-1,04	-1,04	1,07	-1,17
_2608	0		oxidoreductase domain-containing protein	-1,08	-1,07	-1,04	-1,07	-1,26	-1,16	-1,56
_2609	rpoH2		RNA polymerase factor sigma-32	1,04	1,02	-1,04	-1,02	1,02	-1,06	1,18
_2610	rluD		RluA family pseudouridine synthase	1,03	-1,00	-1,09	-1,07	-1,18	-1,09	-1,02
_2611	0		hypothetical protein	1,02	1,00	-1,02	-1,09	-1,09	-1,25	-1,00
_2612	npdA	3.5.1.-	NAD-dependent deacetylase	-1,06	-1,04	1,01	1,03	1,13	1,18	1,07
_2613	0		protein tyrosine phosphatase	-1,02	-1,03	1,00	-1,05	-1,09	1,12	-1,19
_2614	0		hypothetical protein	-1,00	-1,02	1,02	-1,11	1,15	1,34	1,36
_2615	0		ABC-2 type transporter	1,04	1,01	1,02	1,11	-1,06	-1,23	1,03
_2616	0		GcrA cell cycle regulator	1,04	1,04	-1,14	-1,27	-1,47	-1,59	-1,20
_2617	0		hypothetical protein	-1,21	-1,04	-1,15	-1,45	-2,24	-2,12	-1,37
_2618	rimO			1,06	1,05	-1,08	-1,38	-1,31	-1,8	-1,05
_2619	cutA		CutA1 divalent ion tolerance protein	1,05	-1,03	-1,10	-1,23	-1,44	-1,37	-1,04
_2620	0		hypothetical protein	1,11	1,48	2,38	2,85	5,16	3,41	2,23
_2621	0		hypothetical protein	1,69	3,32	6,08	8,99	12,3	8,94	5,63
_2622	0		hypothetical protein	2,01	3,69	6,4	8,28	11,2	9,11	6,01
_2623	0		peptidase M48 Ste24p	1,12	1,02	-1,05	-1,06	1,01	1,07	1,20
_2624	0		hypothetical protein	1,10	1,01	1,11	1,09	1,34	1,98	1,38
_2625	0		hypothetical protein	1,07	1,04	1,11	1,34	1,68	1,23	1,40
_2626	0		major facilitator transporter	1,02	1,02	1,15	-1,20	1,05	1,20	1,13
_2627	0		nitroreductase	1,04	1,08	1,16	1,27	1,69	1,47	1,31
_2628	0		hypothetical protein	1,03	1,02	-1,02	-1,13	-1,02	1,06	1,05
_2629	0		hypothetical protein	1,10	1,09	-1,09	-1,39	-1,28	-1,48	-1,05
_2630	0	5.1.99.1	Methylmalonyl-CoA epimerase	1,07	1,06	-1,14	-1,22	-1,30	-1,71	-1,10
_2631	0		response regulator receiver protein	1,05	-1,04	-1,01	-1,13	1,46	1,45	1,06
_2632	0		hypothetical protein	1,04	1,01	1,14	1,42	1,26	1,10	-1,16
_2633	aspS	6.1.1.12	Aspartate-tRNA ligase	1,14	1,10	-1,26	-1,58	-1,81	-2,63	-1,59
_2634	0		hypothetical protein	-1,13	-1,13	-1,00	-1,14	-1,32	-1,18	-1,26
_2635	0		pentapeptide repeat-containing protein	-1,19	-1,08	-1,09	-1,07	-1,19	-1,11	-1,16
_2636	0		bacteriochlorophyll 4-vinyl reductase	1,53	2,42	4,57	8,21	15,2	11,2	6,01
_2637	0	1.14.13.81	Magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase	1,78	3,04	6,18	12,5	17,7	11,5	6,29
_2638	0		hypothetical protein	-1,03	-1,05	-1,06	1,10	1,24	1,33	1,89
_2639	carB	6.3.5.5	Carbamoyl-phosphate synthase (glutamine-hydrolysing)	1,23	1,22	1,11	-1,24	-1,40	-1,99	-1,14
_2640	0		hypothetical protein	-1,09	-1,00	-1,06	1,19	1,08	1,15	1,04
_2641	tdk	2.7.1.21	thymidine kinase	1,07	-1,01	-1,13	-1,18	-1,07	-1,10	1,06
_2642	0		hypothetical protein	-1,09	-1,07	1,04	1,05	1,06	1,33	-1,24
_2643	0		D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding	-1,03	-1,01	1,02	-1,10	-1,11	-1,01	-1,22
_2644	0		export-related chaperone CsaA	-1,05	-1,06	1,00	1,07	-1,07	1,03	-1,33
_2645	proC	1.5.1.2	pyrroline-5-carboxylate reductase	-1,04	-1,02	1,06	-1,19	1,01	1,13	-1,18
_2646	0		hypothetical protein	-1,03	-1,01	1,19	1,17	1,38	1,53	1,01
_2647	0		hypothetical protein	-1,01	-1,02	-1,12	-1,36	-1,06	-1,05	1,52
_2648	0		hypothetical protein	1,02	1,07	1,07	-1,04	1,21	1,08	1,32
_2649	lgt	2.4.99.-	prolipoprotein diacylglyceryl transferase	1,07	1,05	1,03	-1,03	-1,42	-1,83	-1,02
_2650	0		hypothetical protein	1,03	-1,02	-1,15	-1,21	-1,26	-1,41	-1,00
_2651	0		hypothetical protein	-1,01	-1,04	-1,02	1,00	-1,04	-1,05	-1,13

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_2652	0		hypothetical protein	-1,05	-1,03	1,12	1,11	1,15	1,02	1,07
_2653	0		AsnC family transcriptional regulator	-1,38	-1,32	-1,40	-1,64	-1,84	-1,85	-2,06
_2654	trxB	1.8.1.9	Thioredoxin-disulfide reductase	-1,00	1,01	-1,06	-1,10	-1,20	-1,30	-1,25
_2655	ccpA	1.11.1.5	cytochrome-c peroxidase	1,22	2,01	3,62	4,37	9,29	7,84	9,34
_2656	0	2.7.7.4	sulfate adenylyltransferase	1,02	1,12	-1,31	-1,52	-1,05	-2,34	1,01
_2657	0		hypothetical protein	-1,01	-1,00	-1,01	-1,20	-1,27	-1,52	-1,24
_2658	0		molybdopterin dehydrogenase FAD-binding	-1,03	-1,08	-1,12	1,02	-3,19	-2,45	-3,2
_2659	coxL1	1.2.99.2	carbon-monoxide dehydrogenase (acceptor)	-1,04	-1,08	-1,26	-1,95	-2,99	-2,37	-2,83
_2660	0		2Fe-2S iron-sulfur cluster binding domain-containing protein	-1,06	-1,09	-1,29	-1,76	-3,03	-2,24	-2,76
_2661	0		carbon monoxide dehydrogenase subunit G	-1,09	-1,08	-1,11	-1,29	-2,21	-1,89	-2,15
_2662	0		extracellular solute-binding protein	-1,06	-1,03	-1,13	-1,32	-1,77	-1,51	-2,06
_2663	0		cytochrome c550, putative	-1,09	-1,03	-1,07	-1,08	-1,25	-1,23	-1,15
_2664	0		hypothetical protein	-1,08	-1,04	-1,20	-1,15	-1,42	-1,09	-1,33
_2665	0		YVTN beta-propeller repeat-containing protein	-1,05	-1,00	-1,13	-1,16	-1,32	-1,29	-1,22
_2666	0		hypothetical protein	-1,06	-1,07	-1,08	1,11	-1,71	-1,72	-2,1
_2667	0		ABC transporter related	1,00	1,00	1,02	-1,16	-1,14	1,04	-1,36
_2668	0		ABC-2 type transporter	-1,00	-1,02	-1,05	-1,16	-1,09	1,04	-1,11
_2669	0		Sel1 domain-containing protein	-1,05	-1,07	-1,02	-1,03	1,04	1,26	1,14
_2670	0		ABC transporter related	-1,01	1,02	-1,18	-1,21	-1,07	1,12	-1,05
_2671	0		putative ABC transporter periplasmic solute-binding protein	-1,01	-1,03	-1,05	-1,07	1,04	1,09	-1,03
_2672	0		cytochrome c class I	1,47	2,42	4,67	6,82	12,7	6,9	4,74
_2673	exaA		quinoprotein ethanol dehydrogenase precursor	-1,11	-1,11	-1,06	-1,31	-1,39	-1,47	-1,75
_2674	0		two component LuxR family transcriptional regulator	-1,11	-1,09	-1,04	1,10	-1,02	1,01	-1,17
_2675	0		hypothetical protein	-1,07	-1,03	-1,02	1,03	-1,47	-1,31	-1,97
_2676	0		histidine kinase	1,01	-1,00	1,06	1,10	1,16	1,10	-1,00
_2677	0		GDSL family lipase	1,00	-1,01	-1,02	1,04	1,18	1,52	1,52
_2678	0		ABC transporter related	-1,00	-1,01	-1,04	1,03	1,06	1,28	1,17
_2679	0		hypothetical protein	1,02	1,02	1,00	-1,11	-1,00	1,36	1,60
_2680	gcvP	1.4.4.2	glycine dehydrogenase (decarboxylating)	-1,00	1,03	1,02	-1,05	-1,28	-1,27	1,19
_2681	gcvH		glycine cleavage system protein H	1,03	1,05	-1,10	-1,36	-1,56	-1,63	1,07
_2682	gcvT2	2.1.2.10	aminomethyl transferase	1,05	1,03	-1,08	-1,15	-1,29	-1,50	1,12
_2683	mro	5.1.3.3	Aldose 1-epimerase	-1,09	1,03	1,21	1,22	1,28	1,35	-1,01
_2684	0		hydroxyisourate hydrolase	-1,06	-1,03	1,05	1,14	1,04	1,05	-1,09
_2685	gap3	1.2.1.12	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)	1,10	1,04	1,00	-1,13	-1,03	-1,50	-1,28
_2686	0		UspA domain-containing protein	1,23	1,51	3,3	6,75	9,82	5,76	2,45
_2687	0		pseudoazurin	-1,18	-1,08	1,11	1,23	1,31	1,33	1,28
_2688	appC	1.10.3.-	cytochrome bd-II oxidase subunit 1	-1,04	1,05	1,23	1,50	1,64	1,70	1,57
_2689	cydB	1.10.3.-	cytochrome bd-I oxidase subunit II	-1,01	-1,01	1,14	1,26	1,31	1,57	1,54
_2690	0		hypothetical protein	-1,06	-1,07	1,05	-1,07	-1,05	1,06	-1,08
_2691	0	3.1.2.6	hydroxyacyl glutathione hydrolase	-1,11	-1,03	1,02	-1,09	-1,20	-1,11	-1,34
_2692	0		hypothetical protein	-1,01	-1,04	1,06	-1,13	-1,03	1,10	1,02
_2693	0		hypothetical protein	-1,11	-1,06	-1,06	-1,01	-1,09	1,04	-1,10
_2694	0		cytochrome c family protein, putative	1,26	1,50	3,25	5,8	10	5,82	3,54
_2695	0		putative ureashort-chain amide or branched-chain amino acid uptake ABC transporter periplasmic solute-binding protein precursor	1,02	1,00	-1,01	1,13	1,33	1,58	1,42
_2696	0		inner-membrane translocator	-1,15	-1,03	-1,00	1,12	1,15	1,20	1,32
_2697	0		inner-membrane translocator	-1,03	1,00	1,03	1,07	1,04	1,08	1,13
_2698	0		ABC transporter related	-1,01	-1,01	-1,04	-1,00	-1,00	-1,01	1,10
_2699	0		ABC transporter related	1,10	1,03	-1,14	-1,47	-1,16	-1,52	-1,06
_2700	dhlB	3.8.1.2	(S)-2-haloacid dehalogenase	-1,09	-1,03	1,02	-1,05	-1,11	-1,17	-1,30
_2701	0		alpha/beta hydrolase fold	-1,01	-1,02	-1,02	-1,18	-1,01	-1,09	-1,23
_2702	0		pyridoxal-5'-phosphate-dependent protein beta subunit	1,02	1,00	1,20	1,05	-1,06	-1,05	-1,06
_2703	0		hypothetical protein	1,03	1,10	1,21	1,71	2,21	2,19	2,14
_2704	hemC	2.5.1.61	hydroxymethylbilane synthase	-1,00	1,05	1,06	1,06	1,44	1,16	1,27
_2705	hemE	4.1.1.37	Uroporphyrinogen decarboxylase	-1,04	-1,01	-1,08	-1,17	1,05	1,01	1,13
_2706	0		major facilitator transporter	-1,05	-1,04	-1,08	-1,10	-1,10	1,02	1,14
_2707	metG	6.1.1.10	Methionine-tRNA ligase	1,07	1,05	-1,09	-1,07	-1,21	-1,65	-1,17
_2708	0		PAS/PAC sensor hybrid histidine kinase	1,02	-1,05	-1,02	-1,03	1,00	-1,07	-1,11

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_2709	msrB1	1.8.4.11	peptide-methionine (S)-S-oxide reductase	-1,02	-1,04	-1,09	-1,11	-1,14	1,04	-1,02
_2710	0		hypothetical protein	1,07	1,07	1,00	-1,20	-1,13	-1,23	-1,26
_2711	cobS2	6.6.1.2	cobaltochelatase	1,03	1,05	-1,15	-1,33	-1,44	-1,87	-1,42
_2712	0	2.1.1.17	phosphatidyl ethanolamine N-methyltransferase	-1,01	-1,04	-1,08	-1,06	-1,00	1,08	1,07
_2713	0	2.7.8.8	CDP-diacylglycerol-serine O-phosphatidyl transferase	-1,06	-1,07	-1,16	-1,30	-1,40	-1,54	-1,24
_2714	psd	4.1.1.65	phosphatidylserine decarboxylase	-1,08	-1,05	-1,15	-1,15	-1,39	-1,50	-1,41
_2715	0		DEAD/DEAH box helicase domain-containing protein	-1,08	-1,09	-1,40	-1,54	-1,54	-1,58	1,10
_2716	0		hypothetical protein	-1,01	1,01	1,03	1,07	1,02	1,05	1,13
_2717	0		hypothetical protein	-1,01	-1,01	1,00	-1,17	1,08	1,26	1,22
_2718	0		XRE family transcriptional regulator	-1,01	1,01	-1,08	-1,05	1,02	1,19	1,20
_2719	cobT1	6.6.1.2	cobaltochelatase	1,01	1,00	-1,06	-1,10	-1,12	-1,26	-1,09
_2720	0		endonuclease/exonuclease/phosphatase	-1,01	1,00	-1,05	-1,02	-1,05	-1,06	1,09
_2721	0		peptidase M24	-1,02	-1,02	-1,05	-1,06	1,01	1,03	-1,19
_2722	0		hypothetical protein	1,04	-1,03	1,04	1,20	-1,05	-1,02	1,07
_2723	0		intracellular septation protein A	1,02	1,04	-1,05	-1,02	1,01	-1,14	-1,05
_2724	0		hypothetical protein	-1,01	-1,01	-1,03	-1,09	-1,07	1,07	-1,01
_2725	0		signal recognition particle-docking protein FtsY	-1,04	1,04	-1,05	1,10	-1,20	-1,33	-1,24
_2726	0		hypothetical protein	-1,03	-1,05	1,03	1,07	1,05	1,10	-1,09
_2727	xseA	3.1.11.6	exodeoxyribonuclease VII	1,01	-1,04	1,00	-1,09	1,07	1,09	1,00
_2728	purD	6.3.4.13	Phosphoribosylamine-glycine ligase	1,11	1,13	-1,09	-1,15	-1,31	-1,84	-1,23
_2729	0		Ion transport 2 domain-containing protein	1,03	-1,01	-1,05	-1,09	-1,08	-1,11	-1,20
_2730	0		FG-GAP repeat-containing protein	1,05	1,05	-1,07	-1,23	-1,51	-1,97	-1,13
_2731	0		ferredoxin	1,12	1,12	-1,18	-1,36	-1,63	-2,13	-1,24
_2732	0		nucleic acid binding OB-fold tRNA/helicase-type	1,13	1,01	-1,05	-1,05	-1,08	1,04	1,12
_2733	degP	3.4.21.-	protease do	-1,02	-1,02	-1,06	-1,36	-1,41	-1,15	-1,18
_2734	0		hypothetical protein	1,06	-1,01	-1,03	-1,06	-1,24	1,04	1,14
_2735	hflC		HflC protein	-1,01	-1,02	-1,04	-1,08	-1,37	-1,09	1,00
_2736	hflK		HflK protein	-1,02	-1,06	-1,02	1,01	-1,40	-1,02	1,09
_2737	gor	1.8.1.7	Glutathione-disulfide reductase	-1,02	-1,02	1,01	1,11	-1,21	-1,31	-1,40
_2738	rpiA	5.3.1.6	Ribose-5-phosphate isomerase	-1,07	-1,04	-1,04	1,14	-1,23	-1,35	-1,89
_2739	0		thiamine pyrophosphokinase	-1,09	-1,01	1,02	-1,04	-1,06	1,11	-1,22
_2740	0		putative CheA signal transduction histidine kinase	1,05	1,01	1,10	1,06	1,43	1,43	1,38
_2741	0		hypothetical protein	-1,03	-1,04	-1,11	-1,04	-1,50	-1,8	-1,24
_2742	purA	6.3.4.4	Adenylosuccinate synthase	1,03	-1,02	-1,08	-1,20	-1,34	-1,75	-1,21
_2743	secG		preprotein translocase subunit SecG	1,17	1,13	1,01	-1,11	-1,27	-1,77	-1,21
_2744	pyrG	6.3.4.2	CTP synthase	1,03	1,03	-1,12	-1,51	-1,30	-1,61	-1,12
_2745	0		PhzF family phenazine biosynthesis protein	-1,01	-1,00	-1,21	-1,34	-1,56	-1,67	-1,42
_2746	0		hypothetical protein	1,08	-1,05	1,07	1,28	1,68	1,75	1,8
_2747	0		hypothetical protein	1,02	1,02	1,04	-1,14	1,00	-1,05	-1,06
_2748	gltX	6.1.1.17	Glutamate-tRNA ligase	1,07	1,10	-1,13	-1,46	-1,29	-1,76	-1,14
_2749	0		di-haem cytochrome c peroxidase	-1,06	-1,05	1,13	1,01	-1,07	-1,15	-1,38
_2750	0		hypothetical protein	1,02	1,00	1,01	-1,08	1,10	1,12	1,10
_2751	0		hypothetical protein	-1,09	-1,07	-1,01	1,01	-1,43	-1,61	-1,64
_2752	0		TRAP dicarboxylate transporter- DctP subunit	-1,04	-1,08	-1,16	-1,10	-2,28	-2,43	-2,86
_2753	0		TRAP dicarboxylate transporter, DctM subunit	-1,02	-1,05	-1,27	-1,38	-1,76	-2,06	-1,71
_2754	0		tripartite ATP-independent periplasmic transporter DctQ	1,03	-1,03	-1,14	-1,11	-1,22	-1,49	-1,20
_2755	0		flavin reductase domain-containing protein	-1,01	-1,02	-1,03	-1,13	-1,35	-1,65	-1,26
_2756	0		aldo/keto reductase	-1,01	-1,02	-1,22	-1,15	-1,52	-1,42	-1,33
_2757	ssuD	1.14.14.5	alkanesulfonate monooxygenase	-1,02	-1,07	-1,20	-1,35	-1,43	-1,71	-1,30
_2758	0		GntR family transcriptional regulator	1,03	-1,03	1,01	-1,11	-1,04	-1,03	1,05
_2759	0		oxidoreductase domain-containing protein	-1,06	-1,01	1,02	-1,47	-1,33	-1,34	-1,10
_2760	0	3.1.3.18	phosphoglycolate phosphatase	1,01	1,01	-1,12	-1,02	-1,14	-1,22	-1,22
_2761	0		citrate transporter	-1,05	-1,06	1,02	1,03	1,01	1,05	-1,12
_2762	0		hypothetical protein	1,09	1,13	-1,11	-1,32	-1,69	-2,1	-1,36
_2763	0		hemolysin-type calcium-binding region	-1,11	-1,11	-1,16	-1,41	-1,13	1,03	-1,49
_2764	0		hypothetical protein	-1,01	-1,01	-1,07	1,17	1,05	1,11	1,13
_2765	0		hypothetical protein	-1,00	1,01	-1,04	1,13	-1,04	1,11	1,02
_2766	0		TrkA domain-containing protein	-1,11	-1,06	1,01	-1,01	1,05	1,18	-1,18
_2767	0		hypothetical protein	-1,08	1,06	1,16	1,15	1,47	1,61	1,41
_2768	0		hypothetical protein	1,01	1,07	1,14	1,10	1,48	1,33	1,43
_2769	0		5-formyltetrahydrofolate cyclo-ligase	1,02	-1,02	-1,03	1,07	1,16	1,21	1,16

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_2770	0		magnesium transporter	-1,06	1,01	1,09	1,15	1,03	-1,16	1,01
_2771	guaD	3.5.4.3	guanine deaminase	-1,01	-1,04	1,03	1,02	1,13	1,13	1,02
_2772	0		SCP-like extracellular	1,03	-1,02	1,01	-1,03	-1,21	-1,22	1,00
_2773	0		hydroxydechloroatrazine ethylaminohydrolase	1,02	1,02	-1,05	-1,29	-1,28	-1,30	-1,15
_2774	0		histidinol-phosphate phosphatase, putative	1,01	1,02	-1,00	-1,13	1,03	-1,05	1,01
_2775	0		XRE family transcriptional regulator	1,00	-1,05	1,03	1,11	1,60	1,55	1,06
_2776	0		alcohol dehydrogenase	-1,01	-1,00	1,15	-1,20	-1,13	1,02	-1,09
_2777	0		LysR family transcriptional regulator	-1,03	-1,03	1,01	1,11	1,02	1,14	1,24
_2778	0		hypothetical protein	1,03	1,02	1,03	1,06	1,06	1,14	2,75
_2779	0		hypothetical protein	-1,05	-1,05	-1,03	-1,15	-1,15	1,03	-1,03
_2780	0		hypothetical protein	-1,01	-1,03	1,00	-1,09	1,14	1,26	1,8
_2781	rpmG		50S ribosomal protein L33	1,17	1,22	-1,11	-1,15	-1,30	-1,91	-1,22
_2782	0		PAS domain-containing protein	1,03	-1,08	1,05	1,32	1,51	1,33	1,15
_2783	0		N-acetylmuramyl-L-alanine amidase, negative regulator of AmpC, AmpD	-1,04	-1,02	-1,05	-1,15	-1,32	-1,20	1,02
_2784	0		hypothetical protein	-1,02	-1,01	-1,07	-1,07	-1,52	-1,56	-1,21
_2785	gatA	6.3.5.-	aspartyl/glutamyl-tRNA amidotransferase subunitA"	1,17	1,14	-1,15	-1,45	-1,73	-2,55	-1,30
_2786	gatC	6.3.5.-	aspartyl/glutamyl-tRNA amidotransferase subunitC"	1,16	1,13	-1,13	-1,66	-1,42	-2,23	-1,20
_2787	0		hypothetical protein	-1,15	1,06	1,07	1,14	1,13	1,08	1,19
_2788	0		beta-lactamase domain-containing protein	-1,08	-1,08	-1,04	-1,10	-1,08	-1,02	-1,43
_2789	0		CMP/dCMP deaminase zinc-binding	1,01	-1,02	-1,00	1,06	1,01	1,07	1,10
_2790	0	5.4.99.-	RNA pseudouridine synthase	1,02	1,02	-1,03	-1,21	-1,33	-1,62	-1,11
_2791	0		hypothetical protein	-1,03	-1,05	-1,01	1,10	1,18	1,23	1,15
_2792	0		toxic anion resistance family protein	-1,11	-1,05	-1,03	-1,12	-1,26	-1,15	-1,15
_2793	0		putative lipoprotein	-1,05	-1,06	-1,01	-1,01	-1,23	1,09	-1,19
_2794	0		hypothetical protein	-1,04	-1,03	-1,04	1,00	-1,21	1,04	-1,03
_2795	0		hypothetical protein	1,03	-1,06	-1,06	-1,02	-1,06	1,03	1,01
_2796	0		heat shock protein Hsp20	1,36	2,47	4,81	7,64	14	9,97	6,79
_2797	0	2.7.1.4	fructokinase	-1,30	-1,16	-1,06	-1,04	-1,83	-1,89	-1,85
_2798	dtd			-1,07	-1,07	-1,02	1,05	-1,12	-1,14	-1,15
_2799	fccB	1.8.2.-	sulfide dehydrogenase [flavocytochrome c]flavoprotein chain"	-1,09	-1,07	-1,06	-1,19	-1,69	-1,50	-2,02
_2800	0		cytochrome c class I	-1,10	-1,07	-1,04	-1,61	-1,53	-1,27	-1,78
_2801	0		cytochrome c class I	1,00	-1,04	-1,07	1,04	-1,28	-1,23	-1,54
_2802	0		oxidoreductase molybdopterin binding	-1,07	-1,04	-1,05	1,04	-1,36	-1,56	-1,46
_2803	0		5'-nucleotidase domain-containing protein	-1,02	-1,07	-1,18	-1,08	-1,22	-1,11	-1,37
_2804	soxA1		diheme cytochrome c SoxA	-1,05	-1,09	-1,11	-1,24	-1,73	-1,65	-2,05
_2805	0		sulphur oxidation protein SoxZ	-1,05	-1,07	-1,11	-1,22	-1,81	-1,29	-1,66
_2806	0		sulfur oxidation protein SoxY	-1,05	-1,08	-1,07	-1,09	-1,52	-1,09	-1,43
_2807	0		monoheme cytochrome c SoxX	-1,11	-1,12	-1,13	-1,15	-1,91	-1,49	-2,08
_2808	0		thioredoxin SoxW	-1,02	1,02	1,01	-1,14	1,18	1,09	-1,04
_2809	0		cytochrome c biogenesis protein transmembrane region	-1,05	-1,02	1,01	-1,29	1,20	1,36	1,07
_2810	0		regulatory protein SoxS	-1,02	-1,02	-1,05	-1,01	1,05	1,11	1,04
_2811	0		hypothetical protein	1,01	-1,07	1,04	1,04	-1,06	-1,11	-1,08
_2812	0		ArsR family transcriptional regulator	-1,05	-1,03	1,01	-1,02	-1,10	1,02	-1,22
_2813	0		protein of unknown function DUF395 YeeE/YedE	-1,04	-1,06	-1,02	1,12	-1,12	1,06	1,03
_2814	0		diguanylate cyclase	1,05	1,01	-1,00	1,18	1,76	1,72	1,86
_2815	0		heme NO binding domain-containing protein	1,06	1,01	1,06	1,26	1,82	1,52	1,76
_2816	0		hypothetical protein	-1,10	-1,11	1,03	-1,02	1,01	-1,07	-1,03
_2817	0		trimethylamine methyltransferase	-1,11	-1,04	1,01	1,13	1,12	1,18	1,12
_2818	0		HAD family hydrolase	1,04	1,01	1,02	1,12	1,21	1,43	1,46
_2819	0		hypothetical protein	-1,10	-1,04	-1,02	-1,15	-1,13	1,09	-1,06
_2820	0		response regulator receiver modulated diguanylate cyclase	1,02	-1,02	-1,09	-1,19	-1,07	-1,09	1,02
_2821	0		hypothetical protein	1,10	1,18	1,47	2,02	2,22	1,54	1,97
_2822	0		NUDIX hydrolase	-1,03	1,04	1,17	1,31	1,30	1,23	1,17
_2823	0		aldo/keto reductase	-1,04	1,05	-1,03	1,05	-1,34	-1,53	-1,54
_2824	0		hypothetical protein	-1,01	-1,00	-1,02	1,08	-1,06	-1,16	-1,07
_2825	0		3-hydroxyacyl-CoA dehydrogenase NAD-binding	-1,03	-1,03	1,07	-1,02	1,02	1,07	-1,01
_2826	0		hypothetical protein	1,11	-1,03	-1,00	1,00	-1,02	1,11	1,17
_2827	0		YceI family protein	-1,04	-1,03	-1,05	1,08	1,04	1,13	1,07

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_2828	0		Mg chelatase, subunit ChlI	1,00	-1,02	-1,07	1,02	1,33	1,43	1,19
_2829	gshB	6.3.2.3	Glutathione synthase	1,03	-1,00	-1,03	-1,03	1,16	1,03	1,08
_2830	0		hypothetical protein	1,05	-1,01	-1,02	1,22	1,68	1,73	1,64
_2831	0		uroporphyrin-III C/tetrapyrrole methyltransferase	-1,08	-1,04	1,12	1,12	1,10	1,08	-1,17
_2832	0		extracellular ligand-binding receptor	1,00	-1,00	-1,04	-1,14	-1,11	-1,14	-1,20
_2833	glnD	2.7.7.59	[protein-PII] uridylyltransferase	-1,02	-1,01	1,01	-1,05	-1,15	-1,09	-1,31
_2834	0		integral membrane protein MviN	-1,05	-1,04	1,01	1,16	-1,31	-1,18	-1,04
_2835	0		rhomboid family protein	1,00	-1,01	-1,02	-1,02	-1,12	-1,34	-1,20
_2836	trpS	6.1.1.2	Tryptophan-tRNA ligase	1,16	1,14	-1,08	-1,17	-1,38	-1,94	-1,33
_2837	0		aminotransferase	-1,04	-1,03	-1,00	-1,01	-1,07	-1,20	-1,25
_2838	0		UspA domain-containing protein	-1,10	-1,02	1,04	1,13	-1,11	1,04	-1,25
_2839	0		scaffold protein Nfu/NifU	-1,03	-1,05	-1,13	-1,06	1,00	-1,04	1,64
_2840	0		peptidase M22 glycoprotease	1,00	-1,11	-1,09	-1,04	-1,23	1,04	1,15
_2841	0		ribosomal-protein-alanine acetyltransferase	-1,05	-1,04	-1,07	-1,08	1,04	1,19	1,32
_2842	0		basic membrane lipoprotein	-1,14	-1,11	-1,17	-1,33	-2,24	-1,92	-2,49
_2843	rbsA2	3.6.3.17	Monosaccharide-transporting ATPase	-1,03	-1,09	-1,17	-1,26	-1,64	-1,67	-1,86
_2844	0		inner-membrane translocator	1,02	-1,04	1,03	-1,12	-1,28	-1,26	-1,48
_2845	0		lysine exporter protein LysE/YggA	-1,02	-1,04	1,09	1,01	-1,23	-1,18	-1,29
_2846	0		inner-membrane translocator	-1,04	-1,13	1,09	-1,07	-1,33	-1,29	-1,47
_2847	0		hypothetical protein	-1,03	-1,01	1,05	-1,05	1,28	1,10	1,30
_2848	0		hypothetical protein	1,01	-1,02	1,02	1,11	1,21	1,32	1,18
_2849	0		short-chain dehydrogenase/reductase SDR	-1,03	-1,02	1,05	1,00	-1,01	1,03	-1,14
_2850	0		AAA ATPase	-1,04	-1,03	-1,00	-1,05	1,01	1,05	-1,13
_2851	0		autoinducer synthesis protein	1,10	1,03	1,04	1,21	1,08	1,05	1,15
_2852	0		LuxR family transcriptional regulator	1,02	-1,02	1,00	1,06	-1,30	-1,26	-1,15
_2853	0		crotonyl-CoA reductase	-1,24	-1,22	-1,31	-1,47	-1,57	-1,54	-1,36
_2854	0		phospholipid/glycerol acyltransferase	-1,07	1,03	1,19	1,38	1,54	2	1,57
_2855	mutB	5.4.99.2	Methylmalonyl-CoA mutase	-1,27	-1,19	-1,16	-1,24	-1,14	-1,21	-1,11
_2856	0		hypothetical protein	1,01	-1,02	1,16	1,08	1,02	1,01	1,20
_2857	0		hypothetical protein	-1,06	-1,03	-1,01	-1,24	1,08	1,12	1,01
_2858	deoD	2.4.2.1	purine-nucleoside phosphorylase	-1,01	-1,02	-1,02	1,04	1,06	1,07	-1,03
_2859	0		hypothetical protein	-1,06	-1,03	1,03	1,14	1,02	1,03	1,00
_2860	0		hypothetical protein	1,06	1,04	1,09	1,21	1,15	1,12	1,54
_2861	sdhB	1.3.99.1	succinate dehydrogenase	1,01	1,07	1,15	1,32	1,38	1,34	1,77
_2862	0		hypothetical protein	-1,02	-1,01	1,04	-1,02	1,39	1,64	1,71
_2863	0		hypothetical protein	-1,03	1,01	1,11	1,37	1,58	1,49	1,67
_2864	0		hypothetical protein	1,02	1,04	1,16	1,29	1,61	1,63	1,78
_2865	sdhA	1.3.99.1	succinate dehydrogenase	1,01	1,11	1,30	1,59	2,1	1,62	2,09
_2866	0		succinate dehydrogenase hydrophobic membrane anchor	1,02	1,15	1,36	1,85	2,38	1,69	2,3
_2867	0		succinate dehydrogenase cytochrome b556 subunit	1,02	1,19	1,38	1,63	2,53	1,78	2,29
_2868	0		cytochrome c class II	1,03	-1,11	-1,22	-1,32	-1,58	-1,14	-1,37
_2869	0		gluconate 2-dehydrogenase (acceptor)	1,06	-1,12	-1,13	1,02	-1,17	-1,05	-1,00
_2870	0		hypothetical protein	-1,03	-1,02	1,05	1,02	1,17	1,47	1,55
_2871	0		dehydratase	1,03	-1,00	-1,03	-1,10	-1,36	-1,57	-1,09
_2872	0		hypothetical protein	1,02	1,03	-1,08	-1,03	-1,11	-1,13	-1,11
_2873	0		NnrU family protein	1,02	1,04	-1,03	-1,02	1,01	-1,15	1,04
_2874	0		citrate (pro-3S)-lyase	-1,13	-1,03	-1,07	-1,12	1,34	-1,33	1,16
_2875	0		hypothetical protein	1,06	1,00	1,02	1,08	1,32	1,41	1,25
_2876	mdh	1.1.1.37	malate dehydrogenase	1,02	1,15	1,21	1,16	1,11	-1,39	1,42
_2877	0		hypothetical protein	1,05	1,07	-1,08	-1,39	-1,20	-1,43	1,20
_2878	sucC		succinyl-CoA synthetase beta chain	-1,08	1,09	1,33	1,78	3,48	2,29	3,09
_2879	0		hypothetical protein	-1,01	1,02	1,40	1,83	3,22	2,5	2,66
_2880	0		hypothetical protein	1,04	1,06	1,29	1,89	3,44	2,55	2,77
_2881	0		hypothetical protein	1,01	-1,01	1,19	1,33	2,6	2,47	2,45
_2882	sucD1	6.2.1.5	Succinate-CoA ligase (ADP-forming)	-1,03	1,02	1,20	1,52	2,62	2,39	2,95
_2883	sucA	1.2.4.2	oxoglutarate dehydrogenase (succinyl-transferring)	1,00	1,04	1,11	1,19	2,8	2,28	2,4
_2884	sucB	2.3.1.61	Dihydrolipoyllysine-residue succinyltransferase	1,01	-1,00	1,10	1,17	1,75	1,98	2,36
_2885	0		inner membrane protein	1,04	1,01	1,11	1,23	1,71	2,21	2,22
_2886	lpd		dihydrolipoyl dehydrogenase	-1,03	1,01	1,14	1,34	1,76	2,51	2,43
_2887	gabD	1.2.1.16	Succinate-semialdehyde dehydrogenase [NAD(P)+]	-1,02	1,01	-1,12	-1,41	-1,9	-2,34	-2,46
_2888	0		putative esterase/lipase/thioesterase	1,03	-1,03	-1,02	1,02	-1,03	-1,22	-1,00

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_2889	0		peptidase S58 DmpA	-1,06	-1,01	-1,00	-1,04	-1,08	-1,04	1,03
_2890	0		hypothetical protein	-1,07	-1,07	1,06	-1,11	-1,03	-1,11	-1,33
_2891	fabG		3-ketoacyl-(acyl-carrier-protein) reductase	-1,16	-1,08	1,03	-1,11	-1,15	-1,04	-1,62
_2892	0		heat shock protein Hsp20	-1,00	-1,00	1,05	1,12	1,34	2,4	1,97
_2893	0		peptidase S1 and S6 chymotrypsin/Hap	-1,00	-1,01	1,02	1,09	1,13	1,18	1,66
_2894	0		hypothetical protein	1,04	-1,01	-1,07	-1,21	-1,19	-1,14	-1,21
_2895	0		FAD linked oxidase domain-containing protein	-1,02	-1,04	-1,13	-1,34	-1,22	-1,26	-1,13
_2896	0	1.1.99.14, 1.1.3.15	glycolate dehydrogenase,(S)-2-hydroxy-acid oxidase	-1,04	-1,02	-1,19	-1,48	-1,34	-1,50	-1,43
_2897	0		hypothetical protein	1,02	-1,01	1,02	1,01	-1,02	-1,03	-1,54
_2898	pucC1		PUCC protein	1,04	-1,03	1,04	1,20	1,56	1,34	-1,16
_2899	0		antenna complex alpha/beta subunit	1,01	-1,01	-1,03	-1,02	-1,15	-1,02	-1,76
_2900	pucB		antenna complex alpha/beta subunit	1,00	-1,01	-1,01	-1,04	-1,12	-1,01	-1,91
_2901	0		hypothetical protein	-1,01	-1,04	-1,11	1,18	1,00	-1,02	-1,03
_2902	0		hypothetical protein	-1,06	-1,04	1,10	-1,03	-1,10	-1,04	1,15
_2903	0		hypothetical protein	1,01	-1,04	1,03	1,01	-1,11	1,16	1,15
_2904	0		hypothetical protein	1,04	-1,03	1,03	1,04	-1,03	1,08	1,18
_2905	0		hypothetical protein	1,08	-1,04	-1,03	-1,02	-1,08	1,19	1,29
_2906	0		ATPase	-1,00	-1,06	1,02	-1,06	-1,13	1,09	1,08
_2907	0		hypothetical protein	-1,01	-1,02	1,04	1,08	1,02	-1,04	1,04
_2908	rluE		pseudouridine synthase	-1,04	-1,00	1,06	1,05	-1,02	-1,02	1,00
_2909	polA	2.7.7.7	DNA-directed DNA polymerase	-1,04	1,03	-1,07	-1,16	-1,28	-1,43	-1,57
_2910	0		Hly-III family protein	1,09	-1,16	-1,13	-1,17	-1,10	1,36	1,43
_2911	0		hypothetical protein	1,08	1,07	1,10	1,24	1,34	1,30	1,68
_2912	0		hypothetical protein	1,04	1,13	1,27	1,11	1,64	1,41	1,54
_2913	0		ABC transporter related	1,13	1,06	-1,13	1,00	-1,16	-1,26	1,10
_2914	0		lipase, putative	-1,31	-1,21	-1,23	-1,15	-1,39	1,00	-1,17
_2915	0		NUDIX hydrolase	-1,09	-1,07	1,07	1,01	1,10	1,33	1,08
_2916	0		hypothetical protein	-1,05	-1,04	1,01	-1,07	-1,02	1,06	-1,19
_2917	0		amidohydrolase	1,07	-1,00	-1,10	-1,25	-1,29	-1,41	-1,15
_2918	0		GCN5-related N-acetyltransferase	-1,12	-1,06	-1,01	-1,16	-1,01	1,29	-1,22
_2919	groEL		chaperonin GroEL	-1,07	-1,01	-1,15	-1,20	-3,37	-3,84	-1,84
_2920	0		chaperonin Cpn10	-1,03	1,03	-1,06	-1,13	-3,03	-3,11	-1,62
_2921	0		hypothetical protein	-1,03	-1,03	-1,05	1,08	1,12	1,13	1,06
_2922	0		hypothetical protein	-1,05	1,01	1,02	1,07	1,20	1,32	1,03
_2923	0		5TM Receptors of the LytS-YhcK type transmembrane region	-1,10	-1,16	-1,12	-1,00	1,01	1,48	1,87
_2924	ppaC	3.6.1.1	inorganic diphosphatase	1,18	1,25	1,15	1,03	1,17	-1,29	1,57
_2925	0		HAD family hydrolase	1,01	1,02	-1,08	-1,38	-1,10	-1,34	-1,05
_2926	0		dehydratase	-1,77	-1,60	-1,73	-1,98	-2,33	-2,17	-2,54
_2927	ribF	2.7.1.26, 2.7.7.2	riboflavin kinase,FAD synthetase	1,07	1,04	-1,09	-1,01	-1,29	-1,59	-1,11
_2928	0		hypothetical protein	1,01	-1,01	-1,05	-1,05	-1,27	-1,36	-1,06
_2929	0		alpha/beta hydrolase fold	-1,08	-1,02	-1,01	-1,11	1,01	1,02	-1,10
_2930	0		DSBA oxidoreductase	-1,11	-1,06	1,02	-1,06	-1,03	-1,01	-1,39
_2931	prs	2.7.6.1	ribose-phosphate diphosphokinase	1,10	1,10	1,03	1,10	1,04	-1,57	1,10
_2932	0		hypothetical protein	1,03	1,04	-1,03	1,04	-1,03	-1,22	-1,09
_2933	atpC1	3.6.3.14	H+-transporting two-sector ATPase	1,00	1,05	-1,00	1,11	-2,78	-2,49	-1,26
_2934	atpD2	3.6.3.14	H+-transporting two-sector ATPase	-1,02	1,04	-1,00	-1,06	-2,96	-2,3	-1,20
_2935	atpG2	3.6.3.14	H+-transporting two-sector ATPase	1,01	1,05	-1,12	-1,29	-2,49	-2,25	-1,25
_2936	atpA1	3.6.3.14	H+-transporting two-sector ATPase	1,08	1,15	-1,01	-1,72	-1,82	-2,14	-1,01
_2937	atpH		ATP synthase delta chain	1,19	1,28	1,03	-1,22	-1,33	-2,03	-1,00
_2938	0		hypothetical protein	1,02	1,10	1,19	1,32	1,76	1,61	1,72
_2939	clpA		ATP-dependent Clp protease, ATP-binding subunit clpA	1,01	-1,05	1,06	-1,01	1,16	1,24	1,18
_2940	0		hypothetical protein	-1,04	-1,01	-1,09	-1,31	-1,48	-1,41	-1,35
_2941	0		hypothetical protein	1,03	-1,00	-1,06	-1,13	-1,10	-1,21	-1,13
_2942	0		ChaC family protein	1,13	1,09	-1,10	-1,20	-1,33	-1,72	-1,19
_2943	0		hypothetical protein	1,04	1,04	1,02	-1,06	-1,17	-1,55	-1,09
_2944	0		extensin family protein	-1,07	-1,02	1,02	1,04	-1,15	-1,25	-1,09
_2945	tyrC	1.3.1.43, 1.3.1.12	arogenate dehydrogenase,prephenate dehydrogenase	-1,02	-1,01	-1,05	-1,03	-1,45	-1,65	-1,36
_2946	hisC	2.6.1.9	histidinol-phosphate transaminase	-1,03	-1,00	-1,20	-1,17	-1,50	-2,1	-1,43

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_2947	hss	2.5.1.44	homospermidine synthase	1,03	1,12	-1,23	-1,47	-1,16	-2	-1,12
_2948	rpsD		30S ribosomal protein S4	1,13	1,16	-1,24	-1,60	-1,58	-3,39	-1,19
_2949	0	1.17.4.1	Ribonucleoside-diphosphate reductase	-1,04	1,02	-1,18	-1,25	-1,26	-1,22	-1,52
_2950	0		hypothetical protein	-1,07	-1,04	-1,00	-1,07	-1,12	-1,04	-1,16
_2951	0		pyridoxal-5'-phosphate-dependent protein beta subunit	1,02	-1,02	-1,10	1,13	-1,36	-1,47	-1,12
_2952	panC	6.3.2.1	Pantoate-beta-alanine ligase	-1,03	-1,00	-1,07	-1,06	-1,76	-2,24	-1,74
_2953	hisG	2.4.2.17	ATP phosphoribosyl transferase	-1,02	1,00	-1,02	-1,27	-1,70	-1,76	-1,29
_2954	hisZ		ATP phosphoribosyltransferase regulatory subunit	1,00	1,03	-1,00	-1,18	-1,83	-2,39	-1,43
_2955	hisS	6.1.1.21	Histidine-tRNA ligase	1,12	1,11	-1,25	-1,85	-1,69	-2,39	-1,19
_2956	0		SlyX family protein	1,07	1,01	-1,01	-1,28	1,04	1,08	1,12
_2957	dnaE	2.7.7.7	DNA-directed DNA polymerase	-1,01	-1,03	1,03	1,04	1,10	1,07	-1,15
_2958	xghB	1.17.1.4	xanthine dehydrogenase	-1,05	-1,05	-1,04	1,05	-1,03	-1,02	-1,21
_2959	xdhA	1.17.1.4	xanthine dehydrogenase	-1,00	-1,03	1,04	1,06	-1,05	-1,05	-1,44
_2960	xdhC	1.17.1.4	xanthine dehydrogenase	1,01	-1,02	1,00	-1,07	1,02	1,27	-1,10
_2961	0		ABC transporter related	1,03	-1,07	1,04	-1,00	1,01	1,21	-1,15
_2962	0		inner-membrane translocator	-1,03	-1,03	-1,01	-1,03	-1,12	1,10	-1,22
_2963	0		inner-membrane translocator	1,04	1,00	-1,01	1,17	-1,04	1,23	-1,31
_2964	0		basic membrane lipoprotein	-1,08	-1,04	-1,08	-1,27	-2,11	-2,17	-2,43
_2965	0		hypothetical protein	1,01	1,05	1,13	1,40	1,82	1,91	1,52
_2966	panB	2.1.2.11	3-methyl-2-oxobutanoate hydroxymethyl transferase	-1,05	1,13	1,68	1,91	2,06	2,06	1,35
_2967	0		FAD dependent oxidoreductase	1,02	-1,02	1,02	1,04	1,17	1,29	1,23
_2968	0		hypothetical protein	1,02	-1,03	1,04	1,25	1,64	1,63	1,63
_2969	0		alkylhydroperoxidase	1,01	1,21	1,78	2,35	3,2	1,53	-1,06
_2970	gyaR	1.1.1.26	glyoxylate reductase	-1,10	-1,06	-1,05	1,01	-1,29	-1,28	-1,43
_2971	0		hypothetical protein	-1,01	-1,04	1,16	1,50	1,70	1,05	1,07
_2972	0		putative PAS/PAC sensor protein	-1,09	-1,06	1,02	1,19	1,13	1,45	1,20
_2973	dcp	3.4.15.5	Peptidyl-dipeptidase Dcp	-1,06	-1,02	1,02	1,20	1,20	1,26	1,09
_2974	moeB		UBA/THIF-type NAD/FAD binding protein	-1,03	-1,02	1,08	1,15	1,11	1,08	-1,02
_2975	dut	3.6.1.23	dUTP diphosphatase	1,06	1,01	1,08	1,15	1,14	1,22	1,08
_2976	coaBC	4.1.1.36, 6.3.2.5	phosphopantothenoyl cysteine decarboxylase,phosphopantothenate-cysteine ligase	1,04	1,02	1,09	1,14	1,22	1,04	1,14
_2977	0		uncharacterized iron-regulated protein-like protein	-1,30	-1,44	-1,44	-1,26	1,01	-1,04	1,17
_2978	rpoH2		RNA polymerase factor sigma-32	-2,13	-2,12	-2	-1,88	1,15	-1,25	1,00
_2979	0	2.7.1.156, 2.7.7.62	adenosylcobinamide kinase,adenosylcobinamide-phosphate guanylyltransferase	1,05	1,05	1,00	1,11	-1,03	-1,24	1,02
_2981	0		sulfite oxidase	-1,06	-1,12	-1,47	-1,79	-2,67	-2,57	-2,99
_2982	0		hypothetical protein	-1,03	-1,09	-1,41	-1,84	-2,77	-2,56	-3,14
_2983	0		alcohol dehydrogenase	1,03	-1,04	-1,09	-1,12	-1,22	-1,28	-1,24
_2984	0		glutathione S-transferase family protein	-1,03	1,00	-1,05	1,08	1,02	-1,00	1,07
_2985	0		GntR family transcriptional regulator	-1,07	1,04	1,29	1,43	1,44	1,74	1,32
_2986	0		hypothetical protein	1,07	1,04	1,11	-1,04	-1,11	-1,28	-1,07
_2987	0		hypothetical protein	1,17	1,13	-1,23	-1,52	-1,88	-2,6	-1,56
_2988	0		hypothetical protein	1,14	1,10	-1,23	-1,26	-1,65	-2,24	-1,77
_2989	0		hypothetical protein	-1,09	-1,07	-1,01	1,01	-1,10	-1,23	1,06
_2990	0		LysR family transcriptional regulator	-1,07	-1,12	-1,05	1,04	-1,00	1,14	1,14
_2991	0		hypothetical protein	1,11	1,01	-1,12	-1,10	-1,11	-1,18	-1,03
_2992	dehH	3.8.1.3	haloacetate dehalogenase	-1,00	1,00	-1,09	-1,27	-1,12	-1,16	-1,04
_2993	0		hypothetical protein	-1,04	-1,05	-1,09	-1,09	-1,02	1,19	1,06
_2994	rpsO		30S ribosomal protein S15	1,18	1,16	-1,11	-1,33	-1,62	-2,74	-1,60
_2995	0		hypothetical protein	-1,04	1,00	1,01	1,05	1,06	1,32	1,09
_2996	0		endonuclease/exonuclease/phosphatase	-1,00	-1,03	1,10	1,36	1,07	1,18	-1,06
_2997	pnp	2.7.7.8	polyribonucleotide nucleotidyl transferase	1,01	1,04	1,07	1,01	-1,71	-2,15	-1,27
_2998	0		MscS mechanosensitive ion channel	1,03	1,00	-1,09	-1,26	-1,29	-1,59	-1,24
_2999	fadD1	6.2.1.3	Long-chain-fatty-acid-CoA ligase	1,00	1,01	-1,03	-1,23	-1,52	-1,38	-1,29
_3000	mcd	4.1.1.9	Malonyl-CoA decarboxylase	-1,05	-1,02	-1,13	-1,07	-1,57	-1,54	-1,40
_3001	dctM2		TRAP dicarboxylate transporter, DctM subunit	-1,06	-1,06	-1,12	-1,35	-1,52	-1,40	-1,54
_3002	dctQ4		tripartite ATP-independent periplasmic transporter DctQ	-1,05	-1,11	-1,32	-1,81	-1,88	-1,65	-1,92
_3003	dctP4		TRAP dicarboxylate transporter- DctP subunit	-1,16	-1,13	-1,29	-1,43	-1,77	-1,75	-2,2
_3004	0		GntR family transcriptional regulator	-1,21	-1,05	-1,23	-1,11	-1,05	-1,01	-1,27
_3005	0		hypothetical protein	-1,06	-1,03	1,03	1,02	-1,12	-1,09	-1,05
_3006	rpe	5.1.3.1	ribulose-phosphate 3-epimerase	1,17	1,13	-1,12	-1,14	-1,34	-1,68	-1,18

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_3007	ybgG	3.2.1.24	alpha-mannosidase	1,01	-1,03	-1,03	-1,02	-1,02	-1,01	1,04
_3008	0		ABC transporter related	-1,03	-1,01	1,00	1,04	-1,12	1,08	-1,07
_3009	0		binding-protein-dependent transport systems inner membrane component	1,05	-1,04	1,02	-1,03	-1,10	-1,07	-1,14
_3010	0		binding-protein-dependent transport systems inner membrane component	1,00	-1,05	1,04	-1,08	-1,10	-1,23	-1,12
_3011	0		extracellular solute-binding protein	-1,04	-1,07	-1,12	-1,23	-1,17	-1,21	-1,29
_3012	0		Zn-dependent hydrolase of the beta-lactamase fold	-1,07	1,02	-1,07	1,06	-1,03	1,00	-1,17
_3013	0		hypothetical protein	-1,09	-1,02	1,11	1,11	1,10	1,13	-1,08
_3014	0	1.14.11.18	phytanoyl-CoA dioxygenase	-1,03	1,02	1,04	-1,18	1,12	1,04	1,07
_3015	0		AraC family transcriptional regulator	1,02	1,04	-1,04	1,05	1,03	1,03	1,09
_3016	deoC	4.1.2.4	Deoxyribose-phosphate aldolase	-1,20	-1,09	-1,06	-1,03	-1,19	1,04	-1,50
_3017	ald	1.2.1.3	aldehyde dehydrogenase (NAD+)	-1,02	-1,13	-1,01	-1,02	-1,13	-1,05	-1,31
_3018	0		hypothetical protein	1,07	1,06	-1,12	-1,30	1,01	-1,14	1,06
_3019	0		hypothetical protein	1,01	1,02	1,09	-1,04	1,05	1,01	1,17
_3020	dapE2	3.5.1.18	Succinyl-diaminopimelate desuccinylase	-1,08	-1,01	1,09	1,16	1,16	1,16	-1,06
_3021	puuC	1.2.1.3	aldehyde dehydrogenase (NAD+)	1,02	1,01	-1,02	-1,05	1,03	-1,13	-1,17
_3022	0		ribokinase-like domain-containing protein	1,04	1,06	-1,07	-1,45	-1,56	-1,98	-1,35
_3023	nth	4.2.99.18	DNA-(apurinic or apyrimidinic site) lyase	1,12	1,07	-1,08	-1,24	-1,23	-1,47	-1,12
_3024	ada	2.1.1.63	methylated-DNA-[protein]-cysteine S-methyltransferase	-1,03	-1,02	1,15	1,18	1,07	1,06	1,11
_3025	0		OmpA/MotB domain-containing protein	-1,02	-1,02	-1,10	-1,22	-1,22	-1,34	-1,11
_3026	pdhR		GntR domain-containing protein	-1,12	-1,02	-1,24	-1,83	-1,32	-1,68	-1,53
_3027	atpF2	3.6.3.14	H+-transporting two-sector ATPase	-1,01	1,06	1,05	1,13	-2,68	-3,12	-1,13
_3028	atpX	3.6.3.14	H+-transporting two-sector ATPase	1,02	1,07	1,05	1,07	-2,66	-2,72	-1,18
_3029	atpE2	3.6.3.14	H+-transporting two-sector ATPase	1,03	1,10	1,05	1,00	-2,62	-2,77	-1,16
_3030	atpB1	3.6.3.14	H+-transporting two-sector ATPase	1,15	1,27	1,20	1,18	-1,56	-2,15	1,01
_3031	atpI		ATP synthase F0, subunit I	1,18	1,26	1,19	1,13	-1,37	-1,73	-1,02
_3032	0		heparinase II/III family protein	-1,03	-1,00	1,02	1,02	-1,11	-1,09	-1,04
_3033	rsmB1	2.1.1.-	ribosomal RNA small subunit methyltransferase B	1,04	1,02	-1,14	-1,16	-1,26	-1,52	-1,33
_3034	0		hypothetical protein	1,04	1,04	1,07	1,30	1,30	1,39	1,46
_3035	0		hypothetical protein	-1,72	-1,61	-1,52	-1,32	1,14	-1,26	-1,13
_3036	0		acriflavin resistance protein	-1,04	1,01	-1,07	1,00	-1,03	1,14	1,64
_3037	0		RND family efflux transporter MFP subunit	-1,07	1,02	1,00	-1,05	1,22	1,29	1,98
_3038	0		TetR family transcriptional regulator	1,02	-1,01	-1,03	-1,06	1,16	1,30	1,82
_3039	0		BLUF domain-containing protein	-1,01	1,02	-1,07	1,04	-1,09	-1,03	-1,09
_3040	dapB	1.17.1.-	CDP-6-deoxy-L-threo-D-glycero-4-hexulose-3-dehydrase reductase	1,10	1,07	-1,04	-1,12	-1,31	-1,56	-1,08
_3041	rbfA		ribosome-binding factor A	1,16	1,11	-1,18	-1,18	-1,42	-2,06	-1,29
_3042	truB	5.4.99.25	tRNA pseudouridine55 synthase	1,06	1,08	-1,16	-1,24	-1,41	-1,88	-1,27
_3043	0		hypothetical protein	1,00	-1,02	-1,14	-1,32	-1,78	-2,33	-1,52
_3044	0	3.1.1.73	feruloyl esterase	-1,10	-1,05	1,01	-1,23	-1,47	-1,48	-1,63
_3045	0		glycosyl transferase family protein	-1,00	-1,06	1,04	1,15	-1,15	-1,25	-1,19
_3046	ttuD	1.1.1.81	hydroxypyruvate reductase	-1,13	-1,03	1,00	1,00	-1,30	-1,25	-1,46
_3047	glxR	1.1.1.60	2-hydroxy-3-oxopropionate reductase	-1,04	-1,03	-1,01	-1,02	-1,18	-1,37	-1,64
_3048	0		GntR domain-containing protein	-1,07	-1,02	-1,00	1,06	1,11	1,12	1,03
_3049	0		NAD-dependent epimerase/dehydratase	-1,02	1,03	-1,07	-1,25	-1,51	-1,38	-1,33
_3050	citE2	4.1.3.6	citrate (pro-3S)-lyase	-1,05	-1,08	-1,23	-1,26	-1,32	-1,92	-1,20
_3051	0		hypothetical protein	-1,04	-1,04	1,10	1,05	1,03	-1,03	1,12
_3052	0		hypothetical protein	1,07	1,02	-1,11	-1,02	1,12	1,03	1,24
_3053	0		transposase, putative	-1,00	-1,04	-1,05	1,02	1,00	1,10	1,13
_3054	0		phospholipid/glycerol acyltransferase	-1,01	1,01	-1,03	-1,30	-1,28	-1,20	-1,13
_3055	0		hypothetical protein	1,02	-1,01	-1,05	-1,03	-1,01	-1,06	-1,03
_3056	ftsE		ABC transporter related	1,04	1,05	-1,06	-1,13	-1,21	-1,44	-1,27
_3057	0		Zinc finger-domain-containing protein	-1,04	-1,01	1,05	-1,09	1,04	1,13	1,00
_3058	0		hypothetical protein	-1,01	-1,03	-1,01	-1,02	-1,07	1,03	1,04
_3059	lysA	4.1.1.20	Diaminopimelate decarboxylase	1,02	1,02	-1,06	1,02	-1,11	-1,30	1,01
_3060	0		hypothetical protein	1,04	1,01	1,02	-1,03	-1,28	-1,53	-1,14
_3061	0		hypothetical protein	1,06	-1,01	-1,03	1,09	-1,44	-1,54	-1,18
_3062	argH	4.3.2.1	argininosuccinate lyase	1,14	1,15	-1,11	-1,11	-1,20	-1,71	-1,03
_3063	tlpA		redoxin domain-containing protein	1,02	1,03	-1,12	-1,30	-1,31	-1,18	1,07
_3064	tag	3.2.2.20	DNA-3-methyladenine glycosylase I	1,02	1,01	-1,02	-1,06	1,01	-1,01	1,01

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_3065	0		diguanylate phosphodiesterase	1,02	-1,03	1,05	1,17	1,50	1,88	1,72
_3066	atoB	2.3.1.9	acetyl-CoA C-acetyltransferase	1,08	1,24	1,52	1,95	2,9	1,87	3,2
_3067	fabG1	1.1.1.36	acetoacetyl-CoA reductase	-1,00	1,09	1,28	1,31	1,74	1,39	2,16
_3068	0		DNA-binding transcriptional activator GcvA	1,03	1,01	1,00	1,19	1,31	1,30	1,88
_3069	0		hypothetical protein	-1,11	-1,09	1,12	1,08	-1,19	1,27	-1,18
_3070	0		methyltransferase small	1,05	-1,03	-1,04	-1,22	1,06	1,11	1,08
_3071	0		Beta tubulin, autoregulation binding site	-1,10	-1,04	-1,08	-1,01	-1,18	-1,18	-1,35
_3072	ispB		polyprenyl synthetase	1,06	1,05	-1,08	-1,14	-1,37	-1,66	-1,04
_3073	ispE	2.7.1.148	4-(cytidine 5-diphospho)-2-C-methyl-D-erythritol kinase	-1,00	-1,02	-1,02	-1,01	1,25	1,25	1,14
_3075	ydiS	1.5.5.1	Electron-transferring-flavoprotein dehydrogenase	-1,25	-1,14	-1,47	-2	-1,84	-1,62	-1,49
_3076	greA		transcription elongation factor GreA	-1,02	-1,04	-1,07	-1,01	-1,13	-1,43	-1,74
_3077	0		hypothetical protein	-1,00	-1,01	-1,01	-1,04	-1,14	-1,31	-1,52
_3078	0		AzlC family protein	1,12	1,06	-1,17	-1,16	-1,46	-1,71	-1,39
_3079	0		branched-chain amino acid transport	1,14	1,06	-1,21	-1,27	-1,36	-1,69	-1,13
_3080	0		RND family efflux transporter MFP subunit	1,01	-1,05	1,07	1,19	1,11	1,36	1,25
_3081	0		acriflavin resistance protein	1,03	1,01	1,05	-1,06	1,03	1,18	1,01
_3082	0		hypothetical protein	-1,03	-1,01	-1,05	-1,24	-1,25	-1,08	-1,21
_3083	0		hypothetical protein	1,03	1,13	1,41	1,65	2,06	1,98	1,96
_3084	0		Sua5/YciO/YrdC/YwlC family protein	1,02	1,05	-1,07	-1,12	-1,30	-1,23	-1,05
_3085	0	1.3.99.-	putative acyl-CoA dehydrogenase family protein	-1,64	-1,61	-1,56	-1,44	-1,88	-1,06	-1,41
_3086	0		beta-lactamase domain-containing protein	-1,08	-1,11	1,06	-1,11	-1,12	-1,21	-1,02
_3087	0		aa3 type cytochrome c oxidase subunit IV	1,04	1,13	1,14	1,10	1,14	-1,30	-1,09
_3088	0		hypothetical protein	1,04	1,06	-1,03	-1,09	-1,21	-1,36	-1,11
_3089	moaB		molybdenum cofactor biosynthesis protein B	-1,02	-1,03	1,01	-1,00	-1,08	-1,20	-1,20
_3090	udgA	2.7.7.7	DNA-directed DNA polymerase	1,01	-1,02	1,00	-1,11	-1,03	-1,13	-1,13
_3091	pyrB	2.1.3.2	aspartate carbamoyltransferase	1,10	1,07	1,01	1,09	-1,10	-1,26	-1,25
_3092	0		hypothetical protein	1,06	1,02	-1,04	-1,10	-1,25	-1,29	1,04
_3093	0		hypothetical protein	1,03	1,05	-1,01	-1,02	-1,07	-1,08	1,07
_3094	pyrC1	3.5.2.3	dihydroorotase	-1,03	-1,02	-1,01	-1,06	-1,13	-1,22	1,01
_3095	0	2.3.1.n3	hypothetical protein	1,07	1,00	1,09	1,11	-1,38	-1,48	1,03
_3096	0		hypothetical protein	1,04	-1,04	1,06	1,05	1,18	1,27	1,65
_3097	gsh	6.3.2.2	Glutamate-cysteine ligase	1,07	1,09	-1,13	-1,13	-1,34	-1,62	-1,41
_3098	0		hypothetical protein	1,03	-1,00	-1,05	1,09	-1,10	-1,19	-1,03
_3099	0		16S ribosomal RNA methyltransferase RsmE	-1,02	1,00	1,00	-1,27	-1,07	-1,10	-1,12
_3100	ubiA	2.5.1.-	4-hydroxybenzoate polyprenyltransferase	1,03	1,02	1,02	-1,07	-1,09	-1,31	-1,06
_3101	0		OmpA/MotB domain-containing protein	1,05	1,02	-1,03	1,05	-1,18	-1,45	-1,09
_3102	0		hypothetical protein	1,01	1,06	-1,02	-1,04	-1,22	-1,49	-1,18
_3103	moaE		molybdopterin biosynthesis MoaE protein	-1,00	1,04	-1,04	-1,10	-1,16	-1,41	-1,13
_3104	moaD		molybdopterin converting factor, subunit 1	1,03	1,00	-1,09	-1,10	-1,25	-1,55	-1,14
_3105	pgsA	2.7.8.5	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyl transferase	1,02	1,00	-1,09	-1,32	-1,26	-1,50	-1,14
_3106	rluA		pseudouridine synthase	1,09	1,01	-1,08	-1,21	-1,12	-1,33	1,10
_3107	rhtB		lysine exporter protein LysE/YggA	1,06	1,06	-1,06	-1,01	-1,01	1,03	-1,06
_3108	0		DSBA oxidoreductase	-1,06	-1,05	1,03	-1,12	1,03	-1,03	1,01
_3109	0		hypothetical protein	1,04	1,00	-1,11	-1,40	-1,15	-1,19	-1,15
_3110	0		cyclic nucleotide-binding protein	-1,04	1,01	1,03	1,05	-1,23	-1,28	-1,27
_3111	aslA	3.1.6.1	arylsulfatase	-1,03	-1,06	-1,16	-1,50	-2,06	-1,21	-1,9
_3112	0		nonspecific acid phosphatase	-1,02	-1,03	-1,02	1,06	-1,44	1,10	-1,63
_3113	0		ATPase	1,01	-1,03	1,02	1,03	-1,14	-1,03	-1,12
_3114	0		hypothetical protein	1,05	-1,02	-1,02	-1,06	-1,03	1,20	1,01
_3115	0		hypothetical protein	-1,03	-1,07	1,01	1,06	-1,08	1,20	-1,03
_3116	0		von Willebrand factor type A	1,02	-1,03	-1,03	-1,11	-1,03	1,33	1,03
_3117	0		TPR repeat-containing protein	-1,01	-1,01	1,04	-1,01	1,01	1,15	1,14
_3118	0		hypothetical protein	-1,04	-1,03	1,00	-1,08	1,06	1,34	1,10
_3119	gltA1	2.3.3.1	citrate (Si)-synthase	-1,05	-1,00	-1,05	-1,20	-1,08	1,01	-1,01
_3120	yfdW2	2.8.3.16	formyl-CoA transferase	-1,09	-1,04	-1,07	-1,04	-1,19	-1,38	-1,10
_3121	0		hypothetical protein	-1,21	-1,08	-1,18	-1,12	-1,41	-1,70	-1,45
_3122	0		hypothetical protein	-1,05	-1,12	-1,27	-1,23	-1,42	-1,40	-1,21
_3123	0		hypothetical protein	-1,07	-1,13	-1,14	-1,21	-1,21	-1,24	-1,21
_3124	qseB		two component transcriptional regulator	1,05	-1,01	-1,07	-1,04	1,01	-1,07	1,08
_3125	qseC	2.7.13.3	histidine kinase	1,02	1,09	-1,06	-1,03	-1,12	-1,17	1,07

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_3126	0		putative iron(III) transport system substrate-binding protein	1,01	1,01	-1,04	-1,20	-1,12	1,01	-1,09
_3127	ugpB2		extracellular solute-binding protein	-1,07	-1,10	-1,30	-1,91	-2,92	-2,31	-3,02
_3128	ugpC5	3.6.3.20	glycerol-3-phosphate-transporting ATPase	-1,05	-1,01	-1,14	-1,34	-1,17	-1,03	-1,30
_3129	ugpC1	3.6.3.20	glycerol-3-phosphate-transporting ATPase	-1,06	-1,04	1,06	1,12	-1,35	-1,26	-1,28
_3130	ugpA2		binding-protein-dependent transport systems inner membrane component	1,01	-1,05	-1,07	1,05	-1,26	-1,20	-1,26
_3131	ugpE1		binding-protein-dependent transport systems inner membrane component	-1,02	-1,03	-1,07	1,11	-1,24	-1,15	-1,19
_3132	0		hypothetical protein	1,02	-1,04	-1,07	-1,03	-1,10	-1,02	-1,04
_3133	0		CopY family transcriptional regulator	-1,01	-1,04	-1,01	-1,10	-1,13	-1,23	-1,10
_3134	0		peptidase M56 BlaR1	-1,05	-1,08	1,05	1,14	-1,28	-1,27	-1,49
_3135	0		hypothetical protein	1,01	-1,03	-1,11	-1,06	-1,29	-1,29	-1,28
_3136	0		putative lipoprotein	-1,12	-1,09	1,10	1,23	1,08	1,15	-1,10
_3137	0		hypothetical protein	-1,04	1,01	-1,00	1,05	-1,06	1,04	-1,24
_3138	0		alpha/beta hydrolase fold	1,01	1,03	-1,05	-1,04	-1,01	1,09	1,01
_3139	0		cupin 2 protein	1,00	1,02	1,03	1,08	-1,07	-1,16	-1,04
_3140	0		LacI family transcription regulator	-1,01	-1,03	-1,10	1,04	-1,11	1,04	-1,24
_3141	ugpC3	3.6.3.20	glycerol-3-phosphate-transporting ATPase	-1,01	-1,03	1,02	1,04	-1,14	-1,24	-1,07
_3142	ugpE2		binding-protein-dependent transport systems inner membrane component	-1,01	-1,04	-1,11	-1,11	-1,27	-1,28	-1,26
_3143	ugpA3		binding-protein-dependent transport systems inner membrane component	1,02	-1,03	-1,08	-1,17	-1,23	-1,21	-1,11
_3144	ugpB3		extracellular solute-binding protein	-1,06	-1,03	-1,16	-1,21	-1,38	-1,33	-1,37
_3145	garL	4.1.2.20	2-dehydro-3-deoxyglucarate aldolase	1,06	-1,00	-1,07	1,03	-1,02	1,03	1,07
_3146	accA	6.4.1.2	acetyl-CoA carboxylase	1,04	1,10	-1,06	-1,13	-1,33	-1,82	-1,49
_3147	0		protein of unknown function DUF306 Meta and HslJ	1,03	1,04	-1,07	-1,39	-1,45	-1,91	-1,34
_3148	0		hypothetical protein	-1,09	-1,06	1,02	-1,07	1,03	1,00	1,08
_3149	ddpX	3.4.13.22	D-Ala-D-Ala dipeptidase	-1,09	-1,05	-1,04	-1,17	1,05	1,22	-1,05
_3150	dat	2.6.1.21	D-amino-acid transaminase	1,04	1,04	-1,12	-1,15	-1,20	-1,59	-1,20
_3151	0		LysR family transcriptional regulator	1,05	1,02	-1,03	-1,17	-1,15	-1,24	-1,09
_3152	0		hypothetical protein	-1,03	-1,02	1,32	2,39	3,51	3,21	2,46
_3153	0		TRAP dicarboxylate transporter- DctP subunit	-1,02	-1,01	1,20	1,78	3,08	3,05	2,06
_3154	0		TRAP transporter, transmembrane protein, putative	-1,02	-1,03	1,24	1,81	4,06	4,43	2,99
_3155	0		TRAP dicarboxylate transporter, DctM subunit	-1,00	-1,01	1,25	1,28	3,54	4,24	2,79
_3156	0		hypothetical protein	1,03	-1,01	1,14	1,27	2,98	3,32	2,57
_3157	0		TRAP dicarboxylate transporter- DctP subunit	-1,11	-1,07	-1,07	-1,06	-1,07	1,02	-1,37
_3158	0		tripartite ATP-independent periplasmic transporter DctQ	-1,12	-1,05	-1,05	1,05	-1,03	1,13	-1,32
_3159	0		TRAP dicarboxylate transporter, DctM subunit	-1,09	-1,06	-1,04	-1,05	-1,16	-1,04	-1,07
_3160	0		hypothetical protein	1,05	1,48	2,17	3,01	3,08	2,4	1,62
_3161	napC		NapC/NirT cytochrome c domain-containing protein	1,10	1,67	2,35	3,17	2,9	2,46	1,54
_3162	napB		nitrate reductase cytochrome c-type subunit (NapB)	1,08	1,53	2,22	2,68	2,55	1,83	1,40
_3163	napH		quinol dehydrogenase membrane component	1,17	1,86	2,57	3,65	3,17	2,36	1,59
_3164	napG		MauM/NapG family ferredoxin-type protein	1,24	1,95	2,56	2,4	2,98	2,2	1,48
_3165	napA		periplasmic nitrate reductase NapA	1,33	2,62	3,37	3,42	4,44	2,31	1,73
_3166	napD		NapD family protein	1,31	2,3	2,91	3,09	3,63	2,08	1,33
_3167	napF		ferredoxin-type protein NapF	-1,03	1,41	1,89	2,62	1,36	1,13	1,07
_3168	apbE1		ApbE family lipoprotein	1,29	1,00	1,82	7,07	23,5	17,1	14,3
_3169	cycA1		cytochrome c class I	1,36	-1,07	1,60	3,44	36,1	21,1	27,5
_3170	0		hypothetical protein	1,04	-1,04	-1,00	1,21	6,04	6,72	6,86
_3171	cbiX1		cobalamin (vitamin B12) biosynthesis CbiX protein	1,05	-1,03	1,02	-1,15	9,32	9,36	8,98
_3172	nirN	1.7.2.1	nitrite reductase (NO-forming)	1,12	-1,00	1,28	1,46	14,4	11,7	11,5
_3173	nirJ		radical SAM domain-containing protein	1,11	-1,05	1,28	2,41	6,56	5,6	6,29
_3174	nirH		AsnC family transcriptional regulator	1,33	-1,05	1,83	6,79	16,2	11,6	14,4
_3175	nirG		AsnC family transcriptional regulator	1,13	-1,08	1,44	4,27	20,6	15	12,4
_3176	nirD		AsnC family transcriptional regulator	1,16	-1,08	1,12	1,23	15,5	12,1	12,1
_3177	nirF		cytochrome cd1	1,28	-1,03	1,17	1,84	17,2	14,5	16,3
_3178	nirC		hypothetical protein	1,32	-1,07	1,49	2,47	21,1	14,4	17,4
_3179	nirE	2.1.1.107	uroporphyrinogen-III C-methyltransferase	1,33	-1,06	1,55	3,16	19,5	13,7	16,9
_3180	nirS		nitrite reductase precursor	1,58	-1,29	1,70	7,87	31,6	18,5	28,1
_3182	0		NnrS family protein	1,13	-1,08	1,17	1,40	13,1	11,6	11
_3183	norC		nitric oxide reductase, small subunit	1,63	-1,21	1,65	10,3	47,5	25,9	39,7

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_3184	norB		nitric-oxide reductase	1,52	-1,26	1,36	5,66	30,6	18,4	28,8
_3185	norQ		nitric oxide reductase Q protein	1,33	-1,07	1,23	1,33	16,3	13,4	16,9
_3186	norD		von Willebrand factor type A	1,11	1,00	1,18	1,26	19,2	25,5	28,9
_3187	norE		cytochrome c oxidase subunit III	1,13	-1,00	1,03	1,02	5,81	8,05	7,18
_3188	0		nitric oxide reductase F protein, putative	1,00	-1,00	-1,04	-1,01	8,37	13,4	9,48
_3189	0		cyclic nucleotide-binding protein	1,11	1,21	1,47	1,96	4,47	3,26	2,57
_3190	hemA3	2.3.1.37	5-aminolevulinate synthase	1,39	-1,01	1,86	5,41	11,7	8,43	9,55
_3191	dnr		Crp/FNR family transcriptional regulator	1,16	-1,03	1,64	5,19	12,8	9,87	8,85
_3192	0		hypothetical protein	1,27	1,04	1,96	5,74	14,2	11,5	12,7
_3193	nosR3		FMN-binding domain-containing protein	1,20	1,05	1,75	3,92	11,4	6,06	5,26
_3194	nosZ	1.7.2.4, 1.7.99.6	nitrous-oxide reductase,nitrous-oxide reductase	1,10	-1,05	1,49	2,09	18,4	11,3	7,02
_3195	nosD		periplasmic copper-binding	1,05	-1,00	1,24	1,15	12,8	6,37	3,06
_3196	nosF		ABC transporter related	1,12	-1,05	1,10	1,40	8,36	5,93	3,54
_3197	nosY		nitrous oxide maturation protein NosY	-1,03	-1,05	-1,01	1,29	12,4	7,98	3,11
_3198	nosL		NosL family protein	1,03	1,01	-1,04	1,15	5,88	5,38	2,91
_3199	nosX		ApbE family lipoprotein	-1,05	-1,02	-1,06	1,17	4,6	4,37	2,01
_3200	0		hypothetical protein	1,05	-1,04	1,10	1,07	1,14	1,28	1,05
_3201	0		endoribonuclease L-PSP	1,02	1,02	-1,02	-1,11	1,16	-1,11	-1,12
_3202	uraA		uracil-xanthine permease	-1,02	-1,05	-1,17	1,02	-1,24	-1,06	-1,09
_3203	allA	3.5.3.19	ureidoglycolate hydrolase	1,02	-1,03	1,00	-1,06	-1,02	1,00	-1,02
_3204	0		chitin deacetylase	-1,04	-1,01	-1,06	-1,10	-1,17	1,04	1,06
_3205	0		hydroxyisourate hydrolase	1,04	1,05	-1,06	-1,12	-1,24	-1,05	-1,13
_3206	0		LysR family transcriptional regulator	-1,04	-1,01	-1,16	-1,33	-1,25	1,00	1,12
_3207	0		hypothetical protein	-1,02	1,02	-1,11	-1,22	-1,12	-1,06	-1,07
_3208	0		hypothetical protein	-1,06	1,01	1,14	1,08	1,07	1,16	-1,05
_3209	0		hypothetical protein	-1,03	-1,02	-1,01	1,08	1,00	1,07	-1,05
_3210	ymdC		phospholipase D/transphosphatidylase	1,00	1,03	-1,09	-1,09	-1,16	-1,41	-1,28
_3211	0		putative sulfite oxidase cytochrome subunit	1,02	-1,03	1,04	-1,03	1,10	-1,02	1,11
_3212	0		oxidoreductase molybdopterin binding	-1,10	-1,07	-1,10	1,12	-1,01	1,04	1,05
_3213	0		integrase family protein	1,01	1,00	1,04	1,09	1,00	1,07	1,17
_3214	cas3		CRISPR-associated helicase Cas3	-1,00	-1,01	1,01	1,06	1,03	1,22	-1,06
_3215	cse1		CRISPR-associated Cse1 family protein	-1,02	-1,06	1,00	-1,09	-1,15	1,03	-1,09
_3216	0		hypothetical protein	-1,01	-1,02	-1,05	-1,07	-1,28	1,05	-1,15
_3217	cse3		CRISPR-associated Cse4 family protein	-1,01	-1,03	1,04	1,08	-1,27	-1,02	-1,21
_3218	cas5		CRISPR-associated Cas5 family protein	-1,03	-1,05	1,01	1,06	-1,11	1,14	-1,12
_3219	cse2		CRISPR-associated Cse3 family protein	-1,07	-1,05	1,02	1,02	-1,10	1,02	-1,08
_3220	cas1		CRISPR-associated Cas1 family protein	-1,03	-1,04	1,02	1,11	1,02	1,08	1,02
_3221	cas2		CRISPR-associated Cas2 family protein	1,03	1,01	1,06	1,01	1,18	1,26	1,10
_3222	0		hypothetical protein	-1,01	-1,02	-1,06	1,07	1,01	1,08	1,18
_3223	0		DNA binding domain-containing protein	-1,04	1,02	-1,00	-1,01	1,16	-1,00	1,14
_3224	0		integrase family protein	-1,05	-1,02	1,02	-1,01	1,08	1,04	1,13
_3225	0		hypothetical protein	1,00	1,01	1,07	1,04	1,23	1,32	1,23
_3226	0		hypothetical protein	-1,02	1,01	1,14	1,38	1,49	1,60	1,26
_3227	0		hypothetical protein	-1,09	1,03	1,35	1,76	1,63	1,45	1,24
_3228	dapF	5.1.1.7	diaminopimelate epimerase	1,06	1,14	-1,02	1,05	-1,02	-1,40	-1,07
_3229	0		MiaB-like tRNA modifying enzyme	1,01	1,04	1,01	-1,01	-1,26	-1,44	-1,18
_3230	0		hypothetical protein	-1,01	-1,04	-1,11	1,11	1,05	1,20	1,20
_3231	0		hypothetical protein	-1,06	-1,01	1,01	1,01	-1,08	1,10	1,20
_3232	0		hypothetical protein	-1,13	-1,08	1,10	1,14	1,13	1,33	-1,17
_3233	0		NLP/P60 protein	-1,01	-1,01	1,05	1,04	-1,06	1,05	1,09
_3234	pepA2	3.4.11.1	leucyl aminopeptidase	-1,07	-1,02	1,02	-1,01	-1,12	-1,11	-1,15
_3235	0		hypothetical protein	1,04	1,01	1,03	1,06	1,19	1,45	1,8
_3236	cynT	4.2.1.1	carbonate dehydratase	1,01	1,07	1,22	1,46	2,21	1,78	1,97
_3237	0		hypothetical protein	1,05	1,06	1,08	1,02	1,36	1,16	1,56
_3238	0		hypothetical protein	1,00	1,02	1,07	-1,01	1,28	1,18	1,52
_3239	0		hypothetical protein	1,06	-1,00	-1,05	1,01	1,51	1,51	1,32
_3240	asd	1.2.1.11	Aspartate-semialdehyde dehydrogenase	1,11	1,20	1,32	1,24	1,01	-1,77	1,16
_3241	lpcC		glycosyl transferase group 1	1,03	1,05	1,04	-1,15	-1,17	-1,36	-1,15
_3242	0		hypothetical protein	-1,11	-1,10	1,03	1,03	1,15	1,28	-1,16
_3243	0		hypothetical protein	1,01	-1,03	1,14	1,00	-1,02	1,15	-1,21
_3244	0		transglutaminase domain-containing protein	-1,03	-1,02	1,00	-1,02	1,05	1,18	-1,08

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_3245	0		20S proteasome A and B subunits	1,06	-1,02	-1,05	-1,05	-1,15	-1,40	-1,09
_3246	fliI		FliI/YscN family ATPase	1,03	1,01	1,00	1,14	1,38	1,47	1,30
_3247	flgB		flagellar basal body rod protein FlgB	1,06	1,00	1,01	-1,10	1,65	1,25	1,45
_3248	flgC		flagellar basal body rod protein FlgC	1,02	-1,02	1,04	1,22	1,71	1,37	1,58
_3249	fliE		flagellar hook-basal body protein FliE	1,09	1,03	1,05	1,22	1,86	1,55	1,61
_3250	fliQ		export protein FliQ	1,09	1,03	1,05	1,13	1,66	1,45	1,62
_3251	flgF		flagellar basal body rod protein FlgF	1,07	1,03	1,02	1,10	1,52	1,50	1,59
_3252	flgG		flagellar basal body rod protein FlgG	1,02	-1,03	1,09	1,10	1,34	1,52	1,67
_3253	flgA		flagellar basal body P-ring biosynthesis protein FlgA	1,04	-1,00	1,06	1,17	1,31	1,55	1,69
_3254	flgH		flagellar basal body L-ring protein	1,06	1,02	1,11	1,22	1,23	1,50	1,62
_3255	fliL1		flagellar basal body-associated protein FliL	1,04	1,03	1,05	1,15	1,21	1,49	1,38
_3256	flhB		flagellar biosynthesis protein FlhB	-1,01	1,01	1,03	-1,02	1,01	1,33	1,47
_3257	fliR		type III secretion system inner membrane R protein	1,05	1,00	-1,03	1,05	1,12	1,68	1,53
_3258	flhA		flagellar biosynthesis protein FlhA	-1,01	-1,02	1,03	1,30	1,11	1,56	1,18
_3259	0		hypothetical protein	1,10	1,01	1,06	1,04	1,16	1,28	1,41
_3260	motA		flagellar motor protein MotA	1,06	1,01	1,09	1,16	1,23	1,24	1,45
_3261	0		hypothetical protein	1,02	1,00	1,02	1,22	1,41	1,38	1,25
_3262	0		hypothetical protein	1,07	1,02	1,02	-1,06	1,69	1,39	1,44
_3263	fliL2		flagellar basal body-associated protein FliL	1,07	-1,02	-1,02	-1,05	1,81	1,50	1,41
_3264	fliF		flagellar MS-ring protein	1,05	-1,01	1,02	1,10	1,66	1,47	1,31
_3265	fliH		putative flagellar biosynthesis/type III secretory pathway protein	1,06	1,05	1,04	1,05	1,22	1,31	1,19
_3266	fliN		surface presentation of antigens (SPOA) protein	1,03	-1,01	1,06	-1,06	1,17	1,25	1,22
_3267	fliP		flagellar biosynthesis protein FliP	1,08	1,00	-1,00	-1,05	1,19	1,67	1,36
_3268	0		coenzyme F420 hydrogenase/dehydrogenase beta subunit	-1,04	-1,10	-1,05	1,04	1,57	1,50	1,34
_3269	0		L-carnitine dehydratase/bile acid-inducible protein F	-1,01	1,03	1,21	1,74	1,79	1,40	1,28
_3270	0		CRP/FNR family transcriptional regulator	1,55	2,46	4,63	9,21	12	5,73	4,09
_3271	0		hypothetical protein	-1,05	-1,00	-1,07	-1,08	-1,43	-1,57	-1,59
_3272	0		hypothetical protein	-1,01	1,01	-1,03	-1,00	-1,19	-1,38	-1,17
_3273	0		lipid A biosynthesis acyltransferase	1,01	-1,01	-1,06	-1,01	-1,02	-1,21	1,04
_3274	0		TPR repeat-containing protein	1,00	-1,04	-1,10	-1,25	-1,15	-1,06	-1,03
_3275	aroC	4.2.3.5	chorismate synthase	1,21	1,06	-1,12	-1,10	-1,15	-1,53	1,02
_3276	petC	1.10.2.2	Ubiquinol-cytochrome-c reductase	1,01	1,11	1,14	1,00	1,20	1,00	1,81
_3277	petB	1.10.2.2	Ubiquinol-cytochrome-c reductase	1,07	1,24	1,15	1,15	1,52	1,05	2,03
_3278	petA	1.10.2.2	Ubiquinol-cytochrome-c reductase	1,11	1,23	1,19	1,32	1,37	1,05	1,92
_3279	0	2.5.1.18	glutathione transferase	-1,09	-1,08	1,06	1,13	-1,02	1,15	-1,36
_3280	0		hypothetical protein	-1,09	-1,05	1,03	1,02	-1,02	1,13	-1,03
_3281	0		endonuclease/exonuclease/phosphatase	1,01	-1,01	-1,06	-1,13	-1,17	1,09	1,06
_3282	fdhD	1.2.1.2	formate dehydrogenase	-1,06	-1,04	1,02	1,01	-1,17	-1,14	-1,52
_3283	mobA		molybdopterin-guanine dinucleotide biosynthesis protein A	-1,02	-1,03	1,08	-1,01	-1,01	-1,06	-1,29
_3284	moeA3		molybdopterin-guanine dinucleotide biosynthesis protein B	1,00	1,04	-1,02	-1,09	-1,12	-1,05	-1,31
_3285	trx		thioredoxin domain-containing protein	1,00	1,01	-1,06	-1,26	-1,43	-1,51	-1,34
_3286	ccdA		cytochrome c biogenesis protein transmembrane region	1,07	1,01	-1,11	-1,22	-1,23	-1,33	-1,04
_3287	0		hypothetical protein	1,00	-1,04	-1,07	-1,16	-1,43	-1,41	-1,19
_3288	hup		histone family protein DNA-binding protein	-1,09	-1,04	-1,16	-1,33	-2,37	-2,34	-2,69
_3289	amn	3.2.2.4	AMP nucleosidase	-1,03	-1,04	-1,08	-1,02	-1,06	-1,14	-1,30
_3290	0		glyoxalase/bleomycin resistance protein/dioxygenase	-1,03	-1,03	-1,04	1,00	1,22	1,16	1,86
_3291	0		NAD-dependent epimerase/dehydratase	-1,01	-1,01	1,00	-1,02	-1,07	-1,01	-1,02
_3292	0		hypothetical protein	1,01	-1,01	1,09	1,12	-1,07	-1,01	-1,05
_3293	0		hypothetical protein	-1,01	-1,02	1,00	1,10	-1,30	-1,13	-1,30
_3294	dxs1	2.2.1.7	1-deoxy-D-xylulose-5-phosphate synthase	1,06	1,04	-1,06	-1,33	-1,24	-1,28	-1,30
_3295	ispA	2.5.1.10	(2E,6E)-farnesyl diphosphate synthase	-1,04	-1,02	1,00	-1,09	-1,39	-1,41	-1,53
_3296	xseB	3.1.11.6	exodeoxyribonuclease VII	1,01	-1,02	-1,08	-1,18	-1,30	-1,37	-1,27
_3297	0		histone deacetylase superfamily protein	1,04	1,04	-1,09	-1,30	-1,17	-1,37	-1,19
_3298	0		hypothetical protein	1,01	1,03	-1,04	-1,04	-1,08	1,07	-1,05
_3299	petR		two component transcriptional regulator	-1,05	-1,06	-1,05	-1,06	1,06	1,14	-1,01
_3300	0		MarR family transcriptional regulator	-1,02	-1,07	-1,13	-1,12	1,27	1,20	1,22
_3301	ilvE	2.6.1.42	Branched-chain-amino-acid transaminase	1,02	-1,08	-1,38	-1,56	-1,43	-1,67	-1,16
_3302	0		hypothetical protein	1,01	1,08	1,48	1,79	1,89	2,18	1,64

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_3303	0		hypothetical protein	-1,04	-1,01	1,08	-1,03	1,01	1,10	-1,03
_3304	0		hypothetical protein	-1,01	-1,02	-1,00	-1,01	1,12	1,16	-1,02
_3305	0		hypothetical protein	1,16	-1,00	1,01	1,08	1,12	1,30	1,13
_3306	0		hypothetical protein	-1,01	-1,02	-1,03	1,05	-1,04	1,23	-1,27
_3307	0		hypothetical protein	1,04	-1,05	1,02	1,04	1,03	1,08	-1,00
_3308	gst1	2.5.1.18	glutathione transferase	-1,04	1,00	-1,02	-1,12	1,01	-1,15	-1,20
_3309	mtgA	2.4.2.-	monofunctional biosynthetic peptidoglycantransglycosylase"	-1,04	-1,01	-1,03	-1,06	-1,06	-1,11	1,01
_3310	rssA		patatin	-1,01	-1,00	-1,07	-1,05	-1,16	-1,16	-1,14
_3311	0	2.1.1.-	Replicase large subunit	1,03	1,04	-1,13	-1,06	-1,08	-1,16	-1,02
_3312	0		hypothetical protein	-1,01	-1,04	-1,17	-1,51	-1,54	-1,60	-1,25
_3313	0		hypothetical protein	1,09	1,04	-1,07	-1,08	-1,07	-1,28	1,06
_3314	0		hypothetical protein	1,02	1,03	-1,04	-1,05	-1,16	-1,44	-1,26
_3315	0		hypothetical protein	1,06	-1,04	1,06	1,25	1,56	1,71	1,69
_3316	serB	3.1.3.3	phosphoserine phosphatase	1,15	1,06	-1,10	-1,38	-1,20	-1,72	-1,30
_3317	serC		phosphoserine aminotransferase	1,39	1,16	1,71	3,26	3,84	-1,38	1,52
_3318	serA1	1.1.1.95	phosphoglycerate dehydrogenase	1,19	1,24	1,35	2,25	4,33	-1,96	1,13
_3319	0		metallophosphoesterase	-1,01	1,03	1,28	1,26	1,74	-1,55	-1,08
_3320	0		hypothetical protein	-1,04	-1,04	1,01	1,03	-1,10	-1,02	1,05
_3321	0		CreA family protein	1,02	1,02	-1,07	1,03	1,07	-1,00	1,11
_3322	0		LacI family transcription regulator	-1,22	-1,13	1,02	-1,05	-1,97	-1,69	-1,76
_3323	0		GntR family transcriptional regulator	1,06	1,01	1,18	1,03	1,01	1,07	1,04
_3324	dld2	1.1.2.4	D-lactate dehydrogenase (cytochrome)	1,07	-1,00	-1,04	-1,14	-1,01	1,22	1,10
_3325	sgaA1	2.6.1.45	serine-glyoxylate transaminase	-1,03	1,08	-1,09	-1,24	-1,43	-1,51	-1,29
_3326	dctP3		TRAP dicarboxylate transporter, DctP subunit	-1,03	-1,04	-1,11	-1,08	-2,1	-1,84	-2,26
_3327	dctQ1		tripartite ATP-independent periplasmic transporter DctQ	1,02	-1,00	-1,02	1,01	-1,47	-1,53	-1,38
_3328	dctM4		TRAP dicarboxylate transporter, DctM subunit	1,00	1,01	-1,04	1,07	-1,45	-1,43	-1,55
_3329	0	4.2.1.17	enoyl-CoA hydratase	-1,05	1,00	1,01	-1,20	-1,71	-1,93	-1,45
_3330	yfdW1	2.8.3.16	formyl-CoA transferase	-1,02	1,01	1,00	1,12	-1,06	-1,28	-1,41
_3331	bktB	2.3.1.9	acetyl-CoA C-acetyltransferase	1,05	1,13	1,29	1,31	1,51	1,01	1,30
_3332	0	2.7.13.3	histidine kinase	1,06	1,04	1,05	1,07	1,74	1,36	1,34
_3333	0		hypothetical protein	1,02	1,01	-1,04	-1,07	-1,06	-1,03	-1,08
_3334	recQ	3.6.4.12	DNA helicase	1,02	1,02	1,05	1,15	1,26	1,36	-1,08
_3335	0		protein of unknown function YGGT	-1,04	1,00	1,01	1,04	1,01	-1,07	-1,13
_3336	0		hypothetical protein	-1,11	-1,09	-1,13	-1,01	-1,33	-1,32	-1,11
_3337	0		major facilitator transporter	-1,10	-1,07	-1,03	1,07	-1,11	-1,03	-1,16
_3338	mepA	3.4.24.-	penicillin-insensitive murein endopeptidase	-1,03	-1,02	1,07	-1,06	-1,02	1,16	-1,14
_3339	0		hypothetical protein	-1,02	1,01	-1,00	-1,24	1,07	1,44	-1,03
_3340	0		hypothetical protein	1,06	1,08	-1,15	-1,58	-2	-2,65	-1,89
_3341	rimK		alpha-L-glutamate ligase	1,06	1,02	-1,11	-1,30	-1,33	-1,34	-1,20
_3342	0		peptidyl-tRNA hydrolase domain protein	-1,07	-1,03	-1,02	-1,03	-1,08	-1,12	-1,27
_3343	0		aminotransferase class-III	1,07	1,03	-1,12	-1,15	-1,22	-1,21	-1,06
_3344	0		aminoglycoside phosphotransferase	-1,01	1,00	-1,02	1,06	1,04	1,12	-1,22
_3345	pncB	6.3.4.21	nicotinate phosphoribosyl transferase	-1,02	1,05	1,08	1,31	1,28	1,15	1,24
_3346	0	2.7.13.3	histidine kinase	1,02	-1,01	1,04	-1,02	1,43	1,30	1,15
_3347	pncA	3.5.1.19	nicotinamidase	-1,05	1,03	-1,01	-1,03	-1,34	-1,61	-1,36
_3348	0		rhodanese domain-containing protein	1,11	1,19	1,10	1,23	1,28	-1,15	1,20
_3349	ybbB	2.9.1.-	tRNA 2-selenouridine synthase	1,09	1,02	-1,09	-1,10	-1,02	-1,32	-1,18
_3350	selD	2.7.9.3	selenide, water dikinase	1,07	1,10	1,04	1,15	1,30	1,08	1,34
_3351	0		hypothetical protein	1,15	1,05	-1,05	-1,31	-1,14	-1,18	-1,14
_3352	0		hypothetical protein	1,02	1,00	1,04	1,00	1,04	1,10	1,07
_3353	0		hypothetical protein	-1,00	1,03	1,05	1,23	1,09	1,15	1,08
_3354	0		ABC transporter related	-1,04	1,09	1,13	1,08	1,14	-1,02	1,29
_3355	gyrB	5.99.1.3	DNA topoisomerase (ATP-hydrolysing)	-1,02	-1,00	1,02	-1,15	-1,06	-1,03	-1,06
_3357	0		integrase catalytic region	-1,02	-1,04	-1,08	1,02	1,07	1,18	1,18
_3358	0		hypothetical protein	1,05	-1,01	-1,02	-1,11	-1,03	1,50	1,85
_3359	flbT		flagellar biosynthesis repressor FlbT	1,04	1,00	1,01	1,06	-1,12	1,15	1,68
_3360	flaF		flagellar biosynthesis regulatory protein FlaF	1,04	1,01	-1,08	-1,07	-1,08	1,29	1,67
_3361	fliC		flagellin domain-containing protein	1,04	1,03	-1,02	-1,18	1,08	1,25	1,84
_3362	0		hypothetical protein	1,07	1,00	1,08	-1,02	1,61	1,41	1,51
_3363	0		flagellar protein FlgJ, putative	1,06	-1,00	1,03	1,10	1,45	1,46	1,55

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_3364	0		hypothetical protein	1,08	-1,01	-1,01	1,12	1,49	1,43	1,46
_3365	flgD		flagellar basal body rod modification protein	1,04	-1,00	1,02	-1,08	1,08	1,33	1,38
_3366	0		hypothetical protein	1,04	1,03	-1,05	-1,30	1,09	1,14	1,26
_3367	ubiB		2-polyprenylphenol 6-hydroxylase	1,04	1,06	1,08	1,16	1,24	1,03	1,32
_3368	ubiE	2.1.1.163	demethylmenaquinone methyltransferase	1,03	1,10	1,17	1,42	1,65	1,14	1,38
_3369	mutM	3.2.2.23	DNA-formamidopyrimidine glycosylase	-1,06	-1,01	-1,01	1,01	-1,10	1,06	-1,18
_3370	0	4.2.1.17	enoyl-CoA hydratase	-1,04	-1,00	-1,15	-1,53	-2,06	-2,51	-2,2
_3371	rpsT		30S ribosomal protein S20	1,27	1,26	-1,10	-1,19	-1,32	-2,52	-1,34
_3372	yibN		hypothetical protein	-1,02	-1,05	-1,24	-1,52	-1,89	-1,76	-1,50
_3373	dnaA		chromosomal replication initiation protein	-1,01	-1,06	-1,25	-1,57	-2,08	-1,72	-1,72
_3374	dnaN	2.7.7.7	DNA-directed DNA polymerase	-1,06	-1,01	-1,06	-1,25	-1,53	-1,69	-2,07
_3375	recF		recombination protein F	-1,00	1,01	-1,13	-1,43	-1,15	-1,29	-1,51
_3376	flgI		flagellar basal body P-ring protein	1,02	1,00	1,05	1,05	1,05	1,27	1,34
_3377	flgL		flagellar hook-associated protein FlgL family protein	1,02	-1,03	1,07	1,06	1,01	1,28	1,36
_3378	flgK		flagellar hook-associated protein FlgK	1,05	1,02	-1,04	-1,37	1,05	1,22	1,30
_3379	flgE		hypothetical protein	1,04	1,01	-1,01	1,02	1,26	1,19	1,46
_3380	motB		flagellar motor protein-like protein	1,07	1,03	1,08	1,19	1,46	1,54	1,71
_3381	0		surface antigen (D15)	-1,02	-1,02	-1,08	-1,14	-1,02	-1,20	-1,20
_3382	0		hypothetical protein	-1,02	-1,00	-1,02	-1,04	-1,17	-1,13	-1,25
_3383	0		rhomboid family protein	-1,02	-1,03	-1,02	-1,15	1,08	1,13	1,09
_3384	epsH		methanolan biosynthesis EpsI protein	-1,00	-1,01	-1,04	-1,05	-1,05	1,05	1,10
_3385	0		TPR repeat-containing protein	-1,01	-1,01	-1,11	-1,10	-1,08	-1,23	1,12
_3386	wcaJ	2.7.8.6	Undecaprenyl-phosphate galactose phosphotransferase	-1,05	-1,12	-1,14	1,03	-1,17	-1,13	-1,19
_3387	exeA		AAA ATPase	1,04	1,02	1,00	-1,03	1,36	1,04	1,26
_3388	0		lipopolysaccharide biosynthesis protein	1,05	1,00	-1,06	-1,08	1,09	-1,04	1,19
_3389	0		ATPase involved in chromosome partitioning-like protein	-1,02	1,02	-1,03	1,03	-1,25	-1,06	1,01
_3390	0		metallophosphoesterase	-1,01	-1,02	-1,01	1,05	-1,01	1,05	-1,22
_3391	0		beta-lactamase domain-containing protein	-1,04	-1,04	1,02	-1,05	-1,02	1,09	-1,47
_3392	0		antibiotic biosynthesis monooxygenase	-1,13	-1,09	-1,00	-1,24	-1,16	-1,06	-1,65
_3393	leuB	1.1.1.85	3-isopropylmalate dehydrogenase	-1,03	-1,03	-1,06	-1,05	-1,23	-1,38	-1,42
_3394	0		oxidoreductase domain-containing protein	1,03	-1,03	-1,05	1,03	-1,04	-1,06	-1,07
_3395	dctM3		TRAP C4-dicarboxylate transport system permease DctM subunit	1,03	-1,03	-1,09	-1,04	-1,27	-1,25	-1,31
_3396	dctQ2		tripartite ATP-independent periplasmic transporter DctQ	-1,04	-1,04	-1,09	-1,24	-1,64	-1,48	-1,68
_3397	dctP2		TRAP dicarboxylate transporter- DctP subunit	-1,14	-1,07	-1,21	-1,71	-1,85	-1,71	-2,1
_3398	orfB		ISSpo6, transposase OrfB	-1,02	-1,03	-1,03	-1,07	1,06	1,24	-1,09
_3399	orfA		ISSpo6, transposase orf A	-1,10	-1,09	-1,04	-1,10	-1,11	1,02	-1,39
_3400	ubiG2	2.1.1.64	3-demethylubiquinol 3-O-methyl transferase	1,02	-1,01	-1,03	1,11	1,11	1,12	1,25
_3401	0		hypothetical protein	1,07	1,04	1,08	1,13	1,18	1,27	1,64
_3402	0		serralysin	1,06	1,02	-1,00	-1,12	1,48	1,33	1,73
_3403	0		AMP-dependent synthetase and ligase	-1,04	-1,02	1,02	-1,07	-1,09	-1,14	-1,25
_3404	0		hypothetical protein	1,01	1,12	1,57	1,8	2,25	2,09	1,66
_3405	dsbA2		DSBA oxidoreductase	-1,10	-1,02	-1,05	-1,04	-1,40	-1,43	-1,48
_3406	0		ErfK/YbiS/YcfS/YnhG family protein	1,05	-1,00	-1,12	-1,12	1,20	1,12	1,34
_3407	dsbD		putative suppressor for copper-sensitivity B precursor	1,03	1,03	1,02	1,02	1,42	1,32	1,55
_3408	cycH		TPR repeat-containing protein	1,00	1,06	1,26	1,22	2,16	1,64	1,26
_3409	cycL		cytochrome C biogenesis protein	-1,00	1,08	1,27	1,31	2,33	1,86	1,28
_3410	dsbE		periplasmic protein thiol--disulphide oxidoreductase DsbE	1,02	1,18	1,47	1,59	2,77	2,26	1,41
_3411	cycK		cytochrome c-type biogenesis protein CcmF	1,05	1,20	1,58	1,65	3,23	2,18	1,52
_3412	0		hypothetical protein	1,18	1,52	2,76	4,39	6,12	3,78	2,25
_3413	0		YCII-related	1,23	1,59	3,02	5,5	7,39	4,01	2,3
_3414	gpsA	1.1.1.94	glycerol-3-phosphate dehydrogenase [NAD(P)+]	1,05	1,03	-1,05	-1,03	-1,07	-1,04	-1,01
_3415	gcp	3.4.24.57	O-sialoglycoprotein endopeptidase	1,02	1,04	1,07	1,04	-1,14	-1,35	-1,12
_3416	hemD	4.2.1.75	uroporphyrinogen-III synthase	1,03	1,02	1,03	-1,21	1,03	1,08	1,11
_3417	0		hypothetical protein	-1,07	-1,01	-1,01	-1,13	-1,27	-1,36	-1,45
_3418	0		HemY domain-containing protein	-1,08	-1,03	-1,03	1,05	-1,26	-1,28	-1,40
_3419	0		amidase	-1,08	-1,08	-1,11	-1,23	-1,21	-1,19	-1,43
_3420	glpK	2.7.1.30	glycerol kinase	-1,01	1,03	-1,16	-1,31	-1,61	-1,93	-1,92
_3422	0		hypothetical protein	1,00	1,01	1,02	-1,29	-1,04	-1,06	-1,24

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_3423	rpoE1		ECF subfamily RNA polymerase sigma-24 factor	-1,03	-1,02	1,14	-1,05	1,02	-1,04	-1,17
_3424	0		hypothetical protein	-1,01	-1,01	1,05	1,13	1,05	1,08	-1,07
_3425	0		hypothetical protein	-1,09	-1,03	-1,05	-1,01	-1,29	-1,36	-1,44
_3426	ahcY	3.3.1.1	adenosyl homocysteinase	1,06	1,17	1,06	-1,27	-1,30	-2,16	1,00
_3427	rafI	2.4.1.44	lipopolysaccharide 3-alpha-galactosyl transferase	1,07	1,01	-1,04	1,01	-1,06	-1,09	-1,01
_3428	0		hypothetical protein	-1,01	1,02	1,05	1,06	1,13	1,33	1,01
_3429	0		metal dependent phosphohydrolase	1,05	1,08	-1,07	-1,10	-1,19	-1,51	-1,07
_3430	regA		two component Fis family transcriptional regulator	-1,04	-1,02	-1,18	-1,28	-1,56	-1,60	-1,48
_3431	senC		electron transport protein SCO1/SenC	-1,01	1,15	1,45	1,71	2,06	2,09	1,95
_3432	regB		integral membrane sensor signal transduction histidine kinase	-1,02	-1,03	-1,06	1,01	1,03	1,08	-1,09
_3433	0		PAS domain-containing protein	1,06	-1,01	-1,07	-1,39	1,40	1,30	1,16
_3434	0		hypothetical protein	1,00	-1,01	-1,00	-1,05	-1,02	1,01	1,01
_3435	0		aminoglycoside phosphotransferase	1,06	-1,02	-1,07	-1,05	1,03	-1,01	1,03
_3436	0		nucleotidyl transferase	-1,02	-1,01	1,06	1,01	-1,00	-1,02	1,04
_3437	addB		double-strand break repair protein AddB	1,03	-1,04	1,05	1,11	1,00	1,10	1,04
_3438	addA		double-strand break repair helicase AddA	1,00	-1,02	1,04	1,15	1,11	1,11	-1,02
_3439	trxA1		thioredoxin	-1,00	1,02	-1,02	-1,22	-2,04	-2,52	-1,88
_3440	hslV	3.4.25.2	HslU-HslV peptidase	1,04	1,04	-1,07	-1,39	-1,40	-1,60	-1,22
_3441	hslU		ATP-dependent protease ATP-binding subunit HslU	1,00	1,03	-1,23	-1,43	-1,39	-1,52	-1,33
_3442	0		major facilitator transporter	-1,12	1,02	-1,11	-1,03	-1,35	-1,29	-1,38
_3443	0		Smr protein/MutS2	-1,03	-1,01	-1,00	-1,05	-1,02	1,11	1,05
_3444	mltA	3.2.1.-	membrane-bound lytic murein transglycosylase A	1,02	-1,00	1,01	-1,01	-1,13	-1,03	1,13
_3445	0		import inner membrane translocase subunit Tim44	1,01	1,04	1,04	1,16	-1,04	-1,10	1,04
_3446	fxsA		FxsA cytoplasmic membrane protein	-1,02	-1,00	1,01	1,19	1,11	1,34	1,30
_3447	secB		preprotein translocase subunit SecB	1,08	1,08	-1,25	-1,64	-1,79	-2,62	-1,55
_3448	dnaQ1	2.7.7.7	DNA-directed DNA polymerase	-1,09	-1,02	-1,07	-1,14	-1,19	-1,20	-1,46
_3449	coaE	2.7.1.24	dephospho-CoA kinase	-1,01	-1,00	1,01	-1,35	-1,57	-1,69	-1,29
_3450	aroE	1.1.1.25	shikimate dehydrogenase	1,09	1,09	-1,08	-1,21	-1,17	-1,24	-1,17
_3451	maf		maf protein	1,05	1,02	1,02	1,01	-1,07	-1,26	-1,02
_3452	0		hypothetical protein	1,08	1,10	-1,06	1,05	1,31	-1,02	1,25
_3453	rho		transcription termination factor Rho	1,19	1,15	-1,32	-1,47	-1,34	-2,16	1,16
_3454	trmE			1,04	1,02	-1,23	-1,39	-1,91	-2,23	-1,28
_3455	gidA		tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	1,07	1,03	-1,10	-1,25	-1,8	-2,12	-1,16
_3456	gidB	2.1.1.170	16S rRNA (guanine527-N7)-methyltransferase	-1,06	-1,03	-1,04	1,01	-1,68	-1,86	-1,30
_3457	parA1		cobyrinic acid ac-diamide synthase	-1,02	-1,04	-1,03	-1,01	-1,32	-1,35	-1,25
_3458	parB		parB-like partition protein	-1,03	-1,02	-1,00	-1,22	-1,19	-1,30	-1,20
_3459	0		hypothetical protein	1,02	-1,02	1,01	-1,01	-1,06	-1,18	-1,09
_3460	hemN3	1.3.99.22	coproporphyrinogen dehydrogenase	-1,01	1,01	-1,14	-1,20	-1,36	-1,41	-1,20
_3461	0		endoribonuclease L-PSP	1,01	-1,05	-1,20	-1,39	-1,97	-2,27	-1,58
_3462	ham1	3.6.1.19, 3.6.1.15	Nucleoside-triphosphate diphosphatase,nucleoside-triphosphatase	1,04	1,01	-1,21	-1,33	-1,86	-2,51	-1,55
_3463	rph	2.7.7.56	tRNA nucleotidyl transferase	1,05	1,04	-1,12	-1,22	-1,46	-2,13	-1,36
_3464	hrcA		heat-inducible transcription repressor	1,04	1,02	1,05	1,12	1,05	1,03	1,04
_3465	grpE		GrpE protein	1,11	1,08	-1,09	-1,36	-1,47	-1,92	-1,24
_3466	mutS		DNA mismatch repair protein MutS	-1,04	-1,02	1,03	1,08	1,01	-1,02	-1,18
_3467	maeB	1.1.1.40	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)	1,05	1,05	-1,06	-1,29	-1,34	-1,61	-1,53
_3468	msrA1	1.8.4.11	peptide-methionine (S)-S-oxide reductase	-1,04	-1,08	1,03	-1,00	-1,35	-1,31	-1,15
_3469	0		hypothetical protein	-1,02	-1,01	-1,04	-1,07	1,07	-1,01	-1,19
_3470	0		peptidase M48 Ste24p	1,03	1,01	1,11	1,24	1,34	1,52	1,48
_3471	0		hypothetical protein	1,01	1,01	1,09	1,19	1,20	1,16	1,25
_3472	argG	6.3.4.5	Argininosuccinate synthase	1,28	1,23	-1,14	-1,36	-1,77	-2,8	-1,53
_3473	ilvA	4.3.1.19	threonine ammonia-lyase	-1,02	-1,03	1,05	1,05	1,04	1,00	-1,03
_3474	pcaB	5.5.1.2	3-Carboxy-cis,cis-muconate cycloisomerase	-1,09	-1,01	-1,14	-1,21	-1,10	-1,05	-1,25
_3475	0		hypothetical protein	-1,02	-1,04	1,04	-1,04	-1,16	-1,11	-1,42
_3476	pcaG	1.13.11.3	protocatechuate 3,4-dioxygenase	-1,01	-1,01	1,01	-1,28	-1,06	1,03	-1,11
_3477	pcaH	1.13.11.3	protocatechuate 3,4-dioxygenase	-1,09	1,03	1,05	-1,15	-1,14	-1,22	-1,21
_3478	pcaC	4.1.1.44	4-carboxy muconolactone decarboxylase	1,02	1,02	1,03	1,06	-1,10	-1,10	-1,21
_3479	pobA	1.14.13.2	4-hydroxybenzoate 3-monooxygenase	-1,01	-1,05	1,02	1,01	-1,14	-1,19	-1,21
_3480	modE		ModE family transcriptional regulator	-1,06	1,00	1,10	-1,04	1,02	1,03	1,13
_3481	modA		molybdenum ABC transporter, periplasmic molybdate-	1,03	1,01	-1,01	-1,11	1,06	1,23	1,13

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
			binding protein							
_3482	modB		molybdate ABC transporter permease protein	1,02	1,01	1,01	1,19	-1,07	1,10	1,19
_3483	modC	3.6.3.29	Molybdate-transporting ATPase	-1,04	1,02	1,06	1,09	-1,10	1,14	1,08
_3484	0		Hpt domain-containing protein	1,03	-1,01	-1,04	-1,01	1,37	1,45	1,76
_3485	0		response regulator receiver modulated serine phosphatase	1,08	-1,00	-1,02	1,10	1,47	1,48	1,63
_3486	0		NUDIX hydrolase	1,05	-1,00	-1,12	-1,03	1,00	-1,01	1,04
_3487	hslO		Hsp33 protein	1,02	1,03	1,01	1,23	1,60	1,38	1,65
_3488	0		NUDIX hydrolase	-1,01	1,02	1,07	1,23	1,57	1,29	1,64
_3489	cca		polynucleotide adenylyltransferase region	1,01	-1,01	-1,05	1,20	1,26	1,23	1,52
_3490	0		ABC transporter related	-1,02	-1,01	1,02	1,12	1,14	1,18	1,26
_3491	0		ABC transporter related	1,00	-1,02	-1,01	1,13	1,20	1,33	1,20
_3492	rumA	2.1.1.-	23S rRNA (uracil-5-)-methyltransferase RumA	1,01	1,05	-1,06	-1,07	-1,11	-1,22	-1,09
_3493	0		Ion transport protein	-1,01	1,06	-1,03	-1,16	-1,26	-1,45	1,01
_3494	0		ErfK/YbiS/YcfS/YnhG family protein	-1,02	-1,04	-1,01	-1,10	1,12	1,15	1,15
_3495	0		SCP-like extracellular	-1,03	1,04	1,02	-1,06	1,04	-1,39	-1,11
_3496	0		ErfK/YbiS/YcfS/YnhG family protein	-1,02	1,01	1,03	-1,15	-1,19	-1,32	-1,10
_3498	hemH	4.99.1.1	ferrochelatase	1,07	1,01	-1,11	-1,19	-1,21	-1,41	-1,10
_3499	0		hypothetical protein	1,03	1,05	-1,09	-1,34	-1,25	-1,43	-1,08
_3500	comF		competence protein F, putative	-1,02	-1,08	1,04	1,09	1,45	1,45	-1,09
_3501	crtA		spheroidene monooxygenase	-1,02	-1,04	1,11	1,26	1,57	1,52	1,13
_3502	bchI	6.6.1.1	magnesium chelatase	-1,01	-1,05	1,03	1,03	1,51	1,34	1,19
_3503	bchD	6.6.1.1	magnesium chelatase	1,03	-1,05	1,02	1,05	1,29	1,36	1,14
_3504	bchO	6.6.1.1	magnesium chelatase	1,01	-1,02	1,03	1,12	1,11	1,36	1,05
_3505	0		MarR family transcriptional regulator	1,04	1,06	1,20	1,53	1,82	1,65	1,61
_3506	0		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	-1,00	1,01	1,05	1,11	1,12	1,25	1,17
_3507	grxC		glutaredoxin 3	1,03	1,02	1,05	1,11	1,16	1,30	1,36
_3508	crtI	1.14.99.-	phytoene dehydrogenase	-1,06	-1,08	-1,03	-1,02	1,40	1,30	1,05
_3509	crtB	2.5.1.32	15-cis-phytoene synthase	1,01	-1,02	1,03	1,01	1,19	1,21	-1,02
_3510	tspO		TspO and MBR like protein	1,04	-1,03	1,05	1,06	1,18	1,48	1,06
_3511	0		hypothetical protein	1,04	1,01	1,07	1,11	1,34	1,36	-1,07
_3512	crtC			1,02	1,01	1,09	1,09	1,23	1,15	-1,09
_3513	crtD	1.14.99.-	methoxyneurosporene dehydrogenase	-1,05	-1,07	1,05	1,15	1,33	1,19	-1,29
_3514	crtE	2.5.1.29	geranylgeranyl diphosphate synthase	-1,08	-1,10	1,06	1,10	1,37	1,23	-1,15
_3515	crtF	2.1.1.-	hydroxyneurosporene methyltransferase	-1,01	-1,10	1,03	1,05	1,59	1,33	-1,08
_3516	bchC			-1,00	-1,03	1,05	1,06	1,20	1,11	-1,13
_3517	bchX	1.18.6.1, 1.3.1.33	nitrogenase,protochlorophyllide reductase	1,01	-1,05	-1,05	-1,10	1,21	1,01	-1,44
_3518	bchY		chlorophyllide reductase subunit Y	1,06	-1,01	-1,10	-1,10	-1,25	1,03	-1,33
_3519	bchZ	1.3.1.33	protochlorophyllide reductase	1,07	1,01	-1,05	-1,10	1,12	1,12	-1,51
_3520	pufQ		PufQ cytochrome subunit	1,05	-1,02	1,02	1,10	-1,04	1,15	-1,75
_3521	pufB		antenna complex, alpha/beta subunit	-1,01	-1,01	-1,02	-1,02	-1,14	1,07	-1,20
_3522	pufA		antenna complex alpha/beta subunit	1,02	-1,02	-1,04	1,03	-1,13	1,05	-1,17
_3523	pufL		photosynthetic reaction center subunit L	1,04	-1,01	-1,04	-1,03	-1,08	1,39	-1,49
_3524	pufM		photosynthetic reaction center subunit M	1,03	-1,02	-1,04	-1,04	-1,09	1,30	-1,49
_3525	pufC		photosynthetic reaction center cytochrome c subunit	1,02	-1,02	-1,05	-1,03	-1,11	1,29	-1,52
_3526	dxs2	2.2.1.7	1-deoxy-D-xylulose-5-phosphate synthase	1,05	1,01	-1,02	-1,01	-1,09	1,06	-1,41
_3527	idi	5.3.3.2	Isopentenyl-diphosphate DELTA-isomerase	1,03	1,04	1,14	1,19	1,56	1,75	1,51
_3528	bchP	1.3.1.83	geranylgeranyl diphosphate reductase	1,04	-1,00	1,10	1,09	1,68	2,02	1,45
_3529	pucC2		PUCC protein	-1,00	-1,07	1,08	1,12	2,19	2,14	1,67
_3530	bchG	2.5.1.62	chlorophyll synthase	-1,03	-1,04	1,08	1,27	2,09	2,08	1,66
_3531	ppsR		Fis family transcriptional regulator	1,05	1,01	-1,04	-1,16	1,30	-1,02	-1,01
_3532	ppaA		cobalamin B12-binding domain-containing protein	-1,01	-1,08	-1,07	-1,03	1,35	1,11	1,04
_3533	bchF	4.2.1.-	2-oxoglutarate synthase subunit,2-oxoacid-ferredoxin oxidoreductase subunit CD"	-1,06	-1,06	-1,06	-1,01	1,71	1,49	1,15
_3534	bchN			-1,01	-1,11	-1,05	-1,03	1,46	1,21	-1,00
_3535	bchB			1,01	-1,03	-1,03	-1,10	1,17	1,29	-1,01
_3536	bchH	6.6.1.1, 6.6.1.2	magnesium chelatase,cobaltochelatase	1,01	1,00	1,02	1,03	1,11	1,23	1,01
_3537	chlL			1,01	-1,01	1,00	-1,01	-1,17	1,09	-1,14
_3538	bchM	2.1.1.11	magnesium protoporphyrin IX methyltransferase	1,04	-1,00	1,01	1,11	1,01	1,20	-1,09
_3539	lhaA		PUCC protein	1,05	-1,02	1,05	1,13	1,19	1,43	1,09

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_3540	puhA		photosynthetic reaction center subunit H	1,02	-1,02	-1,01	1,04	1,15	1,48	1,07
_3541	puhB		photosynthetic complex assembly protein	1,03	-1,01	-1,04	-1,04	1,04	1,39	1,04
_3542	puhC		hypothetical protein	1,02	-1,02	-1,05	-1,05	-1,05	1,29	-1,01
_3543	0		hypothetical protein	1,02	1,01	-1,01	-1,05	-1,02	1,25	-1,08
_3544	acsF	1.14.13.81	Magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase	1,01	-1,01	-1,02	-1,05	-1,05	1,21	-1,03
_3545	puhE		hypothetical protein	1,02	1,00	1,05	1,06	1,30	1,60	1,14
_3546	hemA1	2.3.1.37	5-aminolevulinate synthase	-1,06	-1,07	-1,10	-1,11	1,27	1,07	-1,42
_3547	cycA2		cytochrome c class I	-1,05	-1,02	-1,13	-1,33	-2,11	-2,39	-2,5
_3548	0		ABC transporter related	1,06	1,01	-1,05	-1,09	-1,19	-1,26	1,00
_3549	glpQ	3.1.4.46	glycerophospho diester phosphodiesterase	-1,01	-1,02	-1,00	-1,09	-1,17	-1,11	-1,26
_3550	ubiG1	2.1.1.64	3-demethylubiquinol 3-O-methyl transferase	1,01	1,02	1,03	1,03	-1,06	-1,16	1,04
_3551	pip	3.4.11.5	prolyl aminopeptidase	1,00	1,01	-1,04	-1,10	1,06	-1,05	-1,09
_3552	0		extracellular solute-binding protein	-1,01	-1,01	-1,01	-1,03	1,01	1,01	1,04
_3553	acs	6.2.1.1	acetate-CoA ligase	1,02	1,11	1,09	1,16	1,8	1,18	2,28
_3554	adk1	2.7.4.3	adenylate kinase	-1,01	1,01	1,05	-1,14	-1,57	-1,50	1,42
_3555	0		hypothetical protein	1,00	1,04	1,04	1,11	-2	-2,05	-1,16
_3556	0		Na+/solute symporter	-1,00	1,04	-1,02	1,05	-1,72	-1,77	-1,03
_3557	0		CBS domain-containing protein	-1,07	-1,00	1,01	1,15	1,11	1,18	1,11
_3558	0		hypothetical protein	-1,01	1,27	1,72	2,27	3,06	2,77	1,77
_3559	dnaQ2	2.7.7.7	DNA-directed DNA polymerase	1,14	1,35	2,49	6,86	6,89	4,75	2,32
_3560	0		hypothetical protein	1,09	1,11	-1,17	-1,38	-1,42	-2,38	-1,40
_3561	nusA		transcription elongation factor NusA	1,03	1,09	-1,16	-1,88	-1,74	-2,65	-1,73
_3562	0		hypothetical protein	1,03	1,02	-1,06	-1,29	-1,65	-2,19	-1,57
_3563	infB		translation initiation factor IF-2	1,06	1,07	-1,14	-1,33	-1,78	-2,32	-1,52
_3564	mutT	3.6.1.-	mutator MutT protein	-1,00	1,01	-1,09	-1,17	-1,41	-1,55	-1,24
_3565	argJ	2.3.1.35, 2.3.1.1	glutamate N-acetyltransferase,amino-acid N-acetyltransferase	1,01	1,00	-1,13	-1,37	-1,67	-1,82	-1,40
_3566	ppiC	5.2.1.8	Peptidylprolyl isomerase	1,00	1,03	-1,14	-1,32	-1,54	-1,75	-1,43
_3567	secA		preprotein translocase subunit SecA	1,04	1,05	-1,08	-1,13	-1,07	-1,27	1,04
_3568	0		OmpA domain-containing protein	-1,09	-1,01	1,05	1,10	-1,18	1,11	1,05
_3569	radC		DNA repair protein RadC	-1,02	-1,07	-1,06	-1,32	1,15	1,25	-1,05
_3570	dnaJ		chaperone protein DnaJ	1,02	1,01	-1,16	-1,24	-1,39	-1,17	1,06
_3571	dnaK		molecular chaperone DnaK	1,06	1,10	-1,04	-1,01	-1,26	-1,03	1,18
_3572	alkB2		2OG-Fe(II) oxygenase	-1,01	1,01	-1,00	-1,12	1,13	1,17	1,15
_3573	0		ABC-2 type transporter	1,03	-1,01	-1,00	1,12	1,73	1,65	1,33
_3574	cysQ	3.1.3.7	3(2),5-bisphosphate nucleotidase	1,04	1,09	1,08	1,19	1,28	-1,11	1,13
_3575	kdsB	2.7.7.38	3-deoxy-manno-octulosonate cytidylyltransferase	1,02	1,03	1,05	1,02	1,24	-1,06	1,12
_3576	0		glycosyl transferase family protein	1,01	1,03	1,08	-1,10	1,01	-1,01	1,12
_3577	galU	2.7.7.9	UTP-glucose-1-phosphate uridylyltransferase	-1,04	-1,02	-1,03	1,07	1,28	-1,24	-1,07
_3578	0		glycosyl transferase group 1	-1,03	-1,01	-1,01	1,04	1,19	1,10	1,12
_3579	0		hypothetical protein	1,00	-1,00	1,10	-1,20	1,24	1,62	1,33
_3580	0		core-2/I-branching enzyme family protein	1,05	1,00	1,02	-1,02	-1,03	1,51	1,30
_3581	0		hypothetical protein	-1,02	-1,01	1,00	-1,13	-1,03	1,24	-1,08
_3582	ptsN	2.7.1.69	Protein-Npi-phosphohistidine-sugar phosphotransferase	1,03	1,01	-1,05	-1,12	-1,11	-1,16	-1,16
_3583	0		sigma 54 modulation protein/ribosomal protein S30EA	-1,03	-1,01	1,05	-1,17	-1,02	1,11	-1,18
_3584	rpoN		RNA polymerase, sigma 54 subunit, RpoN	-1,02	-1,04	-1,01	1,01	-1,04	1,06	1,09
_3585	0		ABC transporter related	1,02	-1,02	1,01	1,04	-1,11	-1,07	-1,01
_3586	0		cell envelope biogenesis YhbN	1,01	1,02	1,05	1,21	-1,12	-1,20	-1,07
_3587	0		hypothetical protein	-1,03	-1,03	-1,11	-1,07	-1,44	-1,53	-1,41
_3588	yrbH	5.3.1.13	Arabinose-5-phosphate isomerase	1,02	1,03	-1,10	-1,15	-1,23	-1,33	-1,22
_3589	0		3'-5' exonuclease	1,03	1,03	-1,08	-1,10	-1,33	-1,67	-1,48
_3590	0	1.6.5.3	NADH:ubiquinone reductase (H+-translocating)	1,12	1,24	1,48	1,60	2,15	1,35	1,93
_3591	0		prenyl protease-related	1,02	-1,02	1,02	-1,07	1,06	1,15	1,41
_3592	0		Cna B domain-containing protein	-1,04	-1,05	-1,18	-1,28	-1,50	-1,45	-1,75
_3593	uppP	3.6.1.27	Undecaprenyl-diphosphate phosphatase	1,08	1,03	-1,10	1,03	-1,02	-1,02	1,39
_3594	0		hypothetical protein	-1,03	-1,00	-1,03	1,10	1,11	1,20	1,14
_3595	0		ErfK/YbiS/YcfS/YnhG family protein	-1,11	-1,08	-1,06	1,18	1,24	1,29	1,03
_3596	0		multicopper oxidase type 3	1,10	1,07	-1,05	-1,14	-1,10	-1,30	1,24
_3597	0		disulphide bond formation protein DsbB	1,02	1,03	-1,12	-1,01	-1,45	-1,57	1,01
_3598	0		ErfK/YbiS/YcfS/YnhG family protein	1,03	1,02	-1,07	-1,23	-1,31	-1,49	-1,08

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_3600	0		calcium-binding EF-hand-containing protein	-1,07	-1,02	1,01	1,03	1,06	1,12	1,27
_3601	0		hypothetical protein	-1,01	1,02	-1,02	-1,03	-1,16	-1,14	1,05
_3602	0		prolipoprotein diacylglyceryl transferase	-1,03	-1,02	-1,05	-1,21	1,05	1,08	1,14
_3603	0		heavy metal translocating P-type ATPase	-1,08	1,03	-1,09	-1,09	-1,20	-1,25	1,04
_3604	0		amino acid permease-associated region	-1,03	-1,03	1,11	-1,02	-1,18	-1,03	-1,15
_3605	0		hypothetical protein	-1,06	1,01	1,03	1,14	1,06	1,25	1,08
_3606	0		cytochrome c biogenesis protein transmembrane region	-1,04	1,00	-1,05	-1,04	-1,03	-1,01	1,15
_3607	0		ErfK/YbiS/YcfS/YnhG family protein	1,00	1,02	1,04	-1,11	-1,23	-1,04	2,43
_3608	0		hypothetical protein	-1,06	-1,05	-1,04	-1,37	-1,22	-1,20	-1,11
_3609	0		heavy metal translocating P-type ATPase	-1,03	-1,01	-1,08	-1,06	-1,14	-1,20	1,36
_3610	0		hypothetical protein	1,01	1,02	1,02	1,46	1,07	1,06	-1,02
_3611	0		DtxR family iron dependent repressor	-1,05	-1,03	-1,00	1,02	-1,15	-1,23	-1,22
_3612	0		hypothetical protein	-1,02	-1,04	-1,05	-1,00	-1,07	1,00	1,25
_3613	0		apolipoprotein N-acyltransferase	-1,00	1,02	-1,16	1,13	-1,19	-1,01	1,65
_3614	0		lipoprotein signal peptidase	1,00	-1,05	1,11	1,07	-1,15	-1,24	1,42
_3615	0		zinc/iron permease	1,04	1,02	-1,02	1,31	-1,36	-1,43	1,79
_3616	0		hypothetical protein	-1,01	-1,01	1,03	-1,06	-1,43	-1,37	1,63
_3617	0		peptidase M23B	-1,06	-1,04	1,01	-1,04	-1,17	-1,26	1,65
_3618	0		electron transport protein SCO1/SenC	-1,02	-1,01	-1,12	-1,34	-1,19	-1,10	1,64
_3619	0		hypothetical protein	-1,07	-1,01	1,02	-1,08	-1,75	-1,53	1,61
_3620	0		DSBA oxidoreductase	-1,09	-1,08	-1,06	-1,08	-1,48	-1,26	1,82
_3621	0		disulphide bond formation protein DsbB	1,06	1,01	-1,11	-1,03	-1,16	-1,05	1,95
_3622	0		electron transport protein SCO1/SenC	1,01	1,01	-1,18	1,04	-1,30	-1,19	2,06
_3623	0		MerR family transcriptional regulator	-1,02	-1,01	-1,11	1,01	-1,02	1,02	1,21
_3624	0		cation efflux protein	1,02	-1,01	-1,07	1,01	1,09	1,06	1,18
_3625	0		hypothetical protein	-1,07	-1,02	-1,08	1,05	-1,07	1,07	1,65
_3626	0		cation diffusion facilitator family transporter	1,00	1,01	-1,03	-1,17	-1,02	1,00	1,70
_3627	0		hypothetical protein	-1,05	-1,05	-1,05	1,06	-1,15	-1,07	1,25
_3628	0		hypothetical protein	-1,04	-1,05	-1,01	-1,16	-1,17	-1,06	-1,25
_3631	0		AraC family transcriptional regulator	-1,03	-1,02	-1,03	1,11	1,18	1,24	1,17
_3632	0		L-carnitine dehydratase/bile acid-inducible protein F	1,01	-1,03	1,03	1,04	-1,02	1,07	1,11
_3633	0		hypothetical protein	1,01	-1,00	1,03	1,12	1,17	1,09	1,18
_3634	0		hypothetical protein	1,05	-1,01	1,00	1,03	1,08	1,23	1,34
_3635	0		XRE family transcriptional regulator	1,02	-1,00	-1,02	1,02	-1,04	1,12	1,15
_3636	0		hypothetical protein	1,01	-1,01	-1,01	1,14	1,05	1,11	1,11
_3637	0		hypothetical protein	1,07	1,05	-1,08	-1,01	-1,20	-1,36	-1,17
_3638	0		lytic transglycosylase catalytic	1,04	1,02	-1,13	-1,17	-1,17	-1,52	-1,30
_3639	0		conjugal transfer protein TrbC	-1,01	-1,03	-1,20	-1,51	-1,53	-1,8	-1,30
_3640	0		type IV secretory pathway VirB3 family protein	1,01	-1,02	-1,16	-1,42	-1,50	-1,60	-1,25
_3641	0		CagE TrbE VirB component of type IV transporter system	-1,01	-1,05	-1,14	-1,30	-1,72	-1,74	-1,34
_3642	0		hypothetical protein	-1,02	-1,03	-1,11	-1,06	-1,60	-1,53	-1,27
_3643	0		lytic transglycosylase catalytic	-1,02	-1,03	-1,01	1,00	-1,74	-1,58	-1,37
_3644	0		hypothetical protein	-1,02	-1,00	1,01	-1,03	-1,86	-1,71	-1,39
_3645	0		VirB8 family protein	-1,01	-1,01	-1,02	-1,03	-1,99	-1,51	-1,23
_3646	0		conjugal transfer protein TrbG/VirB9/CagX	-1,01	-1,03	-1,03	1,11	-1,85	-1,43	-1,35
_3647	0		conjugation TrbI family protein	-1,03	-1,01	-1,04	-1,08	-1,57	-1,30	-1,25
_3648	0		type II secretion system protein E	-1,00	-1,01	1,02	1,05	-1,49	-1,31	-1,15
_3649	0		hypothetical protein	-1,01	-1,04	1,01	1,07	-1,44	-1,25	-1,25
_3650	0		hypothetical protein	1,01	-1,02	1,06	1,06	-1,39	-1,24	-1,09
_3651	0		TrbL/VirB6 plasmid conjugal transfer protein	1,01	1,00	1,12	1,17	-1,18	-1,13	-1,06
_3652	0		hypothetical protein	1,02	-1,01	1,02	1,16	1,22	1,26	1,18
_3653	0		DNA-directed DNA polymerase	-1,01	1,00	-1,02	1,02	-1,09	-1,01	-1,14
_3654	0		hypothetical protein	1,02	-1,02	1,05	1,12	-1,13	-1,10	-1,23
_3655	0		TRAG family protein	-1,04	-1,03	1,02	1,05	-1,16	-1,00	-1,11
_3656	0		relaxase/mobilization nuclease family protein	-1,01	-1,05	-1,06	-1,28	-1,09	-1,11	-1,27
_3657	0		transposase IS3/IS911 family protein	-1,08	-1,08	-1,12	-1,06	-1,16	-1,07	-1,27
_3658	0		hypothetical protein	-1,05	1,01	-1,20	-1,19	1,02	1,34	1,08
_3659	0		hypothetical protein	-1,06	-1,03	-1,01	1,19	1,09	1,12	1,18
_3660	0		hypothetical protein	-1,02	-1,00	-1,21	1,05	1,11	1,27	1,23
_3661	0		integrase family protein	1,00	-1,04	1,03	1,16	1,06	1,13	-1,13

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_3662	0		putative transposase	-1,02	-1,03	-1,03	1,06	1,08	1,21	1,08
_3664	0		hypothetical protein	-1,03	-1,02	-1,06	-1,36	1,05	1,18	1,27
_3665	0		transcriptional modulator of MazE/toxin, MazF	1,01	-1,02	-1,06	-1,07	1,18	1,36	1,33
_3666	0		hypothetical protein	-1,02	-1,01	1,02	-1,04	1,15	1,45	1,64
_3668	0		hypothetical protein	-1,03	-1,04	1,09	1,36	1,40	1,40	1,79
_3669	0		exopolysaccharide synthesis ExoD	-1,04	1,00	-1,04	-1,08	1,01	1,09	1,16
_3670	0		CaCA family Na(+)/Ca(+) antiporter	-1,13	-1,00	1,10	-1,09	-1,02	1,12	1,12
_3671	0		pentapeptide repeat-containing protein	1,01	-1,03	1,01	1,12	1,14	1,17	1,17
_3672	0		hypothetical protein	1,05	-1,00	1,03	1,07	-1,01	1,17	1,22
_3673	0		hypothetical protein	-1,01	-1,01	-1,02	1,08	1,20	1,15	1,22
_3674	0		cyclic nucleotide-binding protein	-1,03	-1,02	-1,06	1,14	1,09	1,10	-1,09
_3676	0		transposase Tn3 family protein	-1,01	-1,00	1,10	1,05	1,08	1,07	1,04
_3677	0		hypothetical protein	-1,01	-1,01	-1,02	1,12	1,05	-1,02	1,11
_3683	0		resolvase domain-containing protein	-1,08	1,00	1,10	-1,01	-1,00	1,18	1,16
_3684	0		hypothetical protein	-1,09	-1,08	-1,08	-1,34	-1,55	-1,40	-1,84
_3685	0		BioY protein	-1,04	-1,09	-1,09	-1,12	-1,49	-1,32	-1,68
_3686	0		ABC transporter related	1,01	-1,02	-1,08	-1,25	-1,16	-1,00	-1,26
_3687	0		cobalt transport protein	-1,02	-1,03	-1,08	-1,37	-1,33	-1,06	-1,34
_3688	0		BioY protein	-1,04	-1,02	1,17	1,15	1,10	1,09	1,09
_3689	0		hypothetical protein	-1,11	-1,09	-1,22	1,02	-1,09	1,12	1,17
_3690	0		ParB-like nuclease	-1,04	-1,02	-1,05	1,07	1,02	1,10	-1,00
_3691	0		hypothetical protein	-1,13	-1,00	-1,04	-1,08	1,01	1,17	1,05
_3692	0		hypothetical protein	-1,07	-1,03	1,04	1,09	1,08	-1,00	-1,04
_3693	0		hypothetical protein	1,02	-1,00	1,05	1,12	1,09	1,09	1,15
_3695	0		type III restriction protein res subunit	-1,06	-1,02	-1,03	1,00	-1,10	-1,05	-1,43
_3696	0		integrase family protein	1,01	1,01	-1,03	1,19	-1,10	1,03	-1,11
_3697	0		integrase family protein	-1,04	-1,05	1,01	1,07	-1,06	1,05	-1,11
_3698	0		integrase family protein	-1,03	-1,10	1,05	-1,09	-1,51	-1,21	-1,07
_3699	0		putative methylase/helicase	-1,01	-1,01	1,05	1,06	1,10	1,13	1,17
_3700	0		integrase family protein	1,07	1,01	-1,08	-1,15	-1,06	-1,01	-1,14
_3701	0		putative transposase	-1,02	-1,05	-1,05	1,02	1,16	1,11	1,20
_3702	0		fatty acid hydroxylase	1,06	1,02	-1,02	-1,03	-1,01	1,55	1,04
_3707	0		transposase, IS4 family protein	-1,01	-1,01	-1,05	1,19	-1,07	-1,09	-1,15
_3708	0		AraC family transcriptional regulator	-1,06	-1,11	-1,11	-1,31	-1,10	1,13	-1,29
_3709	0		TRAP dicarboxylate transporter, DctM subunit	-1,03	1,02	-1,02	-1,18	-1,11	-1,20	-1,02
_3710	0		tripartite ATP-independent periplasmic transporter DctQ	1,07	1,00	-1,08	-1,39	-1,26	-1,29	-1,14
_3711	0		TRAP dicarboxylate transporter- DctP subunit	-1,04	-1,02	-1,14	-1,05	-1,60	-1,77	-1,48
_3712	0		short-chain dehydrogenase/reductase SDR	1,04	1,03	1,11	1,11	1,05	-1,05	1,03
_3713	0		hypothetical protein	-1,07	-1,07	1,00	1,07	1,10	1,14	-1,14
_3714	0		3-octaprenyl-4-hydroxybenzoate carboxy-lyase	-1,03	-1,01	1,09	1,27	-1,00	-1,01	-1,15
_3715	0		LysR family transcriptional regulator	-1,13	-1,02	-1,02	-1,09	-1,09	1,02	-1,06
_3716	0		UbiD family decarboxylase	1,05	1,01	1,01	-1,09	1,10	1,11	1,27
_3717	0		aldehyde dehydrogenase	1,03	-1,01	-1,01	1,25	1,07	1,07	1,12
_3718	0		AraC family transcriptional regulator	1,05	1,00	1,03	-1,38	-1,01	1,29	1,07
_3719	0		aldehyde oxidase and xanthine dehydrogenase molybdopterin binding	1,07	-1,01	-1,04	-1,25	-1,01	1,12	1,12
_3720	0		molybdopterin dehydrogenase FAD-binding	1,03	1,03	-1,06	1,19	1,06	1,09	1,11
_3721	0		2Fe-2S iron-sulfur cluster binding domain-containing protein	-1,00	1,00	1,10	1,01	1,05	1,03	1,13
_3722	0		AMP-dependent synthetase and ligase	-1,00	1,02	1,10	1,11	1,04	1,07	1,18
_3723	0		enoyl-CoA hydratase/isomerase	-1,04	1,04	1,02	1,21	-1,15	-1,08	1,06
_3724	0		extracellular ligand-binding receptor	1,04	-1,04	-1,02	1,30	1,04	-1,06	1,12
_3725	0		inner-membrane translocator	1,01	1,05	-1,00	1,19	1,18	1,32	1,17
_3726	0		inner-membrane translocator	-1,04	-1,01	-1,08	1,09	1,02	1,11	1,18
_3727	0		ABC transporter related	1,00	-1,02	1,02	1,16	1,01	1,04	-1,02
_3728	0		ABC transporter related	-1,04	1,02	-1,03	1,24	1,12	1,14	1,28
_3729	0		hypothetical protein	1,05	1,01	-1,03	1,08	1,19	1,17	1,22
_3730	0		putative regulator PrlF	-1,00	1,00	-1,05	1,07	1,05	1,00	1,12
_3731	0		hypothetical protein	-1,07	-1,00	-1,03	1,14	1,10	1,18	1,16
_3732	0		hypothetical protein	-1,03	-1,00	1,08	1,23	1,17	1,16	1,03
_3733	0		parB-like partition protein	-1,10	-1,05	-1,00	1,09	1,12	1,21	-1,06

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_3734	0		transposase IS116/IS110/IS902 family protein	-1,05	1,02	1,09	-1,04	-1,14	-1,20	-1,04
_3736	0		integrase catalytic region	-1,03	-1,05	-1,10	-1,25	-1,21	-1,21	-1,15
_3737	0		transposase IS3/IS911 family protein	-1,00	-1,00	-1,08	-1,13	-1,20	-1,05	-1,13
_3738	0		transposase IS116/IS110/IS902 family protein	-1,02	-1,03	1,09	-1,04	1,16	1,18	1,12
_3739	0		integrase catalytic region	1,06	1,02	1,09	-1,08	1,21	1,19	1,10
_3740	0		hypothetical protein	-1,01	-1,03	-1,01	-1,08	1,14	1,33	1,22
_3741	0		hypothetical protein	-1,05	1,01	1,00	1,13	1,02	1,31	1,02
_3742	0		hypothetical protein	-1,05	1,02	-1,02	1,13	1,01	1,10	1,15
_3743	0		replication protein C	1,02	-1,00	-1,04	-1,04	1,00	1,03	-1,06
_3744	0		replication protein B	-1,00	-1,05	-1,06	-1,10	-1,21	-1,32	-1,29
_3745	0		RC102	1,01	-1,00	-1,02	-1,02	1,10	1,03	-1,04
_3746	0		hypothetical protein	-1,06	-1,03	-1,08	1,09	1,03	1,07	1,09
_3747	0		hypothetical protein	1,02	1,02	-1,07	-1,34	1,08	1,09	1,18
_3748	0		resolvase domain-containing protein	-1,05	1,03	1,12	1,07	-1,00	1,09	1,04
_3749	0		CopG/Arc/MetJ family addiction module antidote protein	-1,03	-1,00	1,02	1,04	1,04	-1,04	1,01
_3750	0		plasmid stabilization system protein	1,02	1,00	1,03	1,15	1,07	1,01	1,11
_3751	0		integrase family protein	-1,06	-1,02	1,05	1,25	1,43	1,50	1,11
_3752	0		hypothetical protein	-1,00	-1,01	-1,04	1,01	1,13	1,32	1,32
_3753	0		chromosome segregation and condensation protein ScpB	-1,01	-1,04	-1,09	-1,09	1,25	1,32	1,32
_3754	0		WGR domain-containing protein	-1,02	-1,06	-1,02	1,11	1,19	1,35	1,21
_3755	0		filamentation induced by cAMP protein Fic	-1,00	-1,03	-1,03	-1,04	1,16	1,30	1,16
_3756	0		hypothetical protein	-1,11	-1,12	1,01	1,01	1,04	1,45	-1,30
_3757	0		IS5 family transposase OrfA	1,05	1,04	-1,11	-1,21	-1,10	-1,20	-1,08
_3758	0		transposase IS4 family protein	-1,04	-1,01	-1,06	-1,13	-1,06	-1,09	-1,08
_3759	0		transposase IS116/IS110/IS902 family protein	-1,00	1,03	-1,09	-1,05	-1,17	-1,35	-1,15
_3760	0		hypothetical protein	-1,14	-1,03	-1,03	1,20	1,05	1,24	-1,10
_3761	0		ISSpo6, transposase orf A	-1,08	-1,08	1,03	-1,08	-1,20	-1,08	-1,44
_3762	0		ISSpo6, transposase OrfB	-1,06	-1,02	1,02	-1,04	1,00	1,09	-1,12
_3763	0		hypothetical protein	-1,05	1,07	1,37	1,78	1,82	1,27	1,11
_3764	0		cyclic nucleotide-binding protein	-1,11	-1,03	-1,00	1,02	-1,23	-1,12	-1,25
_3765	0		hypothetical protein	-1,10	-1,03	1,07	1,01	-1,27	-1,35	-1,43
_3766	0		fatty acid hydroxylase	1,01	-1,01	-1,04	1,16	-1,03	1,08	1,09
_3767	0		cation diffusion facilitator family transporter	-1,09	-1,02	-1,03	-1,12	-1,08	-1,10	1,14
_3768	0		SNARE associated Golgi protein	1,01	1,03	-1,09	1,04	1,00	1,12	1,16
_3769	0		hypothetical protein	1,00	1,02	-1,03	1,10	1,03	1,05	1,11
_3770	0		ion transport 2 domain-containing protein	-1,03	1,01	1,07	1,13	1,14	1,26	1,07
_3771	0		hypothetical protein	-1,03	-1,03	-1,02	1,09	-1,04	1,03	-1,05
_3772	0		two component transcriptional regulator	-1,04	1,00	1,05	1,01	1,09	1,04	1,05
_3773	0		integral membrane sensor signal transduction histidine kinase	-1,01	-1,01	-1,06	-1,02	-1,03	-1,14	-1,00
_3774	0		hypothetical protein	1,01	-1,05	1,00	1,07	-1,08	1,01	1,03
_3775	0		cytochrome c-type biogenesis protein CcmF	-1,03	-1,02	-1,05	1,11	-1,18	-1,02	-1,37
_3776	0		periplasmic protein thiol--disulphide oxidoreductase DsbE	-1,04	-1,04	-1,00	1,16	1,01	-1,03	1,04
_3777	0		cytochrome C biogenesis protein	-1,07	-1,01	-1,02	-1,02	-1,11	-1,11	-1,34
_3778	0		TPR repeat-containing protein	-1,03	-1,01	-1,02	1,12	-1,13	-1,14	-1,14
_3779	0		thiol:disulfide interchange protein DsbD 1 precursor	-1,01	-1,05	1,03	1,14	1,27	1,27	1,10
_3780	0		hypothetical protein	-1,03	1,05	1,09	1,29	1,28	1,26	1,04
_3781	0		ErfK/YbiS/YcfS/YnhG family protein	-1,01	1,06	1,05	1,09	-1,22	-1,26	-1,08
_3782	0		cytochrome c class I	1,00	1,02	-1,06	-1,08	-1,28	-1,33	-1,02
_3783	0		putative cytochrome c-like protein	-1,03	-1,02	-1,03	1,06	-1,22	-1,07	1,06
_3784	0	1.1.99.3	gluconate 2-dehydrogenase (acceptor)	-1,01	-1,01	-1,05	-1,39	-1,44	-1,24	-1,14
_3785	0		multicopper oxidase type 3	-1,04	-1,01	1,00	-1,06	-1,37	-1,11	-1,10
_3786	0		cytochrome c class I	-1,05	-1,02	-1,00	1,04	-1,27	-1,20	-1,09
_3787	0		DSBA oxidoreductase	-1,07	-1,00	-1,06	1,05	-1,42	-1,28	-1,44
_3788	0		heavy metal transport/detoxification protein	-1,04	-1,01	1,02	-1,18	-1,38	-1,43	-2,09
_3789	0		heavy metal translocating P-type ATPase	-1,06	-1,01	-1,02	1,03	-1,13	1,01	-1,05
_3790	0		MerR family transcriptional regulator	-1,07	-1,00	-1,12	-1,02	-1,33	-1,24	-1,13
_3791	0		glutaredoxin	1,01	1,02	-1,03	-1,05	1,17	1,12	1,15
_3792	0		extracellular solute-binding protein	-1,11	-1,07	-1,11	-1,05	-1,10	1,22	-1,25

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_3793	0		binding-protein-dependent transport systems inner membrane component	1,02	-1,05	-1,12	-1,07	-1,11	1,13	1,16
_3794	0		binding-protein-dependent transport systems inner membrane component	-1,07	-1,04	-1,05	1,06	1,02	1,05	1,12
_3795	0		oligopeptide/dipeptide ABC transporter, ATPase subunit	-1,09	-1,02	1,05	1,12	-1,14	-1,03	-1,08
_3796	0		oligopeptide/dipeptide ABC transporter, ATPase subunit	1,00	-1,01	-1,06	1,07	-1,06	-1,02	1,12
_3797	0		Asp/Glu racemase	-1,10	-1,03	-1,12	1,12	-1,04	1,06	-1,05
_3798	0		NADH:ubiquinone oxidoreductase complex I intermediate-associated protein 30	-1,14	-1,10	-1,01	1,03	-1,01	1,10	-1,07
_3799	0		HupE/UreJ protein	-1,05	-1,05	1,01	-1,04	-1,16	-1,09	-1,36
_3800	0		hypothetical protein	1,02	-1,01	-1,06	-1,12	-1,09	1,04	-1,14
_3801	0	1.11.1.21	catalase-peroxidase	-1,05	-1,01	-1,17	-1,32	-1,89	-1,99	-1,48
_3802	0		LysR family transcriptional regulator	-1,11	-1,04	-1,06	-1,06	1,03	1,10	1,21
_3803	0		hypothetical protein	-1,18	-1,16	-1,11	-1,06	1,05	1,31	-1,01
_3804	0		LuxR family transcriptional regulator	-1,08	-1,01	-1,09	1,05	1,04	1,19	1,17
_3805	0	1.6.99.5	NADH dehydrogenase (quinone)	1,07	1,19	1,42	1,41	1,98	1,50	1,76
_3806	0		putative monovalent cation/H+ antiporter subunit C	1,02	1,06	1,24	1,08	1,17	1,08	1,32
_3807	0	1.6.99.5	NADH dehydrogenase (quinone)	-1,02	1,03	1,06	1,14	1,21	1,18	1,29
_3808	0		putative monovalent cation/H+ antiporter subunit E	-1,00	1,04	1,09	1,20	1,09	1,15	1,28
_3809	0		multiple resistance and pH regulation protein F	-1,05	1,08	1,09	1,44	1,28	1,38	1,39
_3810	0		monovalent cation/proton antiporter, MnhG/PhaG subunit	1,01	1,04	1,14	1,35	1,26	1,26	1,40
_3811	0	3.7.1.2	fumarylacetoacetase	-1,03	1,00	1,04	-1,03	1,08	1,15	-1,03
_3812	0	1.13.11.5	homogentisate 1,2-dioxygenase	-1,05	-1,05	1,11	1,05	1,15	1,10	1,03
_3813	0		MarR family transcriptional regulator	-1,09	-1,05	-1,03	-1,03	-1,03	1,17	-1,33
_3814	0		beta-lactamase domain-containing protein	-1,08	-1,05	-1,04	-1,24	-1,24	-1,22	-1,42
_3815	0		FAD-dependent oxidoreductase	1,03	-1,02	-1,11	-1,16	-1,10	1,02	-1,12
_3816	0		hypothetical protein	-1,09	-1,04	-1,06	1,07	1,03	-1,00	-1,16
_3817	0	2.3.1.16	acetyl-CoA C-acyltransferase	1,03	-1,00	1,09	1,05	-1,05	-1,11	1,00
_3818	paaA		phenylacetate-CoA oxygenase subunit PaaA	-1,01	1,05	1,15	1,24	1,68	1,60	1,40
_3819	paaB		phenylacetate-CoA oxygenase subunit PaaB	1,01	1,02	1,11	1,25	1,67	1,70	1,52
_3820	0		phenylacetate-CoA oxygenase, PaaI subunit	-1,02	1,05	1,19	1,23	1,49	1,52	1,47
_3821	0		phenylacetate-CoA oxygenase, PaaJ subunit	1,03	-1,03	1,00	1,19	1,30	1,38	1,25
_3822	0		phenylacetate-CoA oxygenase/reductase, PaaK subunit	-1,03	-1,00	1,15	1,23	1,29	1,35	1,37
_3823	0		TetR family transcriptional regulator	1,03	1,01	-1,08	1,04	1,08	1,10	-1,04
_3824	0	6.2.1.30	phenylacetate-CoA ligase	-1,06	-1,04	-1,05	-1,30	-1,23	-1,12	-1,24
_3825	0		phenylacetic acid degradation protein PaaD	-1,03	-1,05	-1,06	-1,00	-1,01	1,15	-1,00
_3826	0		3-hydroxyacyl-CoA dehydrogenase NAD-binding	-1,10	-1,08	-1,17	-1,06	-1,28	-1,30	-1,13
_3827	0		bifunctional aldehyde dehydrogenase/enoyl-CoA hydratase	-1,00	1,02	-1,10	-1,13	-1,03	-1,03	1,06
_3828	0		PaaX family transcriptional regulator	1,06	1,03	1,01	1,07	-1,11	-1,20	1,05
_3830	0	1.1.1.94	glycerol-3-phosphate dehydrogenase [NAD(P)+]	1,02	-1,01	-1,14	-1,00	1,03	1,06	-1,04
_3831	0		sucrose-6F-phosphate phosphohydrolase	-1,03	-1,01	-1,04	-1,22	-1,41	-1,67	-1,21
_3832	0	2.4.1.213	Glucosylglycerol-phosphate synthase	-1,09	-1,03	-1,15	-1,08	-1,70	-1,74	-1,45
_3833	0		phospholipase D/transphosphatidylase	-1,10	-1,02	-1,03	1,07	1,14	1,21	1,27
_3834	0		signal transduction histidine kinase	1,03	-1,01	-1,09	1,21	1,09	1,09	1,32
_3835	0		RNA polymerase sigma factor	1,03	-1,03	-1,01	1,29	1,24	1,21	1,37
_3836	0		hypothetical protein	1,05	-1,02	1,03	1,05	1,31	1,30	1,43
_3837	0		two-component response regulator	1,00	1,00	-1,05	1,08	1,17	1,20	1,26
_3838	0		hypothetical protein	-1,05	-1,03	-1,08	-1,28	1,03	1,19	1,15
_3839	0		Ferritin Dps family protein	1,05	1,00	-1,09	-1,13	-1,14	-1,35	-1,16
_3840	0		thiamine pyrophosphate binding domain-containing protein	1,03	1,01	-1,06	-1,19	-2,18	-2,81	-1,65
_3841	0	1.4.1.4	glutamate dehydrogenase (NADP+)	1,12	1,08	-1,15	-1,50	-1,86	-2,67	-1,51
_3842	0		hypothetical protein	-1,05	-1,01	-1,23	-1,07	1,03	1,05	1,29
_3843	0		hypothetical protein	1,00	1,02	1,01	-1,05	1,33	1,38	1,17
_3844	0		cyclic nucleotide-binding protein	1,06	-1,05	-1,05	1,06	1,20	1,18	1,19
_3847	0		nuclease	1,06	-1,01	-1,05	-1,01	1,10	1,22	1,24
_3848	0		hypothetical protein	-1,04	1,02	1,03	1,01	1,02	1,11	1,20
_3849	0		hypothetical protein	1,00	-1,02	-1,01	-1,04	1,15	1,20	1,25
_3850	0		hypothetical protein	-1,01	-1,02	-1,02	1,11	1,06	1,11	1,15

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_3851	0		hypothetical protein	-1,09	-1,04	-1,03	-1,11	-1,05	1,32	1,16
_3852	0		hypothetical protein	-1,02	-1,04	-1,03	1,04	-1,03	-1,00	-1,02
_3854	0		hypothetical protein	-1,09	-1,05	1,01	1,12	1,20	1,32	1,03
_3855	0		cobyrinic acid ac-diamide synthase	1,03	1,01	-1,15	-1,55	-1,10	1,16	1,12
_3856	0		nuclease	1,02	1,03	-1,08	-1,04	-1,19	-1,06	1,04
_3857	0		polysaccharide biosynthesis protein CapD	1,11	1,07	1,05	1,01	1,27	1,07	1,26
_3858	0		protein of unknown function DUF940 membrane lipoprotein putative	-1,01	-1,03	1,01	1,22	1,44	-1,03	1,19
_3859	0		hypothetical protein	-1,05	-1,00	-1,04	1,03	1,09	-1,08	-1,01
_3860	0		hypothetical protein	-1,05	-1,07	-1,03	-1,22	-1,35	-1,29	-1,22
_3862	0		hypothetical protein	-1,01	1,01	1,06	1,01	1,01	-1,29	-1,14
_3863	0		hypothetical protein	-1,04	-1,03	1,01	1,05	-1,12	-1,13	-1,17
_3864	0		sulfotransferase	-1,08	-1,04	-1,03	-1,00	-1,14	-1,20	-1,18
_3865	0		hypothetical protein	1,02	1,00	1,02	-1,02	-1,14	-1,23	-1,04
_3866	0		glycosyl transferase group 1	-1,00	1,02	-1,09	-1,07	-1,06	-1,36	-1,08
_3867	0		hypothetical protein	1,04	1,04	-1,02	-1,03	1,08	-1,20	1,00
_3868	0		UDP-glucose 4-epimerase	1,04	1,05	-1,08	-1,06	-1,16	-1,46	-1,25
_3869	0		hypothetical protein	-1,09	-1,04	-1,02	-1,02	-1,08	-1,09	-1,14
_3870	0		peptidase S1 and S6 chymotrypsin/Hap	1,01	1,01	-1,05	1,08	-1,00	1,20	1,16
_3871	0		RTX toxins and related Ca2+-binding protein-like protein	1,06	-1,03	-1,01	1,18	1,43	1,35	2,02
_3872	0		hemolysin-type calcium-binding region	1,03	-1,01	-1,05	-1,03	1,08	1,22	1,16
_3873	0		hypothetical protein	1,03	-1,00	-1,10	-1,02	1,13	1,24	1,21
_3874	0		ATP-binding protein	-1,05	-1,02	-1,03	1,01	1,13	1,27	1,11
_3875	0		integrase catalytic region	-1,03	-1,02	-1,04	1,17	1,16	1,66	1,28
_3876	0		resolvase domain-containing protein	-1,02	-1,02	-1,04	1,06	1,15	1,18	1,22
_3877	0	4.1.99.17	phosphomethyl pyrimidine synthase	-1,03	-1,02	-1,14	-1,31	-2,38	-3,24	-3
_3878	0		transposase IS4 family protein	-1,09	-1,07	1,07	1,08	1,10	1,25	-1,07
_3879	0		hypothetical protein	-1,05	-1,08	-1,12	-1,07	-1,17	1,30	-1,19
_3880	0		hypothetical protein	-1,04	-1,02	-1,10	1,05	-1,04	1,14	1,07
_3881	0		hypothetical protein	1,04	-1,01	-1,16	1,05	1,07	1,08	1,09
_3882	0		transposase, putative	-1,05	-1,06	-1,19	-1,26	-1,41	-1,36	-1,74
_3883	0		hypothetical protein	-1,06	-1,07	-1,22	1,08	1,10	1,22	1,01
_3884	0		multi anti extrusion protein MatE	-1,00	1,05	-1,12	1,16	1,05	1,26	1,16
_3885	0		phospholipase D/transphosphatidylase	-1,02	1,01	1,02	1,15	1,18	1,10	1,12
_3886	0		hypothetical protein	1,00	-1,01	-1,09	1,11	1,05	1,18	1,28
_3887	0		cytochrome c class I	1,01	1,01	-1,03	-1,01	1,19	1,20	1,19
_3888	0	1.4.3.2	L-amino-acid oxidase	-1,07	-1,04	1,13	-1,03	-1,04	1,04	1,15
_3889	0		hypothetical protein	-1,06	-1,02	-1,03	1,07	1,00	1,09	1,05
_3890	0		hypothetical protein	-1,00	-1,01	-1,08	1,07	-1,06	1,26	1,08
_3891	0		cytochrome c oxidase subunit I type	-1,06	-1,00	1,08	-1,20	1,12	1,15	1,09
_3892	0		cytochrome c oxidase subunit II	-1,12	1,05	1,03	1,07	1,11	1,09	1,27
_3893	0		cytochrome c class I	-1,12	-1,03	-1,05	1,15	1,14	1,14	1,06
_3894	0		cytochrome c553-like protein	-1,01	1,01	-1,02	1,09	1,19	1,16	1,27
_3895	0	1.1.99.3	gluconate 2-dehydrogenase (acceptor)	-1,04	-1,02	-1,12	1,10	1,16	1,32	-1,03
_3896	0		hypothetical protein	-1,11	-1,02	-1,08	1,13	1,08	1,09	1,04
_3898	0		alpha amylase catalytic region	1,05	-1,03	-1,07	1,18	1,14	1,20	1,26
_3899	0		short-chain dehydrogenase/reductase SDR	-1,06	-1,01	1,03	1,04	1,10	1,04	1,17
_3900	0		short-chain dehydrogenase/reductase SDR	-1,07	-1,01	-1,01	-1,05	1,11	1,09	1,21
_3901	0		acriflavin resistance protein	-1,05	1,03	1,04	1,24	1,10	1,32	-1,02
_3902	0		RND family efflux transporter MFP subunit	-1,04	-1,00	-1,08	1,02	1,10	1,12	1,15
_3903	0		short-chain dehydrogenase/reductase SDR	-1,12	-1,04	-1,01	1,15	1,12	1,24	-1,02
_3904	0		SSS family solute/sodium (Na+) symporter	1,01	-1,06	-1,10	-1,05	1,20	1,21	1,34
_3905	0		MscS mechanosensitive ion channel	-1,06	-1,04	-1,03	1,09	1,20	1,17	1,01
_3906	0		SSS family solute/sodium (Na+) symporter	-1,10	-1,01	1,12	1,05	1,02	1,04	1,18
_3907	0		sodium/calcium exchanger membrane region	-1,06	-1,02	1,02	1,16	1,09	1,18	-1,05
_3908	0		hypothetical protein	1,00	1,02	1,06	1,10	1,10	-1,03	1,12
_3909	0		hypothetical protein	-1,05	-1,00	1,11	1,02	1,15	1,10	1,18
_3910	0		hypothetical protein	-1,07	-1,02	-1,01	1,09	1,18	1,13	1,14
_3911	0	1.3.1.74	2-alkenal reductase	-1,07	-1,01	1,01	1,12	1,08	1,10	1,02
_3912	0		Ferritin Dps family protein	-1,00	-1,02	-1,01	-1,05	1,09	1,05	1,13
_3913	0		TrkA domain-containing protein	-1,00	-1,05	-1,01	-1,02	1,19	1,16	1,16

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_3914	0		cation transporter	1,02	-1,07	-1,05	1,09	1,08	1,14	1,16
_3915	0		hypothetical protein	-1,12	1,03	1,01	1,21	1,03	1,08	-1,04
_3916	0		hypothetical protein	1,06	1,04	1,04	1,21	1,27	1,37	1,30
_3917	0		hypothetical protein	1,02	1,04	1,05	1,09	-1,02	1,06	1,09
_3918	0		hypothetical protein	1,03	-1,00	-1,04	1,15	1,44	1,35	1,50
_3919	0		transposase IS3/IS911 family protein	-1,01	-1,02	1,00	1,13	1,05	1,27	1,13
_3920	0		integrase, catalytic region	-1,01	-1,02	-1,03	1,06	1,05	1,11	1,11
_3921	0		integrase catalytic region	-1,06	-1,05	-1,09	-1,06	1,13	1,15	1,08
_3922	0		transport protein, putative	-1,13	-1,04	-1,02	1,02	-1,01	1,09	-1,02
_3923	0		hypothetical protein	-1,05	-1,03	-1,22	1,02	1,05	1,05	1,05
_3924	0		hypothetical protein	-1,12	1,01	-1,12	1,15	1,15	1,15	1,24
_3925	0		peptidase C26	1,04	1,00	-1,00	1,02	-1,04	1,24	1,13
_3926	0		hypothetical protein	-1,09	-1,04	-1,08	1,17	1,07	1,01	1,22
_3927	0		hypothetical protein	-1,09	-1,05	-1,03	1,15	1,07	1,22	-1,05
_3928	0		homocysteine S-methyltransferase	1,03	1,03	-1,24	-1,16	-1,48	-1,75	-1,17
_3929	0		hypothetical protein	1,03	1,01	1,43	2,34	2,63	2,02	1,78
_3930	0		GntR family transcriptional regulator	-1,06	-1,00	-1,07	-1,28	1,03	1,17	1,29
_3966	0		hypothetical protein	-1,05	-1,07	-1,15	-1,19	-1,35	-1,19	-1,11
_3967	0		ArsR family transcriptional regulator	-1,10	-1,05	1,03	1,08	1,02	-1,05	-1,01
_3968	0		cation efflux protein	-1,03	1,00	-1,22	-1,42	-1,24	-1,31	-1,13
_3969	0		hypothetical protein	1,02	-1,00	1,04	1,06	1,09	1,25	1,34
_3970	0		XRE family transcriptional regulator	1,00	-1,01	1,08	1,13	1,20	1,16	1,25
_3971	0		hypothetical protein	1,01	-1,01	-1,03	1,12	1,16	1,11	1,24
_3972	0		hypothetical protein	1,05	1,04	-1,07	-1,14	-1,20	-1,31	-1,09
_3973	0		lytic transglycosylase catalytic	1,02	1,00	1,01	-1,35	-1,19	-1,73	-1,22
_3974	0		conjugal transfer protein TrbC	-1,02	-1,05	-1,17	-1,38	-1,62	-1,77	-1,22
_3975	0		type IV secretory pathway VirB3 family protein	-1,03	-1,02	-1,17	-1,45	-1,73	-1,67	-1,27
_3976	0		CagE TrbE VirB component of type IV transporter system	-1,02	-1,05	-1,20	-1,39	-1,99	-1,69	-1,33
_3977	0		hypothetical protein	-1,03	-1,05	-1,11	-1,15	-1,98	-1,67	-1,37
_3978	0		lytic transglycosylase catalytic	-1,01	-1,02	-1,04	-1,08	-1,74	-1,49	-1,27
_3979	0		hypothetical protein	-1,01	1,02	-1,07	-1,03	-1,78	-1,50	-1,31
_3980	0		VirB8 family protein	-1,00	-1,03	1,02	-1,04	-2,01	-1,58	-1,29
_3981	0		conjugal transfer protein TrbG/VirB9/CagX	-1,02	-1,02	-1,05	-1,05	-1,93	-1,43	-1,32
_3982	0		conjugation TrbI family protein	-1,02	1,00	-1,03	-1,07	-1,58	-1,44	-1,19
_3983	0		type II secretion system protein E	-1,02	-1,02	1,03	1,24	-1,60	-1,37	-1,16
_3984	0		hypothetical protein	1,01	-1,04	1,04	1,20	-1,39	-1,21	-1,23
_3985	0		TrbL/VirB6 plasmid conjugal transfer protein	1,01	1,03	1,07	1,21	-1,28	-1,11	-1,07
_3986	0		hypothetical protein	-1,00	1,00	1,03	1,03	-1,01	1,34	-1,05
_3989	0		relaxase/mobilization nuclease family protein	-1,01	-1,05	-1,11	-1,14	-1,07	-1,02	1,02
_3990	0		hypothetical protein	-1,04	-1,04	-1,03	-1,26	-1,19	-1,08	-1,14
_3991	0		hypothetical protein	-1,06	-1,01	-1,10	1,05	1,13	1,26	1,21
_3993	0		hypothetical protein	-1,03	-1,05	-1,17	-1,14	1,19	1,15	1,51
_3994	0		hypothetical protein	-1,07	-1,01	-1,07	1,07	1,04	1,28	-1,06
_3995	0		hypothetical protein	-1,08	-1,03	-1,10	-1,04	-1,08	1,05	-1,24
_3996	0		hypothetical protein	1,03	-1,02	-1,08	-1,11	-1,03	1,04	-1,02
_3997	0		hypothetical protein	-1,00	-1,00	-1,05	1,06	1,02	-1,00	-1,06
_3998	0	2.7.7.7	DNA-directed DNA polymerase	1,03	-1,02	1,02	1,12	1,05	1,02	-1,03
_3999	0		ParB-like nuclease	-1,06	-1,01	-1,10	1,29	1,04	1,03	-1,06
_4000	0		hypothetical protein	-1,03	1,04	-1,01	-1,02	1,08	1,22	1,06
_4001	0		hypothetical protein	-1,02	1,01	1,09	1,11	1,18	1,25	1,12
_4002	0		hypothetical protein	1,02	1,00	1,03	1,06	1,09	1,10	1,27
_4003	0		hypothetical protein	1,04	-1,03	1,01	1,16	1,09	1,12	1,11
_4008	0		putative methylase/helicase	1,08	-1,01	-1,01	1,11	1,22	1,19	1,14
_4010	0		hypothetical protein	-1,06	1,00	1,11	-1,09	-1,16	-1,26	-1,02
_4011	0		hypothetical protein	-1,01	1,00	1,01	1,11	1,13	1,13	1,21
_4012	0		putative regulator PrlF	1,01	-1,00	-1,04	1,02	-1,05	-1,12	1,12
_4013	0		RC187	1,05	1,02	1,02	1,07	1,13	1,20	1,20
_4014	0		hypothetical protein	-1,08	1,04	1,02	1,30	1,22	1,31	1,08
_4015	0		parB-like partition protein	-1,04	1,04	-1,08	1,07	1,11	1,21	1,17
_4016	0		hypothetical protein	-1,06	-1,03	1,02	-1,05	1,02	1,10	-1,10
_4017	0		hypothetical protein	-1,07	-1,01	-1,05	1,05	1,13	1,28	1,27

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_4018	0		hypothetical protein	1,01	-1,01	-1,00	1,15	1,09	1,17	1,23
_4019	0		hypothetical protein	1,01	-1,02	1,07	1,17	1,07	1,04	1,14
_4020	0		filamentation induced by cAMP protein Fic	-1,03	-1,01	1,04	1,03	1,14	1,18	1,15
_4021	0		replication initiation protein RepC	-1,01	-1,02	-1,06	-1,02	-1,36	-1,14	-1,34
_4022	0		parB-like partition protein	-1,03	-1,02	-1,13	-1,8	-1,52	-1,38	-1,29
_4023	0		cobyrinic acid ac-diamide synthase	1,02	-1,01	-1,18	-1,64	-1,06	-1,01	-1,14
_4024	0		transcriptional regulator/antitoxin, MazE	-1,03	1,02	-1,09	-1,31	-1,27	1,01	-1,02
_4025	0		hypothetical protein	-1,02	-1,00	-1,12	-1,32	-1,43	-1,10	-1,01
_4026	0		resolvase domain-containing protein	-1,02	-1,02	-1,01	1,11	1,22	1,48	1,39
_4027	0		integrase family protein	-1,06	-1,01	-1,01	1,21	1,40	1,46	1,37
_4067	0		hypothetical protein	1,04	-1,04	-1,05	1,02	1,27	1,64	1,26
_4071	0		parallel beta-helix repeat-containing protein	1,07	1,01	-1,12	-1,13	-1,01	1,14	1,52
_4074	0		transposase IS3/IS911 family protein	1,11	-1,03	-1,05	1,02	1,09	1,35	1,30
_4075	0		hypothetical protein	-1,02	1,01	-1,06	-1,33	-1,23	-1,14	-1,06
_4076	0		capsule polysaccharide export protein	1,02	1,03	1,00	1,05	1,08	1,02	1,14
_4077	0		ABC transporter related	1,02	1,03	1,01	-1,08	1,00	-1,22	1,06
_4078	0		hypothetical protein	1,00	1,01	-1,01	1,14	1,01	1,02	-1,12
_4084	0		resolvase domain-containing protein	-1,03	-1,03	-1,00	-1,08	1,21	1,46	1,38
_4085	0		WGR domain-containing protein	-1,07	-1,06	-1,05	1,06	1,17	1,43	-1,02
_4087	0		plasmid stabilization system protein	-1,00	-1,03	-1,07	-1,40	-1,27	-1,02	1,02
_4088	0		hypothetical protein	1,04	-1,02	-1,14	-1,45	-1,16	1,03	1,04
_4089	0		integrase catalytic region	-1,01	-1,01	-1,04	-1,03	1,00	1,16	1,17
_4090	0		transposase IS3/IS911 family protein	-1,02	-1,02	-1,09	1,02	-1,05	1,20	1,10
_4091	0		hypothetical protein	1,01	-1,02	-1,01	1,19	1,11	1,23	1,19
_4092	0		transposase IS116/IS110/IS902 family protein	1,01	-1,02	-1,07	1,14	-1,01	-1,12	1,14
_4093	0		transposase IS4 family protein	-1,03	-1,00	-1,14	1,02	-1,09	-1,30	-1,10
_4102	0		replication initiation protein RepC	-1,00	1,01	-1,09	-1,26	-1,35	1,22	-1,16
_4104	0		cobyrinic acid ac-diamide synthase	1,02	1,04	-1,11	-1,19	1,22	1,20	1,03
_4105	0		resolvase domain-containing protein	-1,06	1,00	-1,11	-1,23	1,03	1,20	1,08
_4106	0		hypothetical protein	-1,02	-1,05	1,03	1,12	1,10	1,14	1,15
_4107	0		hypothetical protein	-1,06	-1,10	1,09	1,05	1,02	1,08	-1,05
_4108	0		hypothetical protein	-1,04	-1,04	-1,02	1,20	1,15	1,18	-1,02
_4109	0		hypothetical protein	-1,04	-1,04	-1,09	1,16	1,06	1,10	1,04
_4110	0		hypothetical protein	-1,07	-1,07	1,08	-1,07	1,00	-1,02	1,19
_4111	0		integrase family protein	-1,06	-1,04	-1,09	-1,10	-1,02	-1,13	1,06
_4112	0		prevent-host-death family protein	-1,07	-1,04	-1,03	1,09	1,13	1,14	1,01
_4113	0		death-on-curing family protein	-1,06	-1,03	-1,01	1,08	1,21	1,28	1,10
_4114	0	5.1.3.13	dTDP-4-dehydrorhamnose 3,5-epimerase	-1,05	-1,02	1,09	1,39	1,08	-1,24	-1,02
_4115	0		dTDP-glucose 4,6-dehydratase	1,01	1,00	1,10	1,10	1,10	-1,36	-1,13
_4116	0		hypothetical protein	1,01	-1,03	-1,12	-1,14	1,08	-1,07	1,03
_4117	0	1.1.1.133	dTDP-4-dehydrorhamnose reductase	-1,09	-1,01	1,03	1,02	-1,10	-1,17	-1,19
_4118	0		glucose-1-phosphate thymidylyltransferase	-1,04	-1,01	1,04	1,20	1,05	-1,03	-1,17
_4119	0		NAD-dependent epimerase/dehydratase	-1,03	-1,02	-1,02	1,06	1,03	1,09	1,08
_4120	0		sugar transferase	-1,07	-1,03	-1,03	1,04	1,07	1,10	1,07
_4121	0		glycosyl transferase family protein	1,10	1,12	1,01	1,11	-1,03	-1,65	1,16
_4122	0		hypothetical protein	-1,01	1,01	-1,13	-1,05	-1,09	-1,23	1,03
_4125	0		hypothetical protein	-1,05	-1,02	-1,08	-1,17	1,03	-1,03	1,01
_4128	0		hypothetical protein	-1,01	-1,07	1,08	1,09	1,04	1,10	1,03
_4129	0		polysaccharide biosynthesis protein	1,07	1,07	1,13	1,19	1,31	1,15	1,48
_4130	0		parallel beta-helix repeat-containing protein	1,08	1,01	-1,10	-1,47	-1,03	1,27	1,53
_4133	0		oligosaccharide biosynthesis protein Alg14-like protein	-1,01	-1,03	1,06	1,24	1,32	1,07	1,04
_4134	0		glycosyltransferase family 28 protein	1,00	-1,05	-1,05	1,13	1,14	1,21	-1,12
_4136	0		polysaccharide pyruvyl transferase	-1,02	-1,00	-1,06	-1,23	-1,05	-1,11	-1,03
_4137	0		hypothetical protein	1,08	1,02	1,05	1,17	-1,12	-1,06	1,06
_4138	0		hypothetical protein	1,04	-1,01	-1,08	1,01	-1,42	-1,34	-1,11
_4139	0	4.2.1.47	GDP-mannose 4,6-dehydratase	1,00	1,01	-1,01	-1,18	-1,27	-1,14	-1,05
_4141	0		hypothetical protein	1,03	-1,00	-1,08	-1,26	-1,06	-1,08	-1,01
_4142	0		NAD-dependent epimerase/dehydratase	1,04	1,05	-1,09	-1,35	-1,14	-1,34	-1,15
_4143	0		glycosyl transferase family protein	-1,03	-1,02	1,01	-1,08	-1,07	-1,30	-1,06
_4144	0		hexapaptide repeat-containing transferase	-1,07	-1,05	-1,03	1,09	1,11	1,17	1,24
_4145	0		glycosyl transferase family protein	-1,04	-1,00	-1,07	-1,02	-1,10	-1,11	1,25

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_4146	0	2.7.7.22	mannose-1-phosphate guanylyltransferase (GDP)	-1,04	-1,02	-1,08	1,11	1,05	-1,06	1,32
_4147	0		glycosyl transferase family protein	1,02	1,00	1,03	1,02	1,06	1,00	1,16
_4148	0		ABC-2 type transporter	-1,03	-1,03	1,01	-1,11	1,04	-1,10	-1,03
_4149	0		hexapaptide repeat-containing transferase	1,05	1,04	-1,07	1,06	-1,19	-1,48	-1,11
_4150	0		hypothetical protein	-1,00	1,01	-1,06	-1,18	-1,12	-1,30	-1,05
_4152	0		autoinducer synthesis protein	1,13	-1,05	-1,04	-1,00	1,23	1,8	1,30
_4154	0		beta-lactamase domain-containing protein	-1,04	-1,07	-1,02	-1,18	-1,29	-1,28	-1,23
_4155	0		hypothetical protein	-1,04	-1,04	-1,19	-1,38	-1,19	-1,04	-1,14
_4156	0		Fis family GAF modulated sigma54 specific transcriptional regulator	1,01	-1,01	1,10	1,07	1,08	1,10	1,23
_4157	0		monooxygenase protein, putative	-1,09	-1,09	-1,04	-1,06	-1,27	-1,13	-1,63
_4158	0		acetoin reductase	-1,03	-1,01	-1,01	-1,04	-1,11	1,09	1,04
_4159	0		alcohol dehydrogenase	-1,09	-1,02	-1,03	-1,19	-1,09	-1,06	1,20
_4160	0		protochlorophyllide oxidoreductase	1,01	-1,04	-1,02	-1,01	1,36	1,38	1,11
_4161	0		MltA-interacting MipA family protein	-1,02	-1,03	-1,02	-1,03	-1,15	-1,03	-1,04
_4162	0		glycosyl transferase group 1	-1,01	1,00	1,06	1,02	1,33	1,43	1,22
_4163	0		binding-protein-dependent transport systems inner membrane component	1,00	1,06	1,28	1,11	1,66	2,08	1,45
_4164	0		ABC transporter related	1,03	1,05	1,15	1,21	1,40	1,52	1,27
_4165	0		NMT1/THI5-like domain-containing protein	-1,00	1,08	1,36	1,58	1,76	1,86	1,47
_4166	0		hypothetical protein	-1,02	-1,03	-1,05	1,15	-1,01	1,10	1,27
_4167	0		sulfatase	1,11	-1,01	-1,11	1,00	1,01	1,22	1,29
_4168	0		CDP-alcohol phosphatidyltransferase	1,03	-1,04	-1,04	-1,00	-1,01	1,28	1,12
_4169	0		cytochrome B561	1,09	1,01	-1,04	1,05	1,06	1,07	1,21
_4170	0		glucosyltransferase MdoH	-1,06	1,01	-1,05	1,11	1,11	1,14	1,12
_4171	mdoD		glucan biosynthesis protein D	1,04	1,02	-1,11	1,07	-1,01	1,15	1,34
_4172	0		AraC family transcriptional regulator	-1,02	-1,06	1,01	1,06	1,14	1,08	1,01
_4173	0		hypothetical protein	-1,07	1,05	-1,19	1,15	1,05	1,20	1,09
_4174	0		hypothetical protein	-1,09	1,03	-1,07	-1,01	1,04	1,22	1,20
_4175	0		hypothetical protein	-1,05	1,02	1,02	1,13	1,17	1,15	1,18
_4176	0		oxidoreductase FAD/NAD(P)-binding subunit	-1,03	-1,02	-1,12	-1,06	1,08	1,15	-1,08
_4177	0		acetamidase/formamidase	-1,05	-1,01	1,05	-1,02	-1,09	-1,19	-1,09
_4178	0		hypothetical protein	-1,02	-1,00	-1,07	1,14	1,13	1,28	-1,01
_4179	0		hypothetical protein	1,03	-1,04	1,01	1,10	1,15	1,19	-1,03
_4180	0		hypothetical protein	1,01	1,02	1,02	1,06	-1,02	1,13	1,08
_4181	0		hypothetical protein	-1,01	-1,07	-1,09	1,13	1,33	1,37	1,34
_4182	0		MscS mechanosensitive ion channel	1,03	1,00	-1,04	1,13	1,11	-1,04	1,19
_4183	0		hypothetical protein	-1,01	-1,03	1,03	1,00	1,20	1,32	1,39
_4184	0		CsbD family protein	-1,00	-1,00	-1,11	1,12	1,09	1,09	-1,01
_4185	0		GntR domain-containing protein	-1,03	-1,06	-1,07	-1,01	1,04	1,21	1,10
_4186	0		ABC transporter related	-1,03	-1,01	1,05	1,07	-1,02	1,20	1,11
_4187	0		binding-protein-dependent transport systems inner membrane component	-1,06	-1,04	-1,01	1,00	-1,04	1,08	-1,00
_4188	0		binding-protein-dependent transport systems inner membrane component	-1,04	-1,06	1,08	1,01	-1,06	-1,04	-1,01
_4189	0		ABC-type nitrate/sulfonate/bicarbonate transport systems periplasmic components-like protein	-1,03	-1,08	-1,02	-1,09	-1,06	-1,06	-1,13
_4190	0		hypothetical protein	-1,03	-1,01	-1,02	1,03	-1,16	-1,20	1,07
_4191	0		TRAP dicarboxylate transporter, DctP subunit	-1,07	-1,08	-1,09	1,03	-1,41	-1,38	-1,43
_4192	0		tripartite ATP-independent periplasmic transporter DctQ	-1,06	-1,04	-1,04	1,09	-1,02	-1,03	-1,03
_4193	0		TRAP dicarboxylate transporter, DctM subunit	-1,12	-1,00	-1,03	-1,01	-1,16	-1,08	-1,05
_4194	0	2.3.2.2	Gamma-glutamyltransferase	-1,06	-1,03	1,02	1,13	-1,01	1,08	1,12
_4195	0		hypothetical protein	1,02	-1,03	-1,08	1,01	-1,20	-1,12	-1,01
_4196	0		hypothetical protein	-1,03	-1,05	-1,03	1,03	-1,17	-1,17	-1,08
_4197	0		hypothetical protein	-1,02	-1,01	-1,08	-1,10	-1,09	-1,03	1,07
_4198	0		LysR family transcriptional regulator	-1,00	-1,00	-1,09	-1,12	1,04	1,15	1,12
_4199	0		TetR family transcriptional regulator	-1,03	-1,00	1,03	1,06	1,24	1,29	-1,05
_4200	0	1.2.99.2	carbon-monoxide dehydrogenase (acceptor)	1,04	-1,01	-1,04	-1,18	-1,01	1,09	-1,16
_4201	0		2Fe-2S iron-sulfur cluster binding domain-containing protein	1,01	-1,02	-1,05	-1,11	-1,13	-1,07	-1,40
_4202	0	1.2.99.2	carbon-monoxide dehydrogenase (acceptor)	-1,03	1,01	1,01	-1,31	-1,18	-1,06	-1,32
_4203	0		TRAP dicarboxylate transporter- DctP subunit	-1,03	-1,03	-1,02	-1,04	-1,39	-1,34	-1,61

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
_4204	0		hypothetical protein	1,01	1,02	-1,03	-1,01	-1,07	-1,05	-1,13
_4205	0		TRAP dicarboxylate transporter, DctM subunit	-1,01	-1,02	-1,02	1,12	1,04	1,11	1,07
_4206	0		aminotransferase class IV	1,04	1,05	1,00	-1,19	-1,25	-1,41	-1,10
_4207	0		protein of unknown function DUF900 hydrolase family protein	1,03	-1,01	-1,03	1,09	1,18	1,18	1,16
_4208	0		hypothetical protein	1,02	1,00	-1,01	1,04	-1,09	1,02	-1,10
_4209	0		glycerophosphoryl diester phosphodiesterase	-1,16	-1,04	1,03	1,00	-1,15	-1,03	-1,41
_4210	0		PilT domain-containing protein	1,00	-1,02	1,04	-1,05	-1,04	1,16	1,02
_4211	0		hypothetical protein	-1,03	1,03	-1,02	1,00	1,01	1,03	1,11
_4212	0		nuclease	-1,04	-1,01	-1,07	-1,23	-1,20	-1,04	1,07
_4213	0		cobyrinic acid ac-diamide synthase	-1,07	-1,03	-1,12	-1,27	-1,17	-1,05	-1,08
_4214	0		initiator RepB protein	-1,06	-1,02	-1,06	-1,24	-1,26	-1,14	-1,23
_4215	0		hypothetical protein	1,04	-1,01	-1,09	-1,08	-1,31	-1,39	-1,09
_4216	0		hypothetical protein	-1,06	1,00	1,03	-1,35	-1,32	-1,10	-1,05
_4217	0		LacI family transcription regulator	1,04	-1,00	-1,06	1,03	1,13	1,20	1,22
_4218	0		hypothetical protein	-1,10	-1,07	-1,14	-1,34	-1,45	-1,57	-1,35
_4219	0		hypothetical protein	-1,08	-1,04	-1,13	-1,13	-1,37	-1,50	-1,36
_4220	0		hypothetical protein	-1,05	1,00	-1,10	1,12	-1,08	1,06	-1,22
_4221	0	1.1.1.60	2-hydroxy-3-oxopropionate reductase	-1,05	-1,04	1,02	1,10	-1,06	-1,03	-1,08
_4222	0		hypothetical protein	-1,03	-1,02	1,32	1,55	3,31	2,98	2,95
_4223	0		Ferritin Dps family protein	-1,00	1,01	-1,11	-1,03	1,02	1,13	1,78
_4224	0		hypothetical protein	-1,01	1,02	1,24	1,73	7,53	5,76	4,93
_4225	0		hypothetical protein	1,05	1,01	1,24	1,65	4,89	4,31	3,51
_4226	0		hypothetical protein	-1,07	-1,01	1,00	-1,05	1,02	1,11	1,09
_5002	xerC		hypothetical protein	1,00	-1,02	1,07	-1,20	-1,01	1,18	1,02
_5006	0		hypothetical protein	1,06	-1,01	-1,05	1,04	1,06	1,31	1,42
_5007	0		hypothetical protein	-1,10	-1,04	1,04	-1,05	1,01	1,25	-1,10
RDRS00003				-1,05	-1,03	1,12	1,03	1,17	1,28	1,16
RDRS00004				1,05	1,00	-1,04	1,13	-1,10	-1,00	1,14
RDRS00669				-1,03	1,01	-1,05	1,11	1,14	1,06	-1,08
RDRS01331				-1,03	-1,04	-1,00	1,01	-1,20	-1,13	-1,27
RDRS01563				-1,11	-1,04	-1,07	-1,08	-1,36	-1,29	-1,61
RDRS01590				1,02	1,05	1,01	-1,11	-1,31	-1,65	-1,16
RDRS01670				-1,52	-1,60	-1,84	-1,67	-2,3	-2,34	-1,70
RDRS01702				1,00	-1,02	1,09	1,03	-1,05	1,01	1,15
RDRS01750				-1,01	1,02	-1,07	1,15	1,08	1,10	1,10
RDRS01752				-1,06	-1,00	1,02	1,14	1,44	1,49	1,45
RDRS01817				1,02	1,09	1,30	1,43	1,71	1,62	1,45
RDRS01889				-1,07	-1,01	1,08	1,35	1,12	1,36	1,24
RDRS01913				-1,02	-1,02	-1,07	-1,08	-1,09	-1,03	-1,28
RDRS01914				1,00	-1,03	-1,04	-1,30	-1,30	-1,27	-1,23
RDRS01916				-1,06	-1,07	1,06	1,16	-1,04	-1,00	-1,08
RDRS01917				-1,04	-1,02	-1,05	1,14	1,08	1,12	-1,21
RDRS01955				-1,00	-1,03	1,08	1,12	1,08	1,27	1,05
RDRS01965				-1,05	-1,01	1,24	1,10	-1,04	-1,13	1,22
RDRS01967				-1,03	1,04	-1,03	-1,01	-1,48	-1,31	-1,14
RDRS01980				-1,04	-1,04	-1,02	1,15	1,05	1,03	-1,00
RDRS02015				-1,02	-1,05	1,01	1,06	1,20	1,44	1,09
RDRS02037				-1,10	-1,02	-1,02	1,12	1,06	1,15	1,19
RDRS02108				1,00	-1,01	1,09	1,20	1,05	-1,02	-1,00
RDRS02494				-1,07	-1,01	1,00	1,13	1,15	1,19	1,24
RDRS02565				1,00	1,33	1,20	1,03	1,00	-1,19	-1,08
RDRS02974				1,05	1,01	-1,03	-1,13	1,01	-1,02	1,06
RDRS03068				-1,04	-1,06	1,04	1,11	-1,07	-1,06	-1,13
RDRS03175				1,21	1,03	1,52	5,15	13	9	9,07
RDRS03415				-1,04	-1,00	-1,02	1,03	1,06	1,06	-1,11
RDRS03592				-1,01	-1,02	-1,02	1,06	1,06	1,20	1,44
RDRS03603				1,05	1,05	1,04	1,11	1,10	1,06	1,00
RDRS03656				-1,03	-1,03	-1,01	-1,10	1,03	-1,03	-1,26
RDRS03660				1,00	-1,03	1,04	1,13	1,35	1,48	1,9
RDRS03668				1,01	-1,04	1,03	1,24	1,08	1,14	1,17
RDRS03687				1,08	-1,01	-1,14	1,06	1,13	1,28	1,24

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120
RDRS03696				1,00	1,01	1,04	1,20	1,13	1,21	1,15
RDRS03697				1,01	-1,01	-1,06	-1,00	1,08	1,13	1,05
RDRS03757				-1,03	-1,01	-1,00	-1,11	-1,18	-1,20	-1,26
RDRS03821				1,09	-1,02	-1,18	-1,06	1,05	1,08	1,19
RDRS03843				-1,07	-1,03	-1,08	-1,39	-1,06	1,03	1,05
RDRS03851				1,03	1,02	-1,01	1,02	1,07	-1,03	1,05
RDRS03887				-1,07	-1,05	1,04	1,11	1,11	1,12	1,20
RDRS03977				-1,02	-1,07	-1,02	-1,06	1,02	1,27	-1,04
RDRS03978				1,01	-1,02	-1,02	-1,02	-1,10	-1,03	-1,01
RDRS03998				-1,01	-1,02	-1,12	-1,26	-1,11	1,10	1,05
RDRS04039				-1,03	-1,02	-1,09	-1,04	-1,17	-1,05	-1,17
RDRS04058				-1,04	-1,01	-1,07	1,03	1,14	1,14	-1,01
RDRS04059				-1,00	-1,03	-1,04	1,06	-1,07	1,24	-1,05
RDRS04072				-1,03	-1,03	-1,03	-1,27	-1,25	1,01	1,04
RDRS04080				1,00	1,02	-1,10	1,04	1,03	-1,14	1,22
RDRS04081				-1,05	-1,05	1,00	-1,11	-1,04	1,04	-1,15
RDRS04082				1,01	-1,00	1,05	-1,13	1,02	1,27	-1,01
RDRS04086				-1,05	-1,04	1,00	1,21	1,05	1,14	1,13
RDRS04088				1,03	-1,04	-1,19	-1,39	-1,08	1,02	-1,03
RDRS04109				1,02	-1,00	-1,05	-1,09	1,05	1,11	1,06
RDRS04110				-1,01	-1,02	1,00	1,03	1,05	1,10	1,19
RDRS04116				1,01	-1,03	1,08	-1,09	1,01	-1,03	1,06
RDRS04121				1,04	1,02	-1,14	-1,32	-1,05	1,04	1,12
RDRS04132				1,09	1,03	-1,04	-1,03	1,08	1,10	1,30

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120

Table A2: Metabolites in *D. shibae* DFL12T grown under oxygen depletion. The bacterium was grown continuously in a chemostat under aerobic conditions up to the steady state within the exponential growth phase. After oxygen shutdown, the metabolome was analyzed via GC-MS. Data were compared to the situation before oxygen shutdown. A fold change cut off of <0.67 respectively >1.5 and a P-value < 0.05 were applied.

Metabolites	Fold change								
	15 min	30 min		60 min		120 min		240 min	
Amino acids and derivatives									
Alanine	0,77	2,54	*	12,58	**	3,50	**	2,89	**
Arginine"		1,00		0,41		n.d.		n.d.	
Asparagine	0,30	0,35		0,10		0,57		0,41	
Aspartate	0,89	0,62		1,21		0,73		0,71	
beta-Alanine	0,55	1,06		1,00		0,60		0,32	*
Glutamate	0,76	1,03		0,59		0,41	*	0,52	
Glutamine	0,61	1,85		0,71		0,80		1,06	
Glycine	1,17	1,67		1,78		1,47		1,20	
Homoserine"				1,00	**	1,68	*	0,68	**
Isoleucine	1,43	8,34	**	7,26		8,31	**	4,68	**
Leucine	1,08	11,15	**	25,11	*	14,41	**	5,83	**
Lysine	1,07	1,67	*	2,58		1,99	*	1,40	
Methionine	1,89	1,05		1,11		1,41		0,90	
N-acetyl-glutamate	0,97	1,99	*	1,76		2,12	*	2,47	
Ornithine	0,86	0,41		0,57		0,78		0,82	
Phenylalanine	0,84	1,85		1,40		1,39		0,98	
Proline	1,73	2,02		1,58		1,83		4,51	
Pyroglutamate	1,20	0,90		0,89		0,76		0,83	
Sarcosine	0,95	2,18	*	9,81	*	3,39	**	2,07	
Serine	1,75	2,07		5,03		4,08	**	3,66	**
Threonine	1,71	3,78	*	5,03	*	3,66	**	3,41	**
Tyrosine	1,07	0,80		1,07		2,08		1,47	
Valine	1,51	24,27	**	32,69	**	14,88	**	6,92	**
Amino acid metabolism									
3-Aminoisobutanoate	1,72	1,18		0,74		0,49		0,48	
2-Isopropylmalate	0,66	62,45		27,71	**	12,21	**	4,64	
2-Methylmalate	1,91	13,31	**	25,83	*	18,45	**	3,92	**
Polyamines									
Putrescine	0,63	1,54		0,61		1,24		1,15	
Purines, pyrimidines and derivatives									
Adenine	n.d.	2,99		1,25		n.d.		0,03	
Adenosine	0,04	0,10		0,02		n.d.		n.d.	

Metabolites	Fold change									
	15 min		30 min		60 min		120 min		240 min	
Cytosine	0,62		1,42		1,75		1,13		2,69	
Thymine	1,39		0,92		1,00		0,86		0,90	
Uracil	3,09		1,90		1,80		2,18		1,74	
Uridine	0,10		0,14		0,06		0,08		0,05	
Butanoates										
2-Hydroxybutanoate	1,21		0,85		0,66		0,50		0,53	
3-Hydroxybutanoate	0,56		0,87		1,42		2,24	*	2,08	
Fatty acids										
Decanoate	2,17		0,74		0,74		0,86		0,83	
Dodecanoate	0,65		0,96		0,53		0,42		0,78	
3-Hydroxy-decanoate	0,79		1,81		0,84		0,97		1,12	
Hexadecanoate	2,21		1,71		3,37		2,55		1,44	
Octadecanoate	2,79		1,81		4,40		3,30		1,30	
9-Octadecenoate	0,91		0,54		1,34		0,51		1,43	
Tetradecanoate	1,34		1,08		1,50		1,39		1,23	
Lipids										
Ethanolamine	0,78		1,63		0,97		0,98		0,79	
Glycerol-3-phosphate	0,85		0,86		0,93		0,61		1,00	
TCA Cycle										
Aconitate"	1,00		3,34	**	4,78	**	4,86	**	3,20	**
Citrate	0,76		5,61	**	10,88	**	11,30	**	3,80	
Fumarate	1,98		3,84		9,87	*	7,39	**	3,11	*
Malate	1,20		3,71	*	17,99	**	12,58	**	5,08	*
2-Oxoglutarate	0,85		2,26	*	1,10		1,04		1,09	
Succinate	1,20		3,21	**	14,24	**	8,09		3,91	*
Pentose-Phosphate-Pathway										
Ribose	0,43		0,60		0,33		0,50		0,65	
Xylulose-5-phosphate	0,85	0,92	0,62		0,55	0,87	0,58		0,45	*
Gluconeogenesis and Entner-Doudoroff pathway										
Phosphoenolpyruvate	0,75		4,19		4,05		1,74		1,26	
Dihydroxyacetone phosphate	1,03		1,05		0,51		0,96		1,07	
Fructose-6-phosphate	0,59		1,88		3,02		4,36	*	1,85	
Glucose	0,93		0,58	**	0,20	**	0,31	**	0,32	**
Glucose-6-phosphate	1,09		2,72	**	3,23	*	4,79	**	2,05	

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120

Metabolites	Fold change									
	15 min		30 min		60 min		120 min		240 min	
KDG	1,15		2,08		2,63		1,32		1,87	
6-Phosphogluconate	0,97		0,98		n.d.	**	2,52		1,00	
2-Phosphoglycerate	1,00		1,83		2,83		2,02		1,03	
3-Phosphoglycerate	1,00		2,99		4,18	*	2,83		1,37	
Pyruvate	2,97		0,69		3,11		4,40	*	4,21	
Sugars										
N-acetyl-glucosamine	1,07		0,97		1,18		1,34		0,92	
Gulose	1,12		0,87		0,86	0,73	0,73		0,58	**
Mannose	0,98		0,88		2,64		0,65		0,63	
Sucrose	0,37		0,40		0,21		0,31		0,23	
Others										
Adipate	0,14		0,88		0,10		0,24		0,61	
4-Aminobenzoate	0,72		1,11		0,75		0,75		0,53	
Benzoate	1,35		0,97		1,04		1,12		1,01	
Fructose-1-phosphate"			1,00		1,95		n.d.		2,40	
Galacturonate	0,53		0,72		0,48		0,46		0,20	**
Glucoheptonic acid-1,4-lactone	1,32		1,29		0,61		1,15		1,30	
Glutarate	0,97		1,1		3,79		2,24		1,10	
Glycerate	1,00	0,65	0,47	**	0,59	**	1,20	**	0,40	
Glycolate	0,66		0,84		1,27		1,00		1,00	
3-Hydroxypyridine	1,01		0,38		0,49		0,74		1,93	
3-Ketoadipate"			1,00		1,90		2,91	**	1,39	
Lactate	2,01		1,13		2,26		1,36		1,25	
Malic acid-1-methylester	1,19		1,36		2,67		2,60	*	1,67	
2-Methylserine	1,74		1,97		2,74		2,03		2,09	
Nicotinamide	0,92		1,37		1,22		1,02		0,95	
Nicotinate	1,71		1,96		1,34		0,54		0,39	
Octadecanol	0,16		0,57		0,55		1,03		0,26	
Phosphoric acid monomethyl ester	0,53		n.d.		0,73		0,49		0,57	
Succinic-acid-methylester	1,22		0,89		0,88	1,00	1,00		0,96	
Tetradecanol	1,07		0,81		0,60		0,97		1,04	
Toluate	1,27		1,23		1,10		1,27		1,31	
Trehalose	0,50		0,06		0,24		0,04		0,61	

* significant: alpha = 0.05

** significant: alpha = 0.01

Table A3: NCBI access data and data referred to Körner *et al,* 2003. NCBI sequence identification number (GI number), reference number and version, locus tag/ encoded protein, related proteins (Crp/Fnr group), and the name of the host bacterium (organism).*removed record, **removed record cause new assembly of genome, upd: updated record, new: new record found in NCBI database.

GI Number	Reference / Version	Locus Tag/ Encoded Protein	Related Protein	Organism
17989292 new: 499315278	NP_541925.1 new: WP_011005770.1	II947 new: FtrB	Dnr	*Brucella melitensis 16M*
23500056 new: 489056143	NP_699496.1 new: WP_002966284.1	301 new: FtrB	Dnr	*Brucella suis 1330*
14348602	AAK61312.1; AF295359_3	NarR	Dnr	*Paracoccus pantotrophus*
16125659	NP_420223.1	1410 FtrB	Dnr	*Caulobacter crescentus CB15*
23015085*	ZP_00054873.1*	7682	Dnr	*Magnetospirillum magnetotacticum MS-*
23016271*	ZP_00056029.1*	8858	Dnr	*Magnetospirillum magnetotacticum MS-1*
23014003*	ZP_00053845.1*	6629	Dnr	*Magnetospirillum magnetotacticum MS-1*
22966075*	ZP_00013672.1*	670	Dnr	*Rhodospirillum rubrum ATCC11170*
157913491	ABV94924.1	DnrE	Dnr	*Dinoroseobacter shibae DFL 12 = DSM 16493*
6118088	AAF04013.1; AF172325_1	HbaR	Dnr	*Rhodopseudomonas palustrisCGA009*
159045729 new: 501131003	YP_001534523.1 new: WP_012179849.1	DnrD	Dnr	*Dinoroseobacter shibae DFL 12 = DSM 16493*
8119332	AAA69977.2	Nnr	Dnr	*Paracoccus denitrificans DSM413*
16263110 upd	NP_435903.1 upd	1207	Dnr	*Sinorhizobium meliloti 1021*
17936276*	NP_533066.1*	2394	Dnr	*Agrobacterium tumefaciens C58*
21492680 new: 499365890	NP_659754.1 new:WP_011053469.1	Fnr	Dnr	*Rhizobium etli CFN42*
4585795	CAB40903.1	DnrD	Dnr	*Pseudomonas stutzeri ZoBell ATCC14405*
15595724	NP_249218.1	Dnr	Dnr	*Pseudomonas aeruginosa PAO1*
4585799	CAB40906.1	DnrE	Dnr	*Pseudomonas stutzeri ZoBell ATCC14405*
4585802	CAB40908.1	DnrS	Dnr	*Pseudomonas stutzeri ZoBell ATCC14405*
23000226*	ZP_00044165.1*	1891	Dnr	*Magnetococcus sp. MC1*
22998591*	ZP_00042641.1*	332	Dnr	*Magnetococcus sp. MC1*
17549187 new: 499313483	NP_522527.1 new: WP_011004258.1	966	Dnr	*Ralstonia solanacearum GMI1000*
1657803	AAC80174.1	Fnr	Dnr	*Acidithiobacillus ferrooxidans ATCC33020* *new: Acidithiobacillus ferridurans*
23014002*	ZP_00053844.1*	6628	Dnr	*Magnetospirillum magnetotacticum MS-1*
23016270 upd	ZP_00056028.1 upd	8857	Dnr	*Magnetospirillum magnetotacticum MS-1*
16332256 new: 499176690	NP_442984.1 new: WP_010874277.1	Dnr	Dnr	*Synechocystis sp. PCC6803*
23055410*	ZP_00081515.1*	2268	Dnr	*Geobacter metallireducens*
23474021 upd	ZP_00129316.1 upd	929	Dnr	*Desulfovibrio desulfuricans G20*
27380665	NP_772194.1	5554	Dnr	*Bradyrhizobium diazoefficiens USDA 110*
23011566*	ZP_00051889.1*	3006180	Dnr	*Magnetospirillum magnetotacticum MS-1*
157913570	ABV95003.1	DnrF	Dnr	*Dinoroseobacter shibae DFL 12 = DSM 16493*
120356	P29284.1; FLP_LACCA	Flp	Flp	*Lactobacillus casei RNL7*
15673985	NP_268160.1	RcfA	Flp	*Lactococcus lactis ssp. Lactis IL1403*
5804934	CAB53580.1	FlpA	Flp	*Lactococcus lactis ssp. cremoris MG1363*
5804936	CAB53581.1	FlpB	Flp	*Lactococcus lactis ssp. cremoris MG1363*
157910762	ABV92195.1	447	A	*Dinoroseobacter shibae DFL 12 = DSM 16493*
16264406	NP_437198.1	658	A	*Sinorhizobium meliloti 1021*
46193416*	ZP_00004770.2*	656	A	*Rhodobacter sphaeroides 2.4.1*
22958642 upd	ZP_00006309.1 upd	2225	A	*Rhodobacter sphaeroides 2.4.1*
17544909 new: 499309382	NP_518311.1 new: WP_011000157.1	190	Fnr	*Ralstonia solanacearum GMI1000*
22976192*	ZP_00022091.1*	1010	Fnr	*Ralstonia metallidurans CH34*
26990005	NP_745430.1	3287	Fnr	*Pseudomonas putida KT2440*
16129295	NP_415850.1	Fnr	Fnr	*Escherichia coli K12-MG1655*
15596741	NP_250235.1	Anr	Fnr	*Pseudomonas aeruginosa PAO1*
398391	CAA81129.1	FnrA	Fnr	*Pseudomonas stutzeri ZoBell ATCC14405*
27382807	NP_774336.1	7696	FixK	*Bradyrhizobium japonicum USDA110* *new: Bradyrhizobium diazoefficiens USDA 110*
16263120	NP_435913.1	FixK1	FixK	*Sinorhizobium meliloti 1021*

Systematic Name Dshi	Gene Name	EC number	Description	FC5	FC10	FC15	FC20	FC30	FC60	FC120

GI Number	Reference / Version	Locus Tag/ Encoded Protein	Related Protein	Organism
16262861	NP_435654.1	FixK2	FixK	*Sinorhizobium meliloti 1021*
16125005	NP_419569.1	752 new: FixK	FixK	*Caulobacter crescentus CB15*
159043213 new: 501128351	YP_001532007.1 new: WP_012177338.1	660	FnrL	*Dinoroseobacter shibae DFL 12 = DSM 16493*
22960505**	ZP_00008145.1**	FnrL	FnrL	*Rhodobacter sphaeroides 2.4.1*
2623055	AAC46003.1	FnrL	FnrL	*Rhodobacter capsulatus 2.3.1*
15888914	NP_354595.1	FnrN	FnrL	*Agrobacterium tumefaciens C58 new: Agrobacterium fabrum str. C58*
619722	AAA86478.1	FnrN	FnrL	*Rhizobium leguminosarum bv. viciae*
15838141 new: 499196499	NP_298829.1 new: WP_010894039.1	1540	Crp	*Xylella fastidiosa 9a5c*
14581468	AAK38740.1	Crp	Crp	*Aeromonas hydrophila JMP636*
16131236	NP_417816.1	Crp	Crp	*Escherichia coli K12-MG1655*
1161156	AAA85361.1	Crp	Crp	*Mannheimia haemolytica NADC-D60*
15610812	NP_218193.1	3676	CooA	*Mycobactterium tuberculosis H37Rv*
15802719 new: 485669357	NP_288746.1 new: WP_001310375.1	YeiL	YeiL	*Escherichia coli O157-H7-EDL933*
24378661	NP_720616.1	144C	YeiL	*Streptococcus mutans UA159*
53685723**	ZP_00099356.2**	2496	CooA	*Desulfitobacterium hafniense DCB-2*
46202386*	ZP_00053291.2*	3007845	G	*Magnetospirillum magnetotacticum MS-1*
15595472	NP_248966.1	275	G	*Pseudomonas aeruginosa PAO1*
27381072	NP_772601.1	5961	G	*Bradyrhizobium japonicum USDA110 new: Bradyrhizobium diazoefficiens USDA 110*
17227791 new: 499303697	NP_484339.1 new: WP_010994472.1	295	F	*Nostoc sp.PCC7120*
23132570*	ZP_00114355.1*	1875	F	*Prochlorococcus marinus MIT9313*
17231946 new: 499307812*	NP_488494.1 new: WP_010998587.1*	4454	Dnr Nostoc	*Nostoc sp. PCC7120*
23114423**	ZP_00099726.1**	2873	CrpK	*Desulfitobacterium hafniense DCB-2*
20516621	AAM24817.1	Crp	CrpK	*Thermoanaerobacter tengcongensis MB4T new: Caldanaerobacter subterraneus subsp. tengcongensis MB4*
22001021	AAM82249.1	NtcA	NtcA	*Prochlorococcus marinus ssp. pastoris CCMP1378*
23015226*	ZP_00055008.1*	7817	B	*Magnetospirillum magnetotacticum MS-1*
157912828	ABV94261.1	2528	B	*Dinoroseobacter shibae DFL 12 = DSM 16493*
22958740 upd**	ZP_00006405.1 upd**	2322	B	*Rhodobacter sphaeroides 2.4.1*
157912821	ABV94254.1	*2521*	B	*Dinoroseobacter shibae DFL 12 = DSM 16493*
1458102	AAC44402.1	NnrR	NnrR	*Rhodobacter sphaeroides 37713*
22958688 upd**	ZP_00006354.1 upd**	2270	NnrR	*Rhodobacter sphaeroides 2.4.1*
3925389	AAC79437.1	NnrR	NnrR	*Pseudomonas sp. G179*
22961327**	ZP_00008933.1**	602	NnrR	*Rhodopseudomonas palustris CGA009*
27382195	NP_773724.1	NnrR	NnrR	*Bradyrhizobium japonicum USDA110 new: Bradyrhizobium diazoefficiens USDA 110*
23113234**	ZP_00098629.1**	1744	MalR	*Desulfitobacterium hafniense DCB-2*
17432538	AAL39073.1	MalR	MalR	*Bacteroides thetaiotaomicron 5482*
16802160	NP_463645.1	112	D	*Listeria monocytogenes EGDe*
15894789	NP_348138.1	1511	E	*Clostridium acetobutylicum ATCC824*
11465488	NP_045121.1	NtcA	NtcA	*Cyanidium caldarium RK1*
16080784	NP_391612.1	37310	*Fnr B.s.*	*Bacillus subtilis subsp. subtilis str. 168*
16802795	NP_464280.1	753	dd	*Listeria monocytogenes EGDe*
149680	AAA25291.1	PrfA	PrfA	*Listeria monocytogenes EGDe*
27467022	NP_763659.1	104	D	*Staphylococcus epidermidi ATCC12228s*
8894540	CAB95946.1	ArcR	ArcR	*Bacillus licheniformis ATCC14580*
14349119	CAC41344.1	ArcE	ArcR	*Enterococcus faecalis ATCC29212*